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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:43:32 ; Search time 74.6015 seconds  
(without alignments)  
627.306 Million cell updates/sec

Title: US-10-660-357A-1

Perfect score: 649

Sequence: 1 QVQLQSGPGLVKPSTLSL.....WLLPDAFDIGQGTWVTWSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	649	100.0	121	7	ADC99772 Anti-huma
2	649	100.0	121	7	ADC99788 Anti-huma
3	649	100.0	121	7	ADD05376 Anti-MUC1
4	649	100.0	121	7	ADD05392 Anti-MUC1
5	649	100.0	121	7	ADF09814 Human ant
6	649	100.0	121	7	ADF09830 Human ant
7	643	99.1	121	7	ADC99780 Anti-huma
8	643	99.1	121	7	ADD05384 Anti-MUC1
9	643	99.1	121	7	ADF09822 Human ant
10	597	92.0	121	7	ADC99808 Anti-huma
11	597	92.0	121	7	ADD05412 Anti-MUC1
12	597	92.0	121	7	ADF09850 Human ant
13	565.5	87.1	243	8	ADO58076 S9 cell d
14	547	84.3	121	5	ABG92884 Human imm
15	545.5	84.1	121	5	ABB07171 ebvHlgM M
16	545.5	84.1	121	8	ADI26658 Human ant
17	545.5	84.1	122	7	ADP03887 Murine-ex
18	545.5	84.1	122	7	ADP03884 Murine-ex
19	544.5	83.9	122	7	ADP03885 Murine-ex
20	544.5	83.9	122	7	ADP03889 Murine-ex
21	540	83.2	119	2	AAW27554 Human Ab
22	540	83.2	119	6	ABJ18676 Human ant
23	540	83.1	118	8	ADP22272 Antibody
24	540	83.1	123	6	ADA89258 Human ant
25	83.0	83.0	122	7	ADP03931 Murine-ex

ALIGNMENTS

RESULT 1

ADC99772

ID ADC99772 standard; protein; 121 AA.

XX ADC99772;

XX 01-JAN-2004 (first entry)

XX Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 1.

KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.

XX Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudus J;

XX WPI; 2003-587113/55.

XX N-PSDB; ADC99774.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
or condition associated with expression of MUC18 in a patient, e.g.  
tumors, cancers, and other malignancies.

XX Claim 1; SEQ ID NO 1; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising  
a heavy or light chain amino acid or a heavy or light chain variable  
domain where the antibody binds to MUC18. The monoclonal antibody of the  
invention demonstrates cytostatic activity and may be useful for treating  
a disease or condition associated with the expression of MUC18 on the  
cell surface such as tumours, specifically melanoma, oesophageal,  
pancreatic or colorectal tumours, carcinomas, particularly cervical  
carcinomas and cervical intraepithelial neoplasia and cancers including  
colorectal, breast or lung cancer, as well as other malignancies. The  
current sequence is that of the anti-human MUC18 monoclonal antibody

CC heavy chain protein of the invention.  
XX  
SQ Sequence 121 AA;

Query Match 100.0%; Score 649; DB 7; Length 121;

Best Local Similarity 100.0%; Pred. No. 6.4e-46;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLWIGYIYYTWTSNYN 60  
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLWIGYIYYTWTSNYN 60  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
DB 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

QY 121 S 121

DB 121 S 121

RESULT 2  
ADC99788  
ID ADC99788 standard; protein; 121 AA.

XX  
AC ADC99788;

XX  
DT 01-JAN-2004 (first entry)

XX  
DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 17.

XX  
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.

XX  
OS Homo sapiens.

XX  
PN WO2003057838-A2.

XX  
PD 17-JUL-2003.

XX  
PF 26-DEC-2002; 2002WO-US041581.

XX  
PR 28-DEC-2001; 2001US-0346299P.

XX  
PA (ABGE-) ABGENIX INC.

XX  
PI Gudas J;

XX  
WPI; 2003-587113/55.

DR N-PSDB; ADC99790.

XX  
PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
PT or condition associated with expression of MUC18 in a patient, e.g.  
PT tumors, cancers, and other malignancies.

XX  
FS Claim 1; SEQ ID NO 17; 78pp; English.

XX  
CC The invention relates to a novel isolated monoclonal antibody comprising  
CC a heavy or light chain amino acid or a heavy or light chain variable  
CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
CC invention demonstrates cytostatic activity and may be useful for treating  
CC a disease or condition associated with the expression of MUC18 on the  
CC cell surface such as tumours, specifically melanoma, oesophageal,  
CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
CC carcinomas and cervical intraepithelial neoplasia and cancers including  
CC colorectal, breast or lung cancer, as well as other malignancies. The  
CC current sequence is that of the anti-human MUC18 monoclonal antibody  
CC heavy chain protein of the invention.

XX  
SQ Sequence 121 AA;

Query Match 100.0%; Score 649; DB 7; Length 121;  
Best Local Similarity 100.0%; Pred. No. 6.4e-46;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLWIGYIYYTWTSNYN 60  
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLWIGYIYYTWTSNYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
DB 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

QY 121 S 121

DB 121 S 121

RESULT 3  
ADD05376  
ID ADD05376 standard; protein; 121 AA.

XX  
AC ADD05376;

XX  
DT 01-JAN-2004 (first entry)

XX  
DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 1.

XX  
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.

XX  
OS Homo sapiens.

XX  
PN WO2003057006-A2.

XX  
PD 17-JUL-2003.

XX  
PF 26-DEC-2002; 2002WO-US041582.

XX  
PR 28-DEC-2001; 2001US-0346460P.

XX  
PA (ABGE-) ABGENIX INC.

XX  
PI Gudas J, Bar-Eli M;

XX  
WPI; 2003-577496/54.

DR N-PSDB; ADD05378.

XX  
PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
PT associated with melanoma, or increasing survival of an animal having a  
PT metastatic tumor.

XX  
FS Claim 1; SEQ ID NO 1; 87pp; English.

XX  
CC The invention relates to a novel monoclonal antibody used for inhibiting  
CC tumour growth in an animal. The tumour inhibition process comprises  
CC selecting an animal in need of treatment for a tumour, providing a  
CC monoclonal antibody comprising a heavy chain amino acid, where the  
CC antibody consists of any one of 10 fully defined sequences of 117-123  
CC amino acids given in the specification, and where the monoclonal antibody  
CC binds MUC18, and contacting the tumour with the antibody resulting in  
CC inhibited proliferation of the cells. The monoclonal antibody has  
CC cytostatic and can be used in the production of a vaccine. The monoclonal  
CC antibodies against the MUC18 antigen are useful for diagnosing and  
CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or  
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
CC increasing survival of an animal having a metastatic tumour. This  
CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
CC protein of the invention.

XX  
SQ Sequence 121 AA;

Query Match 100.0%; Score 649; DB 7; Length 121;



[illegible]

RESULT 4	
ADD05392	
ID	ADD05392 standard; protein; 121 AA.
XX	
AC	ADD05392;
XX	
DT	01-JAN-2004 (first entry)
XX	
DE	Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 17.
DE	monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW	antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
KW	
XX	
OS	Homo sapiens.
XX	
PN	WO2003057006-A2.
XX	
PD	17-JUL-2003.
XX	
PF	26-DEC-2002; 2002WO-US041582.
XX	
PR	28-DEC-2001; 2001US-0346460P.
PA	(ABGE-) ABGENIX INC.
XX	
PI	Gudas J, Bar-Eli M;
XX	
DR	WPI; 2003-577496/54.
DR	N-PSDB; ADD05394.
XX	
PT	Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT	treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT	associated with melanoma, or increasing survival of an animal having a
PT	metastatic tumor.

RESULT 5  
ADFO9814  
ID ADF09814 standard; protein; 121 AA.  
XX  
XX AC ADF09814;  
XX  
XX DT 12-FEB-2004 (first entry)  
XX  
XX DE Human anti-MUC18 monoclonal antibody heavy chain #1.  
XX  
XX KW cell proliferation inhibition; MUC18 tumour antigen;  
XX KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
XX KW carcinoma; cancer; malignancy; heavy chain; human.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO2003057837-A2.  
XX  
XX PD 17-JUL-2003.  
XX  
XX PF 26-DEC-2002; 2002WO-US041580.  
XX  
XX PR 28-DEC-2001; 2001US-0346414P.  
XX  
XX PA (ABGE-) ABGENIX INC.  
XX  
XX PI Gudas J;  
XX  
XX WPI; 2003-598367/56.  
XX DR N-PSDE; ADF09816.  
XX  
XX PT Inhibiting cell proliferation associated with expression of MUC18 tumour  
XX PT antigen, involves incubating and inhibiting cell by administering anti-  
XX PT MUC18 monoclonal antibody.  
XX  
XX PS Claim 1; SEQ ID NO 1; 83pp; English.

[illegible]

RESULT 6	
ADFO9830	
ID	ADFO9830 standard; protein; 121 AA.
XX	
AC	ADFO9830;
XX	
DT	12-FEB-2004 (first entry)
XX	
DE	Human anti-MUC18 monoclonal antibody heavy chain #5.
XX	
KW	cell proliferation inhibition; MUC18 tumour antigen;
KW	anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW	carcinoma; cancer; malignancy; heavy chain; human.
XX	
OS	Homo sapiens.
XX	
PN	WO2003057837-A2.
XX	
PD	17-JUL-2003.
XX	
PF	26-DEC-2002; 2002WO-US041580.
XX	
PR	28-DEC-2001; 2001US-0346414P.
XX	
PA	(ABGE-) ABGENIX INC.
XX	
PI	Gudas J;
XX	
DR	WPI; 2003-598367/56.
DR	N-PSDB; ADF09832.

PT Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.

PS Claim 1; SEQ ID NO 17; 83pp; English.

The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUC18 tumour antigen-specific monoclonal antibody

Sequence 121 AA;

Query Match	100.0%	Score	649;	DB	7;	Length	121;
Best Local Similarity	100.0%	Pred. No.	6.4e-46;				
Matches	121;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;

[illegible]

QY 121 S 121

Db 121 S 121

## RESULT 7

ADC99780  
ID ADC99780 standard; protein; 121 AA.

AC ADC99780;

DT 01-JAN-2004 (first entry)

Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 9.

anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
 cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
 cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
 lung cancer; human.

xx  
OS  
Homo sapiens.

PN WO2003057838-A2.

17-JUL-2003.

PF 26-DEC-2002; 2002WO-US041581.

PR 28-DEC-2001; 2001US-0346299P.

PA (ABGE-) ABGENIX INC.

PI Gudas J;

DR WPI; 2003-587113/55.

XX  
N-F3DB; ADC3376Z.

PT or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

PS Claim 1; SEQ ID NO 9; 78pp; English.

The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the cell surface such as tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody heavy chain protein of the invention.

Sequence 121 AA;

Query Match 99.1%; Score 643; DB 7; Length 121;  
Best Local Similarity 98.3%; Pred. No. 2e+45;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

**Qy**

1 QVQLQESGPGLVKPSSETISLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYYTWTN<sup>60</sup>

|||

**Dd**

1 QVQLQESGPGLVKPSSETISLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYYTWTN<sup>60</sup>

|||

Qy 121 S 121

Db 121 S 121

## RESULT 8

ADD05384  
ID ADD05384 standard; protein; 121 AA.  
XX AC ADD05384;  
XX DT 01-JAN-2004 (first entry)  
XX DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 9.  
XX KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
XX KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
XX OS Homo sapiens.  
XX PN WO2003057006-A2.  
XX PD 17-JUL-2003.  
XX PF 26-DEC-2002; 2002WO-US041582.  
XX PR 28-DEC-2001; 2001US-0346460P.  
XX PA (ABGE-) ABGENIX INC.  
XX PI Gudas J, Bar-Eli M;  
XX PI WPI; 2003-577496/54.  
XX DR N-PSDB; ADD05386.  
XX DR  
XX PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
XX PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
XX PT associated with melanoma, or increasing survival of an animal having a  
XX PT metastatic tumor.  
XX PS Claim 1; SEQ ID NO 9; 87pp; English.  
XX CC The invention relates to a novel monoclonal antibody used for inhibiting  
XX CC tumour growth in an animal. The tumour inhibition process comprises  
XX CC selecting an animal in need of treatment for a tumour, providing a  
XX CC monoclonal antibody comprising a heavy chain amino acid, where the  
XX CC antibody consists of any one of 10 fully defined sequences of 117-123  
XX CC amino acids given in the specification, and where the monoclonal antibody  
XX CC binds MUC18, and contacting the tumour with the antibody resulting in  
XX CC inhibited proliferation of the cells. The monoclonal antibody has  
XX CC cytostatic and can be used in the production of a vaccine. The monoclonal  
XX CC antibodies against the MUC18 antigen are useful for diagnosing and  
XX CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or  
XX CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
XX CC increasing survival of an animal having a metastatic tumour. This  
XX CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
XX CC protein of the invention.  
XX SQ Sequence 121 AA;  
Query Match 99.1%; Score 643; DB 7; Length 121;  
Best Local Similarity 98.3%; Pred. No. 2e-45;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWISWIRPPGKLEWIGYIYTTTSNNY 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWISWIRPPGKLEWIGYIYTTTSNNY 60  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAAYVYCARDQGWLLPDAFDIWGGTMTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAAYVYCARDQGWLLPDAFDIWGGTMTVTS 120  
QY 121 S 121  
Db 121 S 121  
RESULT 9  
ADF09822

ADF09822 standard; protein; 121 AA.  
XX AC ADF09822;  
XX DT 12-FEB-2004 (first entry)  
XX DE Human anti-MUC18 monoclonal antibody heavy chain #3.  
XX KW cell proliferation inhibition; MUC18 tumour antigen;  
XX KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
XX KW carcinoma; cancer; malignancy; heavy chain; human.  
XX OS Homo sapiens.  
XX PN WO2003057837-A2.  
XX PD 17-JUL-2003.  
XX PF 26-DEC-2002; 2002WO-US041580.  
XX PR 28-DEC-2001; 2001US-0346414P.  
XX PA (ABGE-) ABGENIX INC.  
XX PI Gudas J;  
XX PI WPI; 2003-598367/56.  
XX DR N-PSDB; ADF09824.  
XX DR  
XX PT Inhibiting cell proliferation associated with expression of MUC18 tumour  
XX PT antigen, involves incubating and inhibiting cell by administering anti-  
XX PT MUC18 monoclonal antibody.  
XX PS Claim 1; SEQ ID NO 9; 83pp; English.  
XX CC The invention comprises a method for inhibiting cell proliferation  
XX CC associated with expression of MUC18 tumour antigen. The method involves  
XX CC administering anti-MUC18 monoclonal antibody. The method of the invention  
XX CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
XX CC proliferation associated with the expression of MUC18 tumour antigen, the  
XX CC method is preferably useful for inhibiting tumour metastasis. The method  
XX CC is useful for inhibiting cell proliferation in patients with tumours,  
XX CC carcinomas, cancer and other malignancies. The present amino acid  
XX CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
XX CC monoclonal antibody.  
XX SQ Sequence 121 AA;  
Query Match 99.1%; Score 643; DB 7; Length 121;  
Best Local Similarity 98.3%; Pred. No. 2e-45;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWISWIRPPGKLEWIGYIYTTTSNNY 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWISWIRPPGKLEWIGYIYTTTSNNY 60  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAAYVYCARDQGWLLPDAFDIWGGTMTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAAYVYCARDQGWLLPDAFDIWGGTMTVTS 120  
QY 121 S 121  
Db 121 S 121  
RESULT 10  
ADC99808  
ID ADC99808 standard; protein; 121 AA.  
XX AC ADC99808;  
XX DT 01-JAN-2004 (first entry)  
XX XX

DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 37.  
XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytotastic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
XX lung cancer; human.  
XX Homo sapiens.  
OS  
XX WO2003057838-A2.  
PN  
XX 17-JUL-2003.  
PD  
XX 26-DEC-2002; 2002WO-US041581.  
PF  
XX 28-DEC-2001; 2001US-0346299P.  
PR  
XX (ABGE-) ABGENIX INC.  
PA  
XX Gudas J;  
PI  
XX WPI; 2003-587113/55.  
DR  
XX N-PSDB; ADC99810.  
DR  
XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
PT or condition associated with expression of MUC18 in a patient, e.g.  
PT tumors, cancers, and other malignancies.  
PT  
XX Claim 1; SEQ ID NO 37; 78pp; English.  
PS  
XX The invention relates to a novel isolated monoclonal antibody comprising  
CC a heavy or light chain amino acid or a heavy or light chain variable  
CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
CC invention demonstrates cytostatic activity and may be useful for treating  
CC a disease or condition associated with the expression of MUC18 on the  
CC cell surface such as tumours, specifically melanoma, oesophageal,  
CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
CC carcinomas and cervical intraepithelial neoplasia and cancers including  
CC colorectal, breast or lung cancer, as well as other malignancies. The  
CC current sequence is that of the anti-human MUC18 monoclonal antibody  
CC heavy chain protein of the invention.  
XX  
SQ Sequence 121 AA;  
Query Match 92.0%; Score 597; DB 7; Length 121;  
Best Local Similarity 90.9%; Pred. No. 1.2e-41;  
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSTYYWSWIRQPPGKGLWIGIYIYTTN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSTYYWSWIRQPPGKGLWIGIYIYTTN 60  
QY 61 PSLKSRVTISVDTSKNQFSLKNSVTAADTAVYVCARDPGQWLVPDAFDIWGQGTMTVS 120  
Db 61 PSLKSRVTISVDTSKNQFSLKNSVTAADTAVYVCARDPGQWLVPDAFDIWGQGTMTVS 120  
QY 121 S 121  
Db 121 S 121  
RESULT 11  
ADD05412  
ID ADD05412 standard; protein; 121 AA.  
XX  
AC ADD05412;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 37.  
XX monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
KW

XX Homo sapiens.  
OS  
XX WO2003057006-A2.  
PN  
XX 17-JUL-2003.  
PD  
XX 26-DEC-2002; 2002WO-US041582.  
PF  
XX 28-DEC-2001; 2001US-0346460P.  
PR  
XX (ABGE-) ABGENIX INC.  
PA  
XX Gudas J, Bar-Eli M;  
PI  
XX WPI; 2003-577496/54.  
DR  
XX N-PSDB; ADD05414.  
DR  
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
PT associated with melanoma, or increasing survival of an animal having a  
PT metastatic tumor.  
PT  
XX Claim 1; SEQ ID NO 37; 87pp; English.  
PS  
XX The invention relates to a novel monoclonal antibody used for inhibiting  
CC tumor growth in an animal. The tumor inhibition process comprises  
CC selecting an animal in need of treatment for a tumor, providing a  
CC monoclonal antibody comprising a heavy chain amino acid, where the  
CC antibody consists of any one of 10 fully defined sequences of 117-123  
CC amino acids given in the specification, and where the monoclonal antibody  
CC binds MUC18, and contacting the tumor with the antibody resulting in  
CC inhibited proliferation of the cells. The monoclonal antibody has  
CC cytostatic and can be used in the production of a vaccine. The monoclonal  
CC antibodies against the MUC18 antigen are useful for diagnosing and  
CC treating tumors, inhibiting tumor growth (e.g. melanoma, lung tumor or  
CC tumor metastasis), inhibiting cell invasion associated with melanoma, or  
CC increasing survival of an animal having a metastatic tumor. This  
CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
CC protein of the invention.  
XX  
SQ Sequence 121 AA;  
Query Match 92.0%; Score 597; DB 7; Length 121;  
Best Local Similarity 90.9%; Pred. No. 1.2e-41;  
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSTYYWSWIRQPPGKGLWIGIYIYTTN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSTYYWSWIRQPPGKGLWIGIYIYTTN 60  
QY 61 PSLKSRVTISVDTSKNQFSLKNSVTAADTAVYVCARDPGQWLVPDAFDIWGQGTMTVS 120  
Db 61 PSLKSRVTISVDTSKNQFSLKNSVTAADTAVYVCARDPGQWLVPDAFDIWGQGTMTVS 120  
QY 121 S 121  
Db 121 S 121  
RESULT 12  
ADF09850  
ID ADF09850 standard; protein; 121 AA.  
XX  
AC ADF09850;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human anti-MUC18 monoclonal antibody heavy chain #10.  
XX cell proliferation inhibition; MUC18 tumour antigen;  
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
KW carcinoma; cancer; malignancy; heavy chain; human.  
KW

```

XX OS Homo sapiens.
XX PN WO2003057837-A2.
XX PD 17-JUL-2003.
XX PF 26-DEC-2002; 2002WO-US041580.
XX PR 28-DEC-2001; 2001US-0346414P.
XX PA (ABGE-) ABGENIX INC.
XX PI
XX PT Gudas J;
XX DR WPI; 2003-598367/56.
XX DR N-PSDB; ADF09852.
XX PT
XX PT Inhibiting cell proliferation associated with expression of MUC18 tumor
XX PT antigen, involves incubating and inhibiting cell by administering anti-
XX PT MUC18 monoclonal antibody.
XX PS Claim 1; SEQ ID NO 37; 83pp; English.
XX CC The invention comprises a method for inhibiting cell proliferation
XX CC associated with expression of MUC18 tumour antigen. The method involves
XX CC administering anti-MUC18 monoclonal antibody. The method of the invention
XX CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
XX CC proliferation associated with the expression of MUC18 tumour antigen, the
XX CC method is preferably useful for inhibiting tumour metastasis. The method
XX CC is useful for inhibiting cell proliferation in patients with tumours,
XX CC carcinomas, cancer and other malignancies. The present amino acid
XX CC sequence represents a heavy chain from an MUC18 tumour antigen-specific
XX CC monoclonal antibody.
XX SQ Sequence 121 AA;

Query Match 92.0%; Score 597; DB 7; Length 121;
Best Local Similarity 90.9%; Pred. No. 1.2e-41;
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIRPPGKLEWIGYIYTTSTNNYN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIRPPGKLEWIGYIYTTSTNNYN 60
QY 61 PSLKSRVTISVDTSKNQPSLRSLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQPSLRSLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
QY 121 S 121
Db 121 S 121

S9 cell derived human scFvL-VH protein.
B cell; surface immunoglobulin; Ig; binding site; antigen; human CD28;
closed system; detection laser-beam; catcher tube;
electrochemical device; fluorescence activated cell sorter; FACS;
antibody variable region; human.
Homo sapiens.
WO200404584-A1.

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PD 27-MAY-2004.
XX 12-NOV-2003; 2003WO-EP012664.
XX PR 13-NOV-2002; 2002EP-00025335.
XX PA (MICR-) MICROMET AG.
XX PI Baeuerle P, Hoffmann P, Weinberger S, Kischel R;
XX DR WPI; 2004-449579/42.
XX DR N-PSDB; ADO58077.
XX PT
XX PT Identifying a B cell carrying a surface immunoglobulin molecule having a
XX PT binding site for an antigen of interest, useful for constructing
XX PT therapeutic antibodies, comprises contacting a sample with the antigen
XX PT and a receptor.
XX PS Claim 22; SEQ ID NO 76; 156pp; English.
XX CC The invention relates to a novel method for identifying a B cell carrying
XX CC a surface immunoglobulin (Ig) molecule having a binding site for an
XX CC antigen of interest. The method comprises contacting a sample putatively
XX CC containing the B cell with the antigen of interest and with a receptor
XX CC specifically binding to the Ig molecule, and assessing the presence of
XX CC the detectable signal. The invention further comprises: an antibody
XX CC generated by the method above which is specific for human CD28 or
XX CC comprising an amino acid(s) sequence(s) given in the specification,
XX CC and/or are encoded by a nucleic acid sequence(s) also given in the
XX CC specification; and a device for assessing the presence of a detectable
XX CC signal defined above, where the device comprises a closed system for the
XX CC detection laser-beam and a catcher tube, and where the B cell of interest
XX CC can be collected as a single cell by means of an electrochemical device,
XX CC which is triggered by an electric signal generated by the fluorescence
XX CC activated cell sorter (FACS) device, where the electrochemical device
XX CC moves the nozzle of the steady catcher tube liquid stream for a
XX CC programmed time over a collecting tube, microtiter plate or other
XX CC container after a B cell is sorted. The method is useful for identifying
XX CC a B cell carrying a surface Ig molecule having a binding site for an
XX CC antigen of interest. The method is also useful for cloning of antibody
XX CC variable regions from the identified B cells, which may subsequently be
XX CC employed in the construction of proteins such as antibodies or its
XX CC fragments or derivatives useful in therapeutic approaches. The method is
XX CC useful as an alternative to phage display for the gain of antibodies or
XX CC its fragments. This sequence represents an S2 cell derived human
XX CC polypeptide of the invention.
XX SQ Sequence 243 AA;

Query Match 87.1%; Score 565.5; DB 8; Length 243;
Best Local Similarity 90.1%; Pred. No. 9.5e-39;
Matches 109; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIRPPGKLEWIGYIYTTSTNNYN 60
Db 124 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIRPPGKLEWIGYIYTTSTNNYN 183
QY 61 PSLKSRVTISVDTSKNQPSLRSLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
Db 184 PSLKSRVTISVDTSKNQPSLRSLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 242
QY 121 S 121
Db 243 S 243

RESULT 14
ID ABG92884
XX ABG92884 standard; protein; 121 AA.
XX AC ABG92884;
XX DT 19-NOV-2002 (first entry)

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CC damaged as by trauma. The present sequence represents the ebvHigM  
CC MS119D10 heavy chain variable region amino acid sequence  
XX  
SQ Sequence 121 AA;

Query Match	84.1%;	Score	545.5;	DB	5;	Length	121;
Best Local Similarity	87.6%;	Pred. No.	2.1e-37;				
Matches	106;	Conservative	6;	Mismatches	8;	Indels	1; Gaps 1;

  

Qy	1	QVQLQESGPGLVKRPSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGYIYYTWTSTNYN	60
Db	1	QVQLQESGPGLVKRPSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGYIYYSGSTNYN	60
Qy	61	PSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMTVTS	120
Db	61	PSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCARSAQQQLV-YYFDYWGQGLTVTS	119
Qy	121	\$	121
Db	120	\$	120

Search completed: November 9, 2005, 12:55:23  
Job time : 76.6015 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55 ; Search time 18.802 Seconds  
(without alignments)  
480.403 Million cell updates/sec

Title: US-10-660-357A-1

Perfect score: 649

Sequence: 1 QVQLQSGPGLVKPSETLSL.....WLLPDAFDIWGQGTMTVTSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/PCITUS COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	540	83.2	119	3	US-09-025-769B-39
2	540	83.2	119	3	US-09-025-769B-65
3	540	83.2	119	4	US-09-490-070A-39
4	540	83.2	119	4	US-09-490-070A-65
5	540	83.2	119	4	US-09-490-153-39
6	540	83.2	119	4	US-09-490-153-65
7	540	83.2	119	4	US-09-490-324-39
8	540	83.2	119	4	US-09-490-324-65
9	531.5	81.9	118	3	US-09-025-769B-25
10	531.5	81.9	118	4	US-09-490-070A-25
11	531.5	81.9	118	4	US-09-490-153-25
12	531.5	81.9	118	4	US-09-490-324-25
13	531.5	81.9	120	4	US-09-424-840B-20
14	529.5	81.6	244	3	US-08-918-148-79
15	529.5	81.6	244	4	US-09-138-091A-77
16	515.5	79.4	473	3	US-09-049-672A-4
17	502	77.3	142	2	US-08-480-774A-2
18	500	77.0	117	4	US-09-720-493-2
19	499.5	77.0	139	4	US-09-471-276-837
20	498.5	76.8	122	1	US-08-360-125-11
21	498.5	76.8	122	2	US-08-450-578-11
22	498.5	76.8	122	2	US-09-017-628-11
23	498.5	76.8	122	2	US-09-014-880-11
24	498.5	76.8	122	4	US-08-450-363-11
25	498.5	76.8	122	4	US-09-467-903-11
26	494.5	76.2	487	4	US-09-800-729-145
27	488	75.2	116	3	US-08-545-809A-140

28	485	74.7	119	1	US-08-360-125-5	Sequence 5, Appli
29	485	74.7	119	2	US-08-450-578-5	Sequence 5, Appli
30	485	74.7	119	2	US-09-017-628-5	Sequence 5, Appli
31	485	74.7	119	2	US-09-014-880-5	Sequence 5, Appli
32	485	74.7	119	4	US-08-450-363-5	Sequence 5, Appli
33	485	74.7	119	4	US-09-467-903-5	Sequence 10, Appli
34	484	74.6	119	2	US-08-652-816A-10	Sequence 7, Appli
35	479.5	73.9	172	4	US-09-472-087-7	Sequence 10, Appli
36	479.5	73.9	172	4	US-09-472-087-86	Sequence 86, Appli
37	479	73.8	123	3	US-08-793-450-4	Sequence 4, Appli
38	477	73.5	118	3	US-08-545-809A-142	Sequence 142, App
39	476	73.3	472	3	US-08-793-450-8	Sequence 2, Appli
40	472.5	72.8	139	4	US-09-203-768A-2	Sequence 888, App
41	471	72.6	155	4	US-09-471-276-888	Sequence 6, Appli
42	470.5	72.5	118	4	US-09-343-698-6	Sequence 6, Appli
43	470.5	72.5	118	4	US-08-325-955-6	Sequence 7, Appli
44	469.5	72.3	832	3	US-08-630-820-7	Sequence 7, Appli
45	469.5	72.3	832	4	US-09-273-453-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1  
US-09-025-769B-39  
; Sequence 39, Application US/09025769B  
; Patent No. 630064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-39

Query Match 83.2%; Score 540; DB 3; Length 119;  
Best Local Similarity 86.8%; Pred. No. 7.3e-45;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLEWIGYIYVTWTSNYN 60  
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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLEWIGYIYVTWTSNYN 60  
|  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDINGOGTMTVTS 120  
|  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDINGOGTMTVTS 120  
|  
QY 121 S 121  
|  
Db 119 S 119

## RESULT 2

US-09-025-769B-65  
; Sequence 65, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-65

Query Match 83.2%; Score 540; DB 3; Length 119;  
Best Local Similarity 86.8%; Pred. No. 7.3e-45;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLEWIGYIYVTWTSNYN 60  
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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLEWIGYIYVTWTSNYN 60  
|  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDINGOGTMTVTS 120  
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|  
QY 121 S 121  
|  
Db 119 S 119

Db 119 S 119  
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RESULT 3  
US-09-490-070A-39  
; Sequence 39, Application US/09490070A  
; Patent No. 6696248  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
; STREET: 1666 K Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20006

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-070A-39

Query Match 83.2%; Score 540; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 7.3e-45;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLEWIGYIYVTWTSNYN 60  
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QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDINGOGTMTVTS 120  
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Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDINGOGTMTVTS 120  
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QY 121 S 121  
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Db 119 S 119

## RESULT 4

US-09-490-070A-65  
; Sequence 65, Application US/09490070A

Patent No. 6696248  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
White & McAuliffe  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-070A-65  
Query Match 83.2%; Score 540; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 7.3e-45;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYYTWTSTN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYYSGSTN 60  
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Db 61 PSLSKRVTSVDTSKNQPSLRSLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
QY 121 S 121  
Db 119 S 119  
RESULT 5  
US-09-490-153-39  
Sequence 39, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-153-39  
Query Match 83.2%; Score 540; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 7.3e-45;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYYTWTSTN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYYSGSTN 60  
QY 61 PSLSKRVTSVDTSKNQPSLRSLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
Db 61 PSLSKRVTSVDTSKNQPSLRSLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
QY 121 S 121  
Db 119 S 119  
RESULT 6  
US-09-490-153-65  
Sequence 65, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York

```
/
/
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10021
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/490,153
/ FILING DATE: 24-Jan-2000
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/025,769B
/ FILING DATE: 18-FEB-1998
/ APPLICATION NUMBER: EP 95 11 3021.0
/ FILING DATE: 18-AUG-1995
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: James F. Haley, Jr., Esq.
/ REGISTRATION NUMBER: 27,794
/ REFERENCE/DOCKET NUMBER: MORPHO/5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)596-9000
/ TELEFAX: (212)596-9090
/
/ INFORMATION FOR SEQ ID NO: 65:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 119 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-153-65

Query Match 83.2%; Score 540; DB 4; Length 119;
Best Local Similarity 86.8%; Pred. No. 7.3e-45;
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLWIGIYYTSGSTNN 60
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Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFIMQGGMVTYS 120
QY 121 S 121
Db 119 S 119

RESULT 7
US-09-490-324-39
/ Sequence 39, Application US/09490324
/ Patent No. 6828422
/ GENERAL INFORMATION:
/ APPLICANT: Knappik, Achim
/ Pack, Peter
/ Ilag, Vic
/ Ge, Liming
/ Moroney, Simon
/ Plueckthun, Andreas
/
/ TITLE OF INVENTION: Protein/(Poly)peptide libraries
/ NUMBER OF SEQUENCES: 373
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
/ STREET: 1251 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10021
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
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/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/490,324
/ FILING DATE: 24-Jan-2000
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/025,769
/ FILING DATE: 18-FEB-1998
/ APPLICATION NUMBER: EP 95 11 3021.0
/ FILING DATE: 18-AUG-1995
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: James F. Haley, Jr., Esq.
/ REGISTRATION NUMBER: 27,794
/ REFERENCE/DOCKET NUMBER: MORPHO/5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)596-9000
/ TELEFAX: (212)596-9090
/
/ INFORMATION FOR SEQ ID NO: 39:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 119 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-324-39

Query Match 83.2%; Score 540; DB 4; Length 119;
Best Local Similarity 86.8%; Pred. No. 7.3e-45;
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLWIGIYYTTSNNY 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLWIGIYYTSGSTNN 60
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFIMQGGMVTYS 120
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QY 121 S 121
Db 119 S 119

RESULT 8
US-09-490-324-65
/ Sequence 65, Application US/09490324
/ Patent No. 6828422
/ GENERAL INFORMATION:
/ APPLICANT: Knappik, Achim
/ Pack, Peter
/ Ilag, Vic
/ Ge, Liming
/ Moroney, Simon
/ Plueckthun, Andreas
/
/ TITLE OF INVENTION: Protein/(Poly)peptide libraries
/ NUMBER OF SEQUENCES: 373
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
/ STREET: 1251 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10021
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/490,324
/ FILING DATE: 24-Jan-2000
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/025,769
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;/ FILING DATE: 18-FEB-1998  
;/ APPLICATION NUMBER: EP 95 11 3021.0  
;/ FILING DATE: 18-AUG-1995  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: James F. Haley, Jr., Esq.  
;/ REGISTRATION NUMBER: 27,794  
;/ REFERENCE/DOCKET NUMBER: MORPHO/5  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (212)596-9000  
;/ TELEFAX: (212)596-9090  
;/ INFORMATION FOR SEQ ID NO: 65:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 119 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: protein  
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-324-65  
  
Query Match 83.2%; Score 540; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 7.3e-45;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;  
  
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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIRQPPGKGLWIGIYYTWTSTNYN 60  
  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
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QY 121 S 121  
Db 119 S 119  
  
RESULT 9  
US-09-025-769B-25  
; Sequence 25, Application US/09025769B  
; Patent No. 630064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000

;/ TELEFAX: (212)596-9090  
;/ INFORMATION FOR SEQ ID NO: 25:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 118 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS:  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: protein  
;/ US-09-025-769B-25  
  
Query Match 81.9%; Score 531.5; DB 3; Length 118;  
Best Local Similarity 85.1%; Pred. No. 4.8e-44;  
Matches 103; Conservative 7; Mismatches 8; Indels 3; Gaps 1;  
  
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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIRQPPGKGLWIGIYYTWTSTNYN 60  
  
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QY 121 S 121  
Db 118 S 118  
  
RESULT 10  
US-09-490-070A-25  
; Sequence 25, Application US/09490070A  
; Patent No. 6696248  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
; STREET: 1666 K Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)  
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; APPLICATION NUMBER: US/09/490,070A  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Colin G. Sandercock, Esq.  
; REGISTRATION NUMBER: 31,298  
; REFERENCE/DOCKET NUMBER: 37629-0005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 912-2000  
; TELEFAX: (202) 912-2020  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 118 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

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SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25
Query Match      81.9%; Score 531.5; DB 4; Length 118;
Best Local Similarity 85.1%; Pred. No. 4.8e-44;
Matches 103; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLEWIGIYYTWTSTN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

QY 121 S 121
Db 118 S 118

RESULT 12
US-09-490-324-25
; Sequence 25, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25
Query Match      81.9%; Score 531.5; DB 4; Length 118;
Best Local Similarity 85.1%; Pred. No. 4.8e-44;
Matches 103; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

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QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

QY 121 S 121
Db 118 S 118

RESULT 11
US-09-490-153-25
; Sequence 25, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
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; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-153-25
Query Match      81.9%; Score 531.5; DB 4; Length 118;
Best Local Similarity 85.1%; Pred. No. 4.8e-44;
Matches 103; Conservative 7; Mismatches 8; Indels 3; Gaps 1;
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; Sequence 20, Application US/09424840B			
; Patent No. 6790938			
; GENERAL INFORMATION:			
; APPLICANT: Berchtold, Peter			
; APPLICANT: Escher, Robert F. A.			
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES			
; FILE REFERENCE: 100564-09049			
; CURRENT APPLICATION NUMBER: US/09/424,840B			
; PRIOR FILING DATE: 1999-12-03			
; PRIOR APPLICATION NUMBER: DE 19820663.1			
; PRIOR FILING DATE: 1998-05-08			
; PRIOR APPLICATION NUMBER: DE 19755227.7			
; PRIOR FILING DATE: 1997-12-12			
; PRIOR APPLICATION NUMBER: DE 19723904.8			
; PRIOR FILING DATE: 1997-06-06			
; NUMBER OF SEQ ID NOS: 128			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 20			
; LENGTH: 120			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-424-840B-20			
Query Match 81.8%; Score 531.5; DB 4; Length 120;			
Best Local Similarity 84.4%; Pred. No. 4.9e-44;			
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Db	119	SS	120
RESULT 14			
US-08-918-148-79			
; Sequence 79, Application US/08918148A			
; Patent No. 6342220			
; GENERAL INFORMATION:			
; APPLICANT: Adams, Camellia			
; APPLICANT: W.			
; APPLICANT: Carter, Paul J.			
; APPLICANT: Fendly, Brian M.			
; APPLICANT: Gurney, Austin L.			
; TITLE OF INVENTION: Agonist Antibodies			
; FILE REFERENCE: P0979			
; CURRENT APPLICATION NUMBER: US/08/918,148A			
; CURRENT FILING DATE: 1997-08-25			
; NUMBER OF SEQ ID NOS: 79			
; SEQ ID NO 79			
; LENGTH: 244			
; TYPE: PRT			
; ORGANISM: artificial			
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Best Local Similarity 84.3%; Pred. No. 1.7e-43;			

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Qy	121	S	121
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RESULT 15			
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; Sequence 77, Application US/09138091A			
; Patent No. 6737249			
; GENERAL INFORMATION:			
; APPLICANT: Adams, Camellia W.			
; APPLICANT: Carter, Paul J.			
; APPLICANT: Fendly, Brian M.			
; APPLICANT: Gurney, Austin L.			
; TITLE OF INVENTION: Agonist Antibodies			
; FILE REFERENCE: 9491-013-27			
; CURRENT APPLICATION NUMBER: US/09/138,091A			
; CURRENT FILING DATE: 1998-08-21			
; PRIOR APPLICATION NUMBER: US 60/056,736			
; PRIOR FILING DATE: 1997-08-22			
; NUMBER OF SEQ ID NOS: 77			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 77			
; LENGTH: 244			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: single chain antibody (scFv) fragments			
US-09-138-091A-77			
Query Match 81.6%; Score 529.5; DB 4; Length 244;			
Best Local Similarity 84.3%; Pred. No. 1.7e-43;			
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Db	3	QVQLQSGPGLVKVPSETLSLTCTVSGDSISSYYWSWIRQPPGKGLEWIGIYYSGSTNYN	62
Qy	61	PSLSRVTVISVDTSKNQFSLRLSSVTAADTAVYYCARDQGO-WLLPDAFDIWGGTMVTVS	120
Db	63	PSLSRVTVISVDTSKSQFSLKLSVTAADTAVYYCAR--GRY-----FDVWGRGTMTVVS	115
Qy	121	S	121
Db	116	S	116
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Job time : 19.802 secs			

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:40:37 ; Search time 67.2222 Seconds  
(without alignments)  
753.137 Million cell updates/sec

Title: US-10-660-357A-1  
Perfect score: 649  
Sequence: 1 QVQLQESGPGLVKPKSETLSL.....WLLPDAFDIWGGTMTVTSS 121

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Gapop 10.0 , Gapext 0.5

Searched: 1867879 segs, 418409474 residues  
Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
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15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US10F\_PUBCOMB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	649	100.0	121	14 US-10-330-613-1	Sequence 1, Appli
2	649	100.0	121	14 US-10-330-613-17	Sequence 17, Appli
3	649	100.0	121	14 US-10-330-530-1	Sequence 1, Appli
4	649	100.0	121	14 US-10-330-530-17	Sequence 17, Appli
5	649	100.0	121	16 US-10-660-357-1	Sequence 1, Appli
6	649	100.0	121	16 US-10-660-357-17	Sequence 17, Appli
7	643	99.1	121	14 US-10-330-613-9	Sequence 9, Appli
8	643	99.1	121	14 US-10-330-530-9	Sequence 9, Appli
9	643	99.1	121	16 US-10-660-357-9	Sequence 9, Appli
10	597	92.0	121	14 US-10-330-613-37	Sequence 37, Appli
11	597	92.0	121	14 US-10-330-530-37	Sequence 37, Appli

12	597	92.0	121	16 US-10-660-357-37	Sequence 37, Appli
13	553.5	85.3	118	15 US-10-292-088-142	Sequence 142, App
14	549.5	84.7	118	15 US-10-292-088-109	Sequence 109, App
15	547	84.3	121	14 US-10-067-800-60	Sequence 60, Appli
16	547	84.3	121	18 US-10-994-679-60	Sequence 60, Appli
17	545.5	84.1	121	14 US-10-010-729-11	Sequence 11, Appli
18	545.5	84.1	122	15 US-10-309-762-24	Sequence 24, Appli
19	545.5	84.1	122	15 US-10-309-762-27	Sequence 27, Appli
20	545	84.0	119	17 US-10-937-596-23	Sequence 23, Appli
21	544.5	83.9	122	15 US-10-309-762-25	Sequence 25, Appli
22	544.5	83.9	122	15 US-10-309-762-29	Sequence 29, Appli
23	540	83.2	119	14 US-10-125-687-5	Sequence 5, Appli
24	540	83.2	119	18 US-10-996-191-5	Sequence 5, Appli
25	539.5	83.1	118	17 US-10-371-942-102	Sequence 102, App
26	539	83.0	123	15 US-10-309-762-71	Sequence 71, Appli
27	538.5	83.0	122	15 US-10-309-762-90	Sequence 90, Appli
28	538.5	83.0	141	15 US-10-309-762-4	Sequence 4, Appli
29	536.5	82.7	120	15 US-10-309-762-102	Sequence 102, App
30	536.5	82.7	121	15 US-10-309-762-154	Sequence 154, App
31	536.5	82.7	121	15 US-10-309-762-143	Sequence 143, App
32	536	82.6	119	15 US-10-309-762-11	Sequence 11, Appli
33	536	82.6	125	15 US-10-893-576-37	Sequence 37, Appli
34	534.5	82.4	142	15 US-10-309-762-73	Sequence 73, Appli
35	534.5	82.4	141	15 US-10-309-762-94	Sequence 94, Appli
36	533.5	82.2	116	18 US-10-822-306A-5	Sequence 5, Appli
37	533.5	82.2	124	15 US-10-309-762-26	Sequence 26, Appli
38	533.5	82.2	193	15 US-10-264-049-4331	Sequence 4331, Ap
39	533.5	82.0	118	17 US-10-706-689-10	Sequence 10, Appli
40	532.5	82.0	118	18 US-10-988-360-10	Sequence 10, Appli
41	532.5	82.0	128	15 US-10-173-551-24	Sequence 24, Appli
42	532.5	82.0	120	16 US-10-844-424-20	Sequence 20, Appli
43	531.5	81.9	121	17 US-10-805-177-56	Sequence 56, Appli
44	531.5	81.9	126	14 US-10-067-800-68	Sequence 68, Appli
45	531.5	81.9			

ALIGNMENTS

RESULT 1  
US-10-330-613-1  
; Sequence 1, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; US-10-330-613-1

Query Match	100.0%;	Score 649;	DB 14;	Length 121;
Best Local Similarity	100.0%;	Pred. No. 1.8e-50;		
Matches 121;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	QVQLQESGPGLVKPKSETLSLTCTVSGGSISSYVSWIRPPGKGLWIGYIYTTWSNYN	60	
Db	1	QVQLQESGPGLVKPKSETLSLTCTVSGGSISSYVSWIRPPGKGLWIGYIYTTWSNYN	60	
QY	61	PSLKSRTVISVDTSKNQRSLRSSVTAADTAVYTCARDQGWLLPDAFDIWGGTMTVTVS	120	
Db	61	PSLKSRTVISVDTSKNQRSLRSSVTAADTAVYTCARDQGWLLPDAFDIWGGTMTVTVS	120	
QY	121	S	121	

Db 121 S 121

## RESULT 2

US-10-330-613-17

; Sequence 17, Application US/10330613

; Publication No. US20030147809A1

; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean

; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN

; FILE REFERENCE: ABGENIX.022A

; CURRENT APPLICATION NUMBER: US/10/330,613

; CURRENT FILING DATE: 2002-12-26

; PRIOR APPLICATION NUMBER: 60/346299

; PRIOR FILING DATE: 2001-12-18

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-330-613-17

Query Match 100.0%; Score 649; DB 14; Length 121;

Best Local Similarity 100.0%; Pred. No. 1.8e-50;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIROPKGLWIGIYYTWTSNYN 60

Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIROPKGLWIGIYYTWTSNYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMVTYS 120

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMVTYS 120

QY 121 S 121

Db 121 S 121

## RESULT 3

US-10-330-530-1

; Sequence 1, Application US/10330530

; Publication No. US20030152514A1

; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean

; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES

; FILE REFERENCE: ABGENIX.031A

; CURRENT APPLICATION NUMBER: US/10/330,530

; CURRENT FILING DATE: 2002-12-26

; PRIOR APPLICATION NUMBER: US 60/346414

; PRIOR FILING DATE: 2001-12-18

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-330-530-1

Query Match 100.0%; Score 649; DB 14; Length 121;

Best Local Similarity 100.0%; Pred. No. 1.8e-50;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIROPKGLWIGIYYTWTSNYN 60

Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIROPKGLWIGIYYTWTSNYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMVTYS 120

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMVTYS 120

QY 121 S 121

Db 121 S 121

## RESULT 4

US-10-330-530-17

; Sequence 17, Application US/10330530

; Publication No. US20030152514A1

; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean

; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES

; FILE REFERENCE: ABGENIX.031A

; CURRENT APPLICATION NUMBER: US/10/330,530

; CURRENT FILING DATE: 2002-12-26

; PRIOR APPLICATION NUMBER: US 60/346414

; PRIOR FILING DATE: 2001-12-18

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-330-530-17

Query Match 100.0%; Score 649; DB 14; Length 121;

Best Local Similarity 100.0%; Pred. No. 1.8e-50;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIROPKGLWIGIYYTWTSNYN 60

Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIROPKGLWIGIYYTWTSNYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMVTYS 120

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMVTYS 120

QY 121 S 121

Db 121 S 121

## RESULT 5

US-10-660-357-1

; Sequence 1, Application US/10660357

; Publication No. US20040115205A1

; GENERAL INFORMATION:

; APPLICANT: Bar-Eli, Menashe

; APPLICANT: Green, Larry L.

; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

; FILE REFERENCE: ABGENIX.030C1

; CURRENT APPLICATION NUMBER: US/10/660,357

; CURRENT FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 10/330,580

; PRIOR FILING DATE: 2002-12-26

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-660-357-1

Query Match 100.0%; Score 649; DB 16; Length 121;

Best Local Similarity 100.0%; Pred. No. 1.8e-50;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIROPKGLWIGIYYTWTSNYN 60

Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIROPKGLWIGIYYTWTSNYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMVTYS 120

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVVYCARDQOGWLLPDAFDIWGGTMTVTS 120  
 QY 121 S 121  
 Db 121 S 121

RESULT 6  
 US-10-660-357-17  
 ; Sequence 17, Application US/10660357  
 ; Publication No. US20040115205A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bar-Eli, Menashe  
 ; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
 ; FILE REFERENCE: ABGENIX 030C1  
 ; CURRENT APPLICATION NUMBER: US/10/660,357  
 ; CURRENT FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 10/330,580  
 ; PRIOR FILING DATE: 2002-12-26  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 17  
 ; LENGTH: 121  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 US-10-660-357-17

Query Match 100.0%; Score 649; DB 16; Length 121;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-50;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLWIGYIYYTWTN 60  
 Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLWIGYIYYTWTN 60  
 QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVVYCARDQOGWLLPDAFDIWGGTMTVTS 120  
 Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVVYCARDQOGWLLPDAFDIWGGTMTVTS 120  
 QY 121 S 121  
 Db 121 S 121

RESULT 7  
 US-10-330-613-9  
 ; Sequence 9, Application US/10330613  
 ; Publication No. US20030147809A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gudas, Jean  
 ; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
 ; FILE REFERENCE: ABGENIX.022A  
 ; CURRENT APPLICATION NUMBER: US/10/330,613  
 ; CURRENT FILING DATE: 2002-12-26  
 ; PRIOR APPLICATION NUMBER: 60/346299  
 ; PRIOR FILING DATE: 2001-12-18  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 9  
 ; LENGTH: 121  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 US-10-330-613-9

Query Match 99.1%; Score 643; DB 14; Length 121;  
 Best Local Similarity 98.3%; Pred. No. 6.1e-50;  
 Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLWIGYIYYTWTN 60  
 Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLWIGYIYYTWTN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVVYCARDQOGWLLPDAFDIWGGTMTVTS 120  
 Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVVYCARDQOGWLLPDAFDIWGGTMTVTS 120  
 QY 121 S 121  
 Db 121 S 121

RESULT 8  
 US-10-330-530-9  
 ; Sequence 9, Application US/10330530  
 ; Publication No. US20030152514A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gudas, Jean  
 ; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
 ; FILE REFERENCE: ABGENIX.031A  
 ; CURRENT APPLICATION NUMBER: US/10/330,530  
 ; CURRENT FILING DATE: 2002-12-26  
 ; PRIOR APPLICATION NUMBER: US 60/346414  
 ; PRIOR FILING DATE: 2001-12-18  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 9  
 ; LENGTH: 121  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 US-10-330-530-9

Query Match 99.1%; Score 643; DB 14; Length 121;  
 Best Local Similarity 98.3%; Pred. No. 6.1e-50;  
 Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLWIGYIYYTWTN 60  
 Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLWIGYIYYTWTN 60  
 QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVVYCARDQOGWLLPDAFDIWGGTMTVTS 120  
 Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVVYCARDQOGWLLPDAFDIWGGTMTVTS 120  
 QY 121 S 121  
 Db 121 S 121

RESULT 9  
 US-10-660-357-9  
 ; Sequence 9, Application US/10660357  
 ; Publication No. US20040115205A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bar-Eli, Menashe  
 ; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
 ; FILE REFERENCE: ABGENIX 030C1  
 ; CURRENT APPLICATION NUMBER: US/10/660,357  
 ; CURRENT FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 10/330,580  
 ; PRIOR FILING DATE: 2002-12-26  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 9  
 ; LENGTH: 121  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 US-10-660-357-9

Query Match 99.1%; Score 643; DB 16; Length 121;  
 Best Local Similarity 98.3%; Pred. No. 6.1e-50;  
 Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLWIGYIYYTWTN 60  
 Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLWIGYIYYTWTN 60

Qy	1	QVQLQESGGPGLVKPSETLSLTCTVSGGSISSYYMSWIRQPGKGLEWIGYIYYTWSNYN	60
Dd	1	QVQLQESGGPGLVKPSETLSLTCTVSGGSISSYYMSWIRQPGKGLEWIGYIYYTWTIN	60
Qy	61	PSLKSRTVISDTSKNQFSRLRSSVTAAADTVVYCARGDGQWLPLPAFDINGOGTWMTVS	120
Dd	61	PSLKSRTVISDTSKNQFSRLRSSVTAAADTVVYCARGDGQWLPLPAFDINGOGTWMTVS	120
Qy	121	\$ 121	
Dd	121	\$ 121	

```

RESULT 10
US-10-330-613-37
; Sequence 37, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCES: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2003-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-37

```

Query Match	92.0%;	Score 597;	DB 14;	Length 121;
Best Local Similarity	90.9%;	Pred. NO. 8e-46;		
Matches 110; Conservative	7;	Mismatches 4;	Indels 0;	Gaps 0
Qy	1	QVQLQESGGPGLVKPSETLSLTCTVS	GGSGISYYWSWIRPPGKLEWIGYIYYTWTN	NN 60
Dd	1	QVQLQESGGPGLVKPSETLSLTCTVS	GGSGISTYYWSWIRPPGKLEWIGYIYYTGNTYN	N 60
Qy	61	PSLKSRTVISDVTSKNQFSRLSSVTAADTAVYVCARDQGWLPAFDIWGGQTMTVS		120
Dd	61	PSLKSRTVTSVDTSKNQFSLKINSVTAADTAVYVCARDPGQWLVPDAFDIWGGQTMTVS		120
Qy	121	\$	121	
Dd	121	\$	121	

```

RESULT 11
US-10-330-530-37
; Sequence 37, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330.530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-37

```

Query Match 92.0%; Score 597; DB 14; Length 121;  
Best Local Similarity 90.9%; Pred. No. 8e-46;  
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0

Qy	1	QVQLQESGPGLVKPSETLSLTCTVSSGGSISSYYSWIRQPPCKGLEWIGYIYYTWTSNY	60
Db	1	QVQLQESGPGLVKPSETLSLTCTVSSGGSISSYYSWIRQPPCKGLEWIGYIYYTGNYYN	60
Qy	61	PSLKSRTVISVDTSKNPSFLSLSSVTAADTAVYTCARDGOWLLPDAFDIMCGQTMVTVS	120
Db	61	PSLKSRTVISVDTSKNPSFLKLSNVTAADTAVYTCARDPGQWLVPDAFDIMCGQTMVSVS	120
Qy	121	S 121	
Db	121	S 121	

```

RESULT 12
US-10-660-357-37
; Sequence 37, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660.357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-17

```

Query Match	92.0%;	Score 597;	DB 16;	Length 121;
Best Local Similarity	90.9%;	Pred. No. 8e-46;		
Matches 110;	Conservative 7;	Mismatches 4;	Indels 0;	Gaps 0
Qy	1	QVQLQESGPGLVKPSSETLSLTCTCTVSGSISYYVSWIRQPPKGLEWIGYIYYTWTSNV	60	
Db	1	QVQLQESGPGLVKPSSETLSLTCTCTVSGSISYYVSWIRQPPKGLEWIGYIYYTWTSNV	60	
Qy	61	PSLKSRTVTSVDTSKNQFSLRLSVTTAAADTAVVYCARDQGGWLLPDAFDIWGGQGTWTVS	120	
Db	61	PSLKSRTVTSVDTSKNQFSLKLSNVTTAAADTAVVYCARDPQGWLPDAFDIWGGQGTWTVS	120	
Qy	121	S 121		
Db	121	S 121		

```

RESULT 13
US-10-292-088-142
; Sequence 142, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 142
; LENGTH: 118

```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-142

Query Match      85.3%; Score 553.5; DB 15; Length 118;
Best Local Similarity 87.6%; Pred. No. 6.2e-42;
Matches 106; Conservative 7; Mismatches 5; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYVTWTSNYN 60
   |||||
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYVTWTSNYN 60
   |||||

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTVS 120
   |||||
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDYGDY---NWFDPWGGQTLVTVS 117
   |||||

QY 121 S 121
Db 118 S 118
```

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RESULT 14
US-10-292-088-109
; Sequence 109, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-109
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Query Match      84.7%; Score 549.5; DB 15; Length 118;
Best Local Similarity 87.6%; Pred. No. 1.4e-41;
Matches 106; Conservative 5; Mismatches 7; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYVTWTSNYN 60
   |||||
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYVTWTSNYN 60
   |||||

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTVS 120
   |||||
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDYGG---NSYFDWGGQTLVTVS 117
   |||||

QY 121 S 121
Db 118 S 118
```

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RESULT 15
US-10-067-800-60
; Sequence 60, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRs) HDGMR10
; FILE REFERENCE: 1488.1150001
; CURRENT APPLICATION NUMBER: US/10/067,800
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; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-60

Query Match      84.3%; Score 547; DB 14; Length 121;
Best Local Similarity 86.0%; Pred. No. 2.4e-41;
Matches 104; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYVTWTSNYN 60
   |||||
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYVTWTSNYN 60
   |||||

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTVS 120
   |||||
Db 61 PSLKSRVTMSVDTSKNRFSLRLSSVTAADTAVYYCARDRGSSWYPDAFDIWGGQTMVTVS 120
   |||||

QY 121 S 121
Db 121 S 121

Search completed: November 9, 2005, 12:42:57
Job time : 68.2222 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2005, 12:25:58 ; Search time 13.0401 seconds  
(without alignments)  
892.802 Million cell updates/sec

Title: US-10-660-357A-1  
Perfect score: 649  
Sequence: 1 QVQLQESGPGLVKPSSETLSL.....WLLPDAFDIWGQTMVTWVS 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	543	83.7	140	2 I37782	Ig variable region
2	536	82.6	155	2 S31512	Ig heavy chain - h
3	533	82.1	130	2 S31690	Ig heavy chain v r
4	533	82.1	155	2 S31511	Ig heavy chain - h
5	526.5	81.1	139	2 S31586	Ig heavy chain v r
6	518.5	79.9	130	2 S30534	Ig heavy chain v r
7	512.5	79.0	137	2 S31676	Ig heavy chain v r
8	509.5	78.5	118	2 S20780	Ig heavy chain v r
9	505	77.8	147	2 S13519	Ig heavy chain v r
10	498.5	76.8	140	2 S78052	Ig heavy chain pre
11	495	76.3	135	2 S78051	Ig heavy chain pre
12	490	75.5	105	2 S44125	Ig lambda chain v
13	489	75.3	97	2 S26906	Ig heavy chain v r
14	489	75.3	146	2 S09711	Ig heavy chain v r
15	488	75.2	116	2 B26340	Ig heavy chain pre
16	486	74.9	97	2 S12416	Ig heavy chain v r
17	486	74.9	121	2 S44113	Ig heavy chain v r
18	485	74.7	140	2 A49045	Ig heavy chain v r
19	481	74.1	123	2 S30530	Ig heavy chain v r
20	481	74.1	139	2 S31696	Ig heavy chain v r
21	477	73.5	118	2 A26340	Ig heavy chain pre
22	474.5	73.1	129	2 S44114	Ig heavy chain v r
23	473.5	73.0	126	2 S47010	Ig heavy chain v r
24	473.5	73.0	145	2 S78055	Ig heavy chain pre
25	468.5	72.2	118	2 S24443	Ig heavy chain v r
26	467	72.0	99	2 S26802	Ig heavy chain v r
27	467	72.0	99	2 S26803	Ig heavy chain v r
28	467	72.0	220	2 A49444	Ig gamma-1 heavy c
29	466	71.8	97	2 PH0876	Ig heavy chain v r

ALIGNMENTS

RESULT 1

I37782  
Ig variable region (VDJ) (clone T23-9) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
C:Accession: I37782; S25476  
R:Demaison, C.; Chastagner, P.; There, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A:Title: Somatic diversification in the heavy chain variable region genes expressed by F;46-128/Domain: immunoglobulin homology <IMM>  
A:Accession: I37782  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140 <RES>  
A:Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F;46-128/Domain: immunoglobulin homology <IMM>

Query Match 83.7%; Score 543; DB 2; Length 140;  
Best Local Similarity 86.0%; Pred. No. 3.5e-41;  
Matches 104; Conservative 5; Mismatches 12; Indels 0; Gaps 0;  
  
QY 1 QVQLQESGPGLVKPSSETLSLCTVSGGSISSYVWSWIRPPGKLEWIGYIVYTWTSNYN 60  
DB 20 QVQLQESGPGLVKPSSETLSLCTVSGGSISSYVWSWIRPPGKLEWIGYIVYSGSTNYN 79  
  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAIVYCARDQGOQMLLPDAFDIWGQTMVTWS 120  
DB 80 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAIVYCARHNSSSWYGRYFDYWGQTLVTWS 139  
  
QY 121 S 121  
DB 140 S 140

RESULT 2

S31512  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S31512  
R:Chastagner, P.; Demaison, C.; There, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA aut  
A:Reference number: S31509  
A:Accession: S31512  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <CHA>  
A:Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Ig heavy chain V r  
Ig heavy chain V-I  
Ig heavy chain V r  
Ig heavy chain V r  
Ig heavy chain V-I  
Ig heavy chain V r  
Ig heavy chain V r  
Ig heavy chain V r  
Ig heavy chain V-D  
Ig heavy chain pre  
Ig heavy chain V r  
Ig V-D-J region (N  
hypothetical hybri  
Ig heavy chain V r  
Ig heavy chain V r  
Ig heavy chain V-I  
Ig heavy chain V-J

F;47-129/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match	82.6%;	Score 536;	DB 2;	Length 155;
Best Local Similarity	82.9%;	Pred. No. 1.6e-40;		
Matches 102;	Conservative 7;	Mismatches 12;	Indels 2;	Gaps 1;
Qy	1	QVQLQESGPGLVKPESETLSLTCTVSGGISISSYYSWIRQPPGKGLEWIGYIYYTWTSNYN	60	
Db	33	QVQLQESGPGLVKPESETLSLTCTVSGGISISSYYSWIRQPPGKGLEWIGYIYYTGSATYN	92	
Qy	61	PSLKSRTVISVDTSKNPSFLRLSVTTAADTAVYVCARDQG--QVLLPDAPDIWGQGTWVT	118	
Db	93	PPILKSRTVISVDTSKNPSFLKVSSTTAADTAVYVCARGGISISSWYVYGDWVGQGTWVT	152	
Qy	119	VSS 121		
Db	153	VSS 155		

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RESULT 3
S31690
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31690
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougeteau, M.; Tonnelie, C.
Submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31690
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-130 <CDI>
A/Cross-references: EMBL:Z14199; NID:G30984; PIDN:CAA78568.1; PID:G30985
C/Superfamily: immunoglobulin v region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:20-102/Domain: immunoglobulin homology <IMW>

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	Query Match	82.1%	Score 533;	DB 2;	Length 130;
	Best Local Similarity	84.0%	Pred. No. 2.5e-40;		
	Matches 105;	Conservative 5;	Mismatches 11;	Indels 4;	Gaps 1
Qy	1	QVQLQESGPGLVKPSETLSLTCTVSGGSISSVYKSWIRPPCKGLEWIGYIYYTWTSTNN	60		
Db	6	QVQLQESGPGLVKPSETLSLTCTVSGGSISSVYKSWIRPPCKGLEWIGYIYYTWTSTNN	65		
Qy	61	PSLSRVTIISVDTKKNQPSFLRLSSVTAADTAVYVCARDQGQWL-----LPDAFDIWGQGTM	116		
Db	66	PSLSRVTIISVDTKKNQPSFLRLSSVTAADTAVYVCARDQGQWL-----LPDAFDIWGQGTL	125		
Qy	117	VTVSS 121			
Db	126	VTVSS 130			

RESULT 4

S31511  
IG heavy chain - human

C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S31511  
R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992.

A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto

A:Reference number: S31509  
A:Accession: S31511  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <CHA>  
A:Cross-references: EMBL:X69866; NID:g33094; PID:CAA49500.1; PID:g33095  
C:Superfamily: immunoglobulin v region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:47-129/Domain: immunoglobulin homology <IMM>

Query Match	82.1%;	Score 533;	DB 2;	Length 155;
Best Local Similarity	83.7%;	Pred. No. 3e-40;		
Matches 103;	Conservative 5;	Mismatches 13;	Indels 2;	Gaps 1
Qy	1	QVQLQESGPGLVKPSETLSLTCTVSGSISYYVSWIRQPPKGLIEWIGYIYTWTSNYN	60	
Db	33	QVQLQESGPGLVKPSETLSLTCTVSGSISYYVSWIRQPPKGLIEWIGYIYTWTSNYN	92	
Qy	61	PSLKSRTVISDTSKNQFSLRLSVTTAADTAVYVCARDQG--QWLLPDAFDIWGGTWMVT	118	
Db	93	PPLKSRTVISDTSKNQFSLKSVSVTTAADTAVYVCAREGGISSWDYDGMDVWGQTTVT	152	
Qy	119	VSS 121		
Db	153	VSS 155		

RESULT 5

S31586

Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C/Accession: S31586

R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougetreau, M.; Tonnelles, C.

A/Submitted to: The EMBL Data Library, June 1992

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31586

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-139 <CUI>

A/Cross-references: EMBL:Z14196; NID:g30978; PID:CAA78565.1; PID:g30979

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:34-116/Domain: immunoglobulin homology <IMM>

Query Match	81.1%;	Score 526.5;	DB 2;	Length 139;
Best Local Similarity	86.0%;	Pred. No. 1e-39;		
Matches 104;	Conservative 6;	Mismatches 10;	Indels 1;	Gaps 1;

  

Qy	1	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYMSWIRPPKGLGLEWIGIYYTWTSSNN	60
Db	20	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYMSWIRPPKGLGLEWIGIYYTWTSSNN	79
Qy	61	PSLKSRYTISVDTSKNQFSLRLSVTTAADTAVYICARDQGWLLPDAFDIWGGTMTVTS	120
Db	80	PSLKSRYTMSVDTSKNQFSLKLSVTTAADTAVYICARG-GLGIRRGAFDIWGGTMTVTS	138
Qy	121	S 121	
Db	139	S 139	

```

RESULT 6
S30534
IG heavy chain V region - human
C:Species: Homo sapiens (man)
C:date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1995
C:Accession: S30534
R:Marlette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30534
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <MAR>
A:Cross-references: EMBL:Z18320
C:Superfamily: immunoglobulin V region; immunoglobulin homology
K:Keywords: heterotrimer; immunoglobulin
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 79.9% Score 518.5 DB 2: Length 130:

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Best Local Similarity 81.5%; Pred. No. 4.8e-39;
Matches 106; Conservative 6; Mismatches 9; Indels 9; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGIS--SYNYSWIRQPPGKGLEWIGYIYTWTSN 58
Db 1 QVQLQESGPGLVKPSQTLSTLTCTVSGGISISGGSYYSWIRQPPGKGLEWIGRIYTSNSTN 60
QY 59 YNPSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCARDQGO-WL-----LPDAFDIW 111
Db 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARDKGGFWGYYTNSRAAFDIW 120
QY 112 QGGMVTWVS 121
Db 121 QGGMVTWVS 130

RESULT 7
S31676
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31676
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31676
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137 <CUI>
A;Cross-references: EMBL:Z14182; NID:G31031; PIDN:CAA78551.1; PID:G31032
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 512.5; DB 2; Length 137;
Best Local Similarity 83.5%; Pred. No. 1.7e-38;
Matches 101; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISISSYYSWIRQPPGKGLEWIGYIYTWTSN 60
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGISISSYYSWIRQPPGKGLEWIGRIYTSNSTN 79
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGOGLLPDAFDIWGGTMTVTS 120
Db 80 PSLKSRVTMSVDTSKNQFSLKLSVTAADTAVYYCARDAP---LMYGMVWGQGTIVTS 136
QY 121 S 121
Db 137 S 137

RESULT 8
S20780
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20780
R;Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Description: Analysis of human cord blood Ig heavy chain Iga and IgG repertoire.
A;Reference number: S20764
A;Accession: S20780
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-118 <MOR>
A;Cross-references: EMBL:Z11958; NID:G33893; PIDN:CAA78015.1; PID:G33894
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 78.5%; Score 509.5; DB 2; Length 118;
Best Local Similarity 81.0%; Pred. No. 2.7e-38;

Best Local Similarity 81.5%; Pred. No. 4.8e-39;
Matches 106; Conservative 6; Mismatches 9; Indels 9; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISISSYYSWIRQPPGKGLEWIGYIYTWTSN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISISGGSYYSWIRQPPGKGLEWIGRIYTSNSTN 60
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGOGLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTMSVDTSKNQFSLKLSVTAADTAVYYCARDGR---DGGFDIWGGQGTIVTS 117
QY 121 S 121
Db 118 S 118

RESULT 9
S13519
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S13519
R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A;Reference number: S13519; MUID:91187691; PMID:2011536
A;Accession: S13519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-147 <MOR>
A;Cross-references: EMBL:X56158; NID:G37724; PIDN:CAA39626.1; PID:G37725
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;41-125/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 505; DB 2; Length 147;
Best Local Similarity 82.1%; Pred. No. 8.6e-38;
Matches 101; Conservative 7; Mismatches 11; Indels 4; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISISSYYSWIRQPPGKGLEWIGYIYTWTSN 58
Db 27 QVQLQESGPGLVKPSSETLSLTCTVSGGISISSYYSWIRQPPGKGLEWIGSIYSGSTY 86
QY 59 YNPSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCARDQGOGLLPDAFDIWGGTMTV 118
Db 87 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARPL-LW-FGELFDIWGGQGTIVT 144
QY 119 VSS 121
Db 145 VSS 147

RESULT 10
S78052
Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78052; S32717
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78052
A;Molecule type: mRNA
A;Residues: 1-140 <HAR>
A;Cross-references: EMBL:X54441; NID:G37815; PIDN:CAA38308.1; PID:G930118
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and
patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S23717
A;Molecule type: mRNA
A;Residues: 15-111 <HAW>
A;Cross-references: EMBL:X54441
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## RESULT 14

Query Match 75.3%; Score 489; DB 2; Length 146;  
Best Local Similarity 74.0%; Pred. No. 2.2e-36;  
Matches 97; Conservative 11; Mismatches 9; Indels 14; Gaps 3;

```
QY      59 YNP SLK RVT ISVDTSKN QFSRLRSSVTAADTAVYYCAR-----DQG WLLPDAFDI   110  
       |||||:||||::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db      80 YNP SLR RVT ISVDTSKN QFSLKLGSVTAADTAVYYCARVLRSITSISQSYVM----DV   135
```

## RESULT 15

Query Match 75.2%; Score 488; DB 2; Length 116;  
Best Local Similarity 93.8%; Pred. No. 2.le-36;  
Matches 91; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 61 PSLKSRVTISVDTSKNQFSRLSSVTAADTAVYYCAR 97  
|||:|||||

Db 80 PSLKSRVTISVDTSKNQFSRLSSVTAADTAVYYCAR 116

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:46:52 ; Search time 62.4712 Seconds  
(without alignments)  
991.843 Million cell updates/sec

Title: US-10-660-357A-1

Perfect score: 649

Sequence: 1 QVQLQESGPGVLPKSETSL.....WLLPDAFDIWGQGTMTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	516	79.5	476	2	Q6GMX1 homo sapien
2	515	79.4	119	2	Q9UL73 homo sapien
3	508.5	78.4	465	2	Q6GMX6 homo sapien
4	501.5	77.3	620	2	Q96EY0
5	498.5	76.8	477	2	Q6GMX7
6	495	76.3	139	2	Q86SX2
7	493.5	76.0	478	2	Q7Z379
8	482.5	74.3	150	2	Q95973
9	472.5	72.8	576	2	Q6P418
10	472	72.7	492	2	Q7Z374
11	460.5	71.0	496	2	Q96KX8
12	454.5	70.0	146	1	HV21 HUMAN
13	451	69.5	595	2	Q8WUX4
14	451	69.5	597	2	Q6GMX5
15	451	69.5	597	2	Q9BU10
16	451	69.5	625	2	Q96AA6
17	450	69.3	478	2	Q6NTH3
18	449	69.2	597	2	Q9BQB8
19	445	68.6	117	1	HV2G HUMAN
20	444	68.4	129	1	HV2F HUMAN
21	435.5	67.1	130	2	Q81ZD7
22	416.5	64.2	116	2	Q7Z3Y6
23	411.5	63.4	122	2	Q9UL75
24	407	62.7	479	2	Q99M22
25	398	61.3	476	2	Q6MZK7
26	394.5	60.8	136	2	Q6LBQ5
27	394	60.2	137	1	HV46 MOUSE
28	390.5	60.2	473	2	Q8TC63
29	375	57.8	113	1	HV47 MOUSE
30	372	57.3	262	2	Q65Z11
31	369.5	56.9	482	2	Q91X92

32	366.5	56.5	116	1	HV60 MOUSE
33	355	54.7	117	1	HV62_MOUSE
34	354.5	54.6	116	1	HV61_MOUSE
35	348	53.6	118	2	Q9UL74
36	348	53.6	144	1	HV43_MOUSE
37	347.5	53.5	118	2	Q811U5
38	345.5	53.2	121	2	Q99NG4
39	343.5	52.9	135	1	HV02_XENLA
40	333	51.3	121	2	Q9UL96
41	332	51.2	470	2	Q6PJA4
42	330.5	50.9	613	2	Q8WUK1
43	328.5	50.6	118	2	Q9UL91
44	324.5	50.0	606	2	Q6GMV2
45	320	49.3	240	2	Q65ZC9

#### ALIGNMENTS

RESULT 1  
Q6GMX1 PRELIMINARY; PRT; 476 AA.  
AC Q6GMX1  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
ON NCBI\_TaxID=9606;  
RX MDLLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RP Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]  
PP SEQUENCE FROM N.A.  
RC SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073773; AAH73773.1; -.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00409; Ig; 2.  
DR SMART; SM00407; Igc1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.

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KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DD59D CRC64;

Query Match 79.5%; Score 516; DB 2; Length 476;
Best Local Similarity 79.7%; Pred. No. 3.6e-43;
Matches 102; Conservative 10; Mismatches 8; Indels 8; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISS--YYKSWIRPPGKGLWIGIYYTWTN 58
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: |||
20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSGYYKSWIRPPGKGLWIGIYYSGSTY 79
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: |||

QY 59 YNPSLKRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGW----LLPDAFDIWQ 113
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: |||
80 YNPSLKRVTISLDTSKNQFSLKNSVTAADTAVYFCAR-AGVWGSRFSAIDGFNIWGQ 138
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: |||

QY 114 GTWMTVSS 121
Db |||||
139 GTWMTVSS 146

RESULT 2
Q9UL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]

SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RC MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035041; AAD56277.1; -.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;

Query Match 79.4%; Score 515; DB 2; Length 119;
Best Local Similarity 82.6%; Pred. No. 1e-43;
Matches 100; Conservative 8; Mismatches 11; Indels 2; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYKSWIRPPGKGLWIGIYYTWTN 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: |||
1 QVQLQESGPGLVKPSSETLSLTCTVSGGSICSYKSWIRPPGKGLWIGIYYSGSTNYT 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: |||

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWQGGTMTVTS 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: |||
61 PSLKSRVTISVDRSKNQFSLKLTSLTAADTAVYFCAR-LSNW-GPYFYDWQGGTLTVTS 118
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: |||

QY 121 S 121
Db 119 S 119

RESULT 3
Q6GMX6 PRELIMINARY; PRT; 465 AA.
ID Q6GMX6
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AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]

SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RC MEDLINE=22388357; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton A., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]

SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RC Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS0290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 78.4%; Score 508.5; DB 2; Length 465;
Best Local Similarity 81.8%; Pred. No. 2e-42;
Matches 99; Conservative 8; Mismatches 9; Indels 5; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYKSWIRPPGKGLWIGIYYTWTN 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: |||
20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYKSWIRPPGKGLWIGIRITSGSTNN 79
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: |||

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWQGGTMTVTS 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: |||
80 PSLKSRVTISVDTSKNQFSLKLTSLTAADTAVYVCARGRTY-----FDYWQGGTLTVTS 134
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: |||

QY 121 S 121
Db 135 S 135

RESULT 4
Q96EY0
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ID Q96EY0 PRELIMINARY; PRT; 620 AA.
AC Q96EY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011857; AAH11857.2; -.
DR PIR; S15590; S15590.
DR HSP; P01820; IG7J.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR Pfam; SM00409; IG; 2.
DR SMART; SM00407; IG1; 4.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00407; IG1; 3.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;

Query Match 77.3%; Score 501.5; DB 2; Length 620;
Best Local Similarity 82.0%; Pred. No. 1.4e-41;
Matches 100; Conservative 6; Mismatches 13; Indels 3; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVWSWIRQPPGKLEWIGYIYTWTSNYN 60
DB 27 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVWSWIRQPPGKLEWIGYIYTWTSNYN 86
QY 61 PSLKSRVTVISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPD-AFDIWGGTMTVY 119
DB 87 PSLKSRVTVISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPD-AFDIWGGTMTVY 144
QY 120 SS 121
DB 145 SS 146
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RESULT 5

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Q6GMX7 PRELIMINARY; PRT; 477 AA.
ID Q6GMX7;
AC Q6GMX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073765; AAH73765.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR Pfam; SM00409; IG; 3.
DR SMART; SM00407; IG1; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;

Query Match 76.8%; Score 498.5; DB 2; Length 477;
Best Local Similarity 81.0%; Pred. No. 2e-41;
Matches 98; Conservative 8; Mismatches 12; Indels 3; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVWSWIRQPPGKLEWIGYIYTWTSNYN 60
DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVWSWIRQPPGKLEWIGYIYTWTSNYN 79
QY 61 PSLKSRVTVISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPD-AFDIWGGTMTVY 120
DB 80 PSLKSRVTVISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPD-AFDIWGGTMTVY 136
QY 121 S 121
DB 137 S 137
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2



AC Q6P4I8;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE IGH domain protein.  
 GN Name=IGHD;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalak U., Smillius D.E., Schnerch J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC063384; A063384.1; -;  
 DR HSSP; P01820; 1A7N.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 2.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00409; IG1; 1.  
 DR SMART; SM00407; IG1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
 SQ SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;  
 Query Match 72.8%; Score 472.5; DB 2; Length 576;  
 Best Local Similarity 76.2%; Pred. No. 1e-38;  
 Matches 96; Conservative 9; Mismatches 10; Indels 11; Gaps 3;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIS--SSYVSWIRPPGKGLWIGIYVYVTSNY 59  
 DB 27 QVQLQESGPGLVKPSSETLSLTCTVSGSIS--SSYVSWIRPPGKGLWIGIYVYVTSNY 86  
 QY 60 NPSLKSRTVISVDTSKNQFSLRLSSVTAADTAATVAVYCARDQGLWLPDAP-----DINGQGT 115  
 DB 87 NPSLKSRTVISVDTSKNQFSLRLSSVTAADTAATVAVYCARDQGLWLPDAP-----DINGQGT 140  
 QY 116 MVTVSS 121  
 DB 141 TVTVSS 146  
 RESULT 10

Q7Z374  
 ID Q7Z374 PRELIMINARY; PRT; 492 AA.  
 AC Q7Z374;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein DKFZp686C02218 (Fragment).  
 GN Name=DKFZp686C02218;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human rectum tumor;  
 RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobo G., Han M., Wiemann S.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX538077; CAD98001.1; -;  
 DR HSSP; P01820; 1G7J.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;  
 Query Match 72.7%; Score 472; DB 2; Length 492;  
 Best Local Similarity 75.4%; Pred. No. 9.5e-39;  
 Matches 95; Conservative 9; Mismatches 12; Indels 10; Gaps 4;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIS--SYVSWIRPPGKGLWIGIYVYVTSN 58  
 DB 32 QVQLQESGPGLVKPSSETLSLTCTVSGSIS--SYVSWIRPPGKGLWIGIYVYVTSN 91  
 QY 59 YNPGLKSRVTISVDTSKNQFSLRLSSVTAADTAATVAVYCARD-QGQ--WLPDAPDINGQGT 115  
 DB 92 YNPGLKSRVTISVDTSKNQFSLRLSSVTAADTAATVAVYCARD-QGQ--WLPDAPDINGQGT 146  
 QY 116 MVTVSS 121  
 DB 147 LVTVSS 152  
 RESULT 11  
 Q96KX8  
 ID Q96KX8 PRELIMINARY; PRT; 496 AA.  
 AC Q96KX8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE MGC27165 protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016369; AAH16369.1; -.
DR HSP; P01876; IOWO.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 71.0%; Score 460.5; DB 2; Length 496;
Best Local Similarity 74.0%; Pred. No. 1.4e-37;
Matches 94; Conservative 8; Mismatches 16; Indels 9; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSI--SSYVMSWIRPPGKGLIEWIGIYYTWTSN 58
Db 20 QLQLQESGPGLVKPSSETLSLTCTVSGGSISSSYVMSWIRPPGKGLIEWIGIYYTWTSN 79
QY 59 YNPGLSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARD---QGWLLPDAFDPF 114
Db 80 YNPGLSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDHYSRSGR---TGAIDYWGQG 136
QY 115 TMVTVSS 121
Db 137 TLVTVSS 143

RESULT 12
ID HV21 HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.2; -.
DR PIR; G34964; G34964.
DR HSP; P01861; 1A0Q.

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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146 Ig heavy chain V-II region ARH-77.
FT DOMAIN 20 117 V segment.
FT DOMAIN 118 127 D segment.
FT DOMAIN 128 146 J segment.
FT DISULFID 42 115 By similarity.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Query Match 70.0%; Score 454.5; DB 1; Length 146;
Best Local Similarity 72.2%; Pred. No. 1.4e-37;
Matches 91; Conservative 11; Mismatches 19; Indels 5; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSYVMSWIRPPGKGLIEWIGIYYTWTSN 60
Db 21 QVQLQWAGAGLVKPSSETLSLTCAVFGSGFGYVMSWIRPPGKGLIEWIGIINHSSTNYK 80
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARD---QGWLLPDAF---DIWGQGT 115
Db 81 TSLKSRVTISLDTSKNLFSLKLSVTAADTAVYVCARGLLRGMDVDVYVGMVWGQGT 140
QY 116 MVTVSS 121
Db 141 TVTVSS 146

RESULT 13
Q8WUX4 Q8WUX4 PRELIMINARY; PRT; 595 AA.
ID Q8WUX4;
AC Q8WUX4;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.2; -.
DR PIR; G34964; G34964.
DR HSP; P01861; 1A0Q.

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DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 595 AA; 0D4B50776545714E CRC64;

Query Match 69.5%; Score 451; DB 2; Length 595;
Best Local Similarity 69.8%; Pred. No. 1.5e-36;
Matches 90; Conservative 10; Mismatches 17; Indels 12; Gaps 2;

QY 1 QVQLQESGGLVSPSEKLSLTCTVSGGSISSYWSWIRQPPGKLEWIGIYYTWTNYYN 60
DB 27 QVQLQWAGAGLLKPESETLSLTCTGVYGGSGFYWSWIRQPPGKLEWIGIINHSNSTN 86
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCAR-----DQGWLLPDADF 112
DB 87 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARVITRASPFGTDGRY----GMDVWG 142
QY 113 QGTMTVTVSS 121
DB 143 QGTMTVTVSS 151

RESULT 14
Q6GMX5 . PRELIMINARY; PRT; 597 AA.
ID Q6GMX5 AC Q6GMX5
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullaby S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073767; AH73767.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.

DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG; 2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 2A1E75F6AE8D5230 CRC64;

Query Match 69.5%; Score 451; DB 2; Length 597;
Best Local Similarity 69.8%; Pred. No. 1.5e-36;
Matches 90; Conservative 10; Mismatches 17; Indels 12; Gaps 2;

QY 1 QVQLQESGGLVSPSEKLSLTCTVSGGSISSYWSWIRQPPGKLEWIGIYYTWTNYYN 60
DB 20 QVQLQWAGAGLLKPESETLSLTCTGVYGGSGFYWSWIRQPPGKLEWIGIINHSNSTN 79
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCAR-----DQGWLLPDADF 112
DB 80 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARVITRASPFGTDGRY----GMDVWG 135
QY 113 QGTMTVTVSS 121
DB 136 QGTMTVTVSS 144

RESULT 15
Q9BU10 . PRELIMINARY; PRT; 597 AA.
ID Q9BU10 AC Q9BU10
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullaby S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
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DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; C1-set; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG_LIKE; 5.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.  
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;  
  
Query Match 69.5%; Score 451; DB 2; Length 597;  
Best Local Similarity 69.8%; Pred. No. 1.5e-36;  
Matches 90; Conservative 10; Mismatches 17; Indels 12; Gaps 2;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYYTWTSTN 60  
  ||||: ||:||||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 20 QVQLQQMGAGLLKPSSETLSLTGCVYGSFSGYWSWIRPPGKGLEWIGIHNHSGSTN 79  
  ||||: ||:||||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCAR-----DQGWLLPDPADPIWG 112  
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 80 PSLKSRVTISVDTSKQSLKLSVNAADTAVYYCARVITRASPGTDGRY---GMDVWG 135  
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QY 113 QGTMTVTVSS 121  
Db 136 QGTMTVTVSS 144
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Search completed: November 9, 2005, 13:05:46  
Job time : 64.4712 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:43:32 ; Search time 72.1353 Seconds  
(without alignments)  
627.306 Million cell updates/sec

Title: US-10-660-357A-5

Perfect score: 625

Sequence: 1 QVQLQSGPGPLVKPSQTL...ARGGDGKYKQGQTLVTSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001s:\*

5: Geneseq2002s:\*

6: Geneseq2003as:\*

7: Geneseq2003bs:\*

8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	625	100.0	117	7	Adc99776 Anti-huma
2	625	100.0	117	7	Add05380 Anti-MUC1
3	625	100.0	117	7	Adf09818 Human ant
4	604	96.6	117	7	Adc99804 Anti-huma
5	604	96.6	117	7	Add05408 Anti-MUC1
6	604	96.6	117	7	Adf09846 Human ant
7	587	93.9	117	7	Adc99784 Anti-huma
8	587	93.9	117	7	Add05388 Anti-MUC1
9	587	93.9	117	7	Adf09826 Human ant
10	571.5	91.4	118	7	Adp03968 Murine-ex
11	571	91.4	123	7	Adp03870 Murine-ex
12	567.5	90.8	120	7	Adp03974 Murine-ex
13	567.5	90.8	120	7	Adp03873 Murine-ex
14	561	89.8	120	4	Aab62775 Human HIV
15	559.5	89.5	121	7	Adj80377 Antibody
16	559	89.4	119	7	Adp03970 Murine-ex
17	557	89.1	122	4	Aab62765 Human HIV
18	556.5	89.0	123	4	AAB62745 Human HIV
19	556.5	89.0	124	7	Adp03935 Murine-ex
20	555.5	88.9	110	7	Adp03934 Murine-ex
21	555.5	88.9	122	7	Adp03977 Murine-ex
22	555	88.8	121	7	Adp03981 Antibody
23	555	88.8	123	2	Aaw78433 Heavy cha
24	555	88.8	123	5	Abb97976 Heavy cha
25	555	88.8	123	7	Adg88414 anti-Ob-R

## ALIGNMENTS

## RESULT 1

ADC99776  
ID ADC99776 standard; protein; 117 AA.

XX AC ADC99776;

XX AC  
DT 01-JAN-2004 (first entry)

XX DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 5.

XX KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
XX KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
XX KW lung cancer; human.

XX OS Homo sapiens.

XX PN WO2003057838-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041581.

XX PR 28-DEC-2001; 2001US-0346299P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J;

XX DR WPI; 2003-587113/55.

XX DR N-PSDB; ADC99778.

XX PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

XX PS Claim 1; SEQ ID NO 5; 78pp; English.

XX CC The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the cell surface such as tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody

Adp03869 Murine-ex  
Adp03868 Murine-ex  
Adp03876 Murine-ex  
Adp03875 Murine-ex  
Adp03871 Murine-ex  
Aaau81276 Human trk  
Adp03872 Murine-ex  
Adp22366 Human ant  
Adp03882 Murine-ex  
Adp45608 Human Bly  
Adg96435 Single ch  
Adp45983 Human Bly  
Adg96810 Single ch  
Adp03961 Murine-ex  
Adp03969 Murine-ex  
Adq91396 Amino aci  
Aaau81273 Human trk  
Aay15126 Anti-muri  
Adp22124 Human ant  
Adp22104 Human ant

CC heavy chain protein of the invention.

XX Sequence 117 AA;

Query Match 100.0%; Score 625; DB 7; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.7e-45; Mismatches 0; Indels 0; Gaps 0;

Matches 117; Conservative 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKLEWIGYIYSGSTY 60

DB 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKLEWIGYIYSGSTY 60

QY 61 YNPPLSKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVTVSS 117

DB 61 YNPPLSKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVTVSS 117

RESULT 2

ADD05380

ID ADD05380 standard; protein; 117 AA.

XX AC

XX ADD05380;

DT 01-JAN-2004 (first entry)

XX DE

DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 5.

XX KW

KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;

KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.

XX OS

OS Homo sapiens.

XX PN

PN WO2003057006-A2.

XX PD

PD 17-JUL-2003.

XX PF

PF 26-DEC-2002; 2002WO-US041582.

XX PR

PR 28-DEC-2001; 2001US-0346460P.

XX PA

PA (ABGE-) ABGENIX INC.

XX PI

PI Gudas J, Bar-Eli M;

XX DR

DR WPI; 2003-577496/54.

XX DR

DR N-PSDB; ADD05382.

XX PT

PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and

PT treating tumors, inhibiting tumor growth, inhibiting cell invasion

PT associated with melanoma, or increasing survival of an animal having a

PT metastatic tumor.

XX PS

PS Claim 1; SEQ ID NO 5; 87pp; English.

XX CC

CC The invention relates to a novel monoclonal antibody used for inhibiting

CC tumour growth in an animal. The tumour inhibition process comprises

CC selecting an animal in need of treatment for a tumour, providing a

CC monoclonal antibody comprising a heavy chain amino acid, where the

CC antibody consists of any one of 10 fully defined sequences of 117-123

CC amino acids given in the specification, and where the monoclonal antibody

CC binds MUC18, and contacting the tumour with the antibody resulting in

CC inhibited proliferation of the cells. The monoclonal antibody has

CC cytotostatic and can be used in the production of a vaccine. The monoclonal

CC antibodies against the MUC18 antigen are useful for diagnosing and

CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or

CC tumour metastasis), inhibiting cell invasion associated with melanoma, or

CC increasing survival of an animal having a metastatic tumour. This

CC sequence represents an anti-MUC18 antibody heavy chain, variable region,

CC protein of the invention.

XX SQ

SQ Sequence 117 AA;

Query Match 100.0%; Score 625; DB 7; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.7e-45;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKLEWIGYIYSGSTY 60

DB 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKLEWIGYIYSGSTY 60

QY 61 YNPPLSKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVTVSS 117

DB 61 YNPPLSKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVTVSS 117

RESULT 3

ADF09818

ID ADF09818 standard; protein; 117 AA.

XX AC

AC ADF09818;

XX DT

DT 12-FEB-2004 (first entry)

XX DE

DE Human anti-MUC18 monoclonal antibody heavy chain #2.

XX KW

KW cell proliferation inhibition; MUC18 tumour antigen;

KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;

KW carcinoma; cancer; malignancy; heavy chain; human.

XX OS

OS Homo sapiens.

XX PN

PN WO2003057837-A2.

XX PD

PD 17-JUL-2003.

XX PF

PF 26-DEC-2002; 2002WO-US041580.

XX PR

PR 28-DEC-2001; 2001US-0346414P.

XX PA

PA (ABGE-) ABGENIX INC.

XX PI

PI Gudas J;

XX DR

DR WPI; 2003-598367/56.

XX DR

DR N-PSDB; ADF09820.

XX PT

PT Inhibiting cell proliferation associated with expression of MUC18 tumour

PT antigen, involves incubating and inhibiting cell by administering anti-

PT MUC18 monoclonal antibody.

XX PS

PS Claim 1; SEQ ID NO 5; 83pp; English.

XX CC

CC The invention comprises a method for inhibiting cell proliferation

CC associated with expression of MUC18 tumour antigen. The method involves

CC administering anti-MUC18 monoclonal antibody. The method of the invention

CC is useful for inhibiting cell (e.g. melanoma or tumour cell)

CC proliferation associated with the expression of MUC18 tumour antigen, the

CC method is preferably useful for inhibiting tumour metastasis. The method

CC is useful for inhibiting cell proliferation in patients with tumours,

CC carcinomas, cancer and other malignancies. The present amino acid

CC sequence represents a heavy chain from an MUC18 tumour antigen-specific

CC monoclonal antibody.

XX SQ

SQ Sequence 117 AA;

Query Match 100.0%; Score 625; DB 7; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.7e-45;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKLEWIGYIYSGSTY 60

DB 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKLEWIGYIYSGSTY 60

QY 61 YNPPLSKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVTVSS 117

DB 61 YNPPLSKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVTVSS 117

DT	01-JAN-2004	(first entry)
XX	Anti-MUC18 antibody heavy chain variable region protein, SEQ ID NO 33.	
DE	monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;	
XX	antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.	
KW		
OS	Homo sapiens.	
XX		
XX	WO2003057006-A2.	
XX		
PD	17-JUL-2003.	
XX		
PF	26-DEC-2002; 2002WO-US041582.	
XX		
PR	28-DEC-2001; 2001US-0346460P.	
XX		
PA	(ABGE-) ABGENIX INC.	
XX		
PI	Gudas J, Bar-Eli M;	
XX		
DR	WPI; 2003-577496/54.	
DR	N-PSDB; ADD05410.	
XX		
PT	Use of monoclonal antibodies against MUC18 antigen, for diagnosing and	
PT	treating tumors, inhibiting tumor growth, inhibiting cell invasion	
PT	associated with melanoma, or increasing survival of an animal having a	
PT	metastatic tumor.	
XX		
PS	Claim 1; SEQ ID NO 33; 87pp; English.	
XX		
CC	The invention relates to a novel monoclonal antibody used for inhibiting	
CC	tumour growth in an animal. The tumour inhibition process comprises	
CC	selecting an animal in need of treatment for a tumour, providing a	
CC	monoclonal antibody comprising a heavy chain amino acid, where the	
CC	antibody consists of any one of 10 fully defined sequences of 117-123	
CC	amino acids given in the specification, and where the monoclonal antibody	
CC	binds MUC18, and contacting the tumour with the antibody resulting in	
CC	inhibited proliferation of the cells. The monoclonal antibody has	
CC	cytostatic and can be used in the production of a vaccine. The monoclonal	
CC	antibodies against the MUC18 antigen are useful for diagnosing and	
CC	treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or	
CC	tumour metastasis), inhibiting cell invasion associated with melanoma, or	
CC	increasing survival of an animal having a metastatic tumour. This	
CC	sequence represents an anti-MUC18 antibody heavy chain, variable region,	
CC	protein of the invention.	
XX		
SQ	Sequence 117 AA;	
	Query Match 96.6%; Score 604; DB 7; Length 117;	
	Best Local Similarity 94.0%; Pred. No. 1.le-43;	
	Matches 110; Conservative 7; Mismatches 0; Indels 0; Gaps 0	
Qy	1 QVQLQSGPGLVFPSTLSLTCTVSGSGISGGTTHWSWIHQHPKGLIEWIGYIYSGSTY 60	
	:     :     :     :     :     :     :     :	
Db	1 QVQLQSGPGLVFPSETLSLTCTVSGSGISGGTTHWSWIHQHPKGLIEWIGYIYSGSTY 60	
	:     :     :     :     :     :     :	
Qy	61 YNPSLKSRVITISVDTSKNQFSLKLSVTAADTAVYVCARGDGYKYGQGLTLTVSS 117	
	:     :     :     :     :     :     :     :	
Db	61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYVCARGDGYKYGQGLTLTVSS 117	
	:     :     :     :     :     :     :     :	
RESULT 6		
ADF09846		
ID	ADF09846 standard; protein; 117 AA.	
XX		
AC	ADF09846;	
XX		
AC		
XX		
DT	12-FEB-2004 (first entry)	
XX		
DE	Human anti-MUC18 monoclonal antibody heavy chain #9.	
XX		
KW	cell proliferation inhibition; MUC18 tumour antigen;	





XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
 PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
 PT associated with melanoma, or increasing survival of an animal having a  
 PT metastatic tumor.

PS Claim 1; SEQ ID NO 13; 87pp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting  
 CC tumor growth in an animal. The tumour inhibition process comprises  
 CC selecting an animal in need of treatment for a tumour, providing a  
 CC monoclonal antibody comprising a heavy chain amino acid, where the  
 CC amino acids given in the specification, and where the monoclonal antibody  
 CC binds MUC18, and contacting the tumour with the antibody resulting in  
 CC inhibited proliferation of the cells. The monoclonal antibody has  
 CC cytostatic and can be used in the production of a vaccine. The monoclonal  
 CC antibodies against the MUC18 antigen are useful for diagnosing and  
 CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or  
 CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
 CC increasing survival of an animal having a metastatic tumour. This  
 CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
 CC protein of the invention.

XX Sequence 117 AA;

Query Match 93.9%; Score 587; DB 7; Length 117;  
 Best Local Similarity 94.0%; Pred. No. 2.9e-42;  
 Matches 110; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
 Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
 Qy 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGDGYKYWGQGLTVTVSS 117  
 Db 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGDGYKYWGQGLTVTVSS 117

RESULT 9

ID ADF09826  
 AC ADF09826; protein; 117 AA.

DT 12-FEB-2004 (first entry)

XX Human anti-MUC18 monoclonal antibody heavy chain #4.

XX cell proliferation inhibition; MUC18 tumour antigen;  
 KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
 KW carcinoma; cancer; malignancy; heavy chain; human.

XX Homo sapiens.

XX WO2003057837-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041580.

XX 28-DEC-2001; 2001US-0346414P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-598367/56.

XX N-PSDB; ADF09828.

XX Inhibiting cell proliferation associated with expression of MUC18 tumor  
 PT antigen, involves incubating and inhibiting cell by administering anti-  
 PT MUC18 monoclonal antibody.

XX

PS Claim 1; SEQ ID NO 13; 83pp; English.

XX The invention comprises a method for inhibiting cell proliferation  
 CC associated with expression of MUC18 tumour antigen. The method involves  
 CC administering anti-MUC18 monoclonal antibody. The method of the invention  
 CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
 CC proliferation associated with the expression of MUC18 tumour antigen, the  
 CC method is preferably useful for inhibiting tumour metastasis. The method  
 CC is useful for inhibiting cell proliferation in patients with tumours,  
 CC carcinomas, cancer and other malignancies. The present amino acid  
 CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
 CC monoclonal antibody.

XX Sequence 117 AA;

Query Match 93.9%; Score 587; DB 7; Length 117;  
 Best Local Similarity 94.0%; Pred. No. 2.9e-42;  
 Matches 110; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
 Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60

Qy 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGDGYKYWGQGLTVTVSS 117  
 Db 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGDGYKYWGQGLTVTVSS 117

RESULT 10

ID ADF03968

XX ADF03968 standard; protein; 118 AA.

XX ADF03968;

XX 29-JUL-2004 (first entry)

XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138.

XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytostatic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX Unidentified.

XX WO2003048328-A2.

XX 12-JUN-2003.

XX 02-DEC-2002; 2002WO-US038550.

XX 03-DEC-2001; 2001US-0337275P.

XX (ABGE-) ABGENIX INC.

XX Gudas J, Foltz I, Handa M, Gallo M;

XX WPI; 2003-523295/49.

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX Example 2; SEQ ID NO 138; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mab)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytostatic activity and may be useful for treating a tumour,

CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.

XX SQ Sequence 118 AA;

Query Match 91.4%; Score 571.5; DB 7; Length 118;  
Best Local Similarity 94.1%; Pred. No. 6.1e-41;  
Matches 111; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
QY 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYICAR-GGDGYKYGQGTLLVTSS 117  
DB 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYICARYYGGSDYWGQGTLLVTSS 118

RESULT 11

ADP03870

ID ADP03870 standard; protein; 123 AA.

XX AC ADP03870;

XX DT 29-JUL-2004 (first entry)

XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 10.

XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
XX KW cytosolic; colorectal neoplasm; renal cell carcinoma;  
XX KW cervical intraepithelial squamous neoplasia;  
XX KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
XX KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX OS Unidentified.

XX PN WO2003048328-A2.

XX PD 12-JUN-2003.

XX PF 02-DEC-2002; 2002WO-US038550.

XX PR 03-DEC-2001; 2001US-0337275P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J, Foltz I, Handa M, Gallo M;

XX DR WPI; 2003-523295/49.

XX PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX PS Claim 1; SEQ ID NO 10; 89pp; English.

XX CC The invention relates to a novel isolated monoclonal antibody (mAb)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cytostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a

CC transgenic mouse strain.

XX SQ Sequence 123 AA;

Query Match 91.4%; Score 571; DB 7; Length 123;  
Best Local Similarity 90.2%; Pred. No. 7e-41;  
Matches 111; Conservative 1; Mismatches 5; Indels 6; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
QY 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYICARCGDGY-----KYWGQGTLLVT 114  
DB 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYICARAGKYGSGSYLDYWGQGTLLVT 120

QY 115 VSS 117

DB 121 VSS 123

RESULT 12

ADP03974

ID ADP03974 standard; protein; 120 AA.

XX AC ADP03974;

XX DT 29-JUL-2004 (first entry)

XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.  
XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
XX KW cytosolic; colorectal neoplasm; renal cell carcinoma;  
XX KW cervical intraepithelial squamous neoplasia;  
XX KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
XX KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX OS Unidentified.

XX PN WO2003048328-A2.

XX PD 12-JUN-2003.

XX PF 02-DEC-2002; 2002WO-US038550.

XX PR 03-DEC-2001; 2001US-0337275P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J, Foltz I, Handa M, Gallo M;

XX DR WPI; 2003-523295/49.

XX PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX PS Example 2; SEQ ID NO 144; 89pp; English.

XX CC The invention relates to a novel isolated monoclonal antibody (mAb)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cytostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.

SQ Sequence 120 AA;  
 Query Match 90.8%; Score 567.5; DB 7; Length 120;  
 Best Local Similarity 91.0%; Pred. No. 1.4e-40;  
 Matches 111; Conservative 2; Mismatches 2; Indels 7; Gaps 2;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKGLEWIGYIYSGSTY 60  
 Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKGLEWIGYIYSGSTY 60  
 Qy 61 YNPSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARGDGYKY-----WGQGLTVTV 115  
 Db 61 YNPSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCAR--DGYNWYFDLWGRGLTVTV 118  
 Qy 116 SS 117  
 ||  
 Db 119 SS 120

RESULT 13  
 ADP03873  
 ID ADP03873 standard; protein; 120 AA.  
 XX  
 AC ADP03873;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.  
 XX  
 KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytosolic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003048328-A2.  
 XX  
 PD 12-JUN-2003.  
 XX  
 PF 02-DEC-2002; 2002WO-US038550.  
 XX  
 PR 03-DEC-2001; 2001US-0337275P.  
 XX  
 XX (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas J, Foltz I, Handa M, Gallo M;  
 XX  
 DR WPI; 2003-523295/49.  
 XX  
 PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX  
 PS Claim 1; SEQ ID NO 13; 89pp; English.  
 XX  
 CC The invention relates to a novel isolated monoclonal antibody (mAb)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytostatic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.  
 XX  
 SQ Sequence 120 AA;

Query Match 90.8%; Score 567.5; DB 7; Length 120;  
 Best Local Similarity 91.0%; Pred. No. 1.4e-40;  
 Matches 111; Conservative 2; Mismatches 2; Indels 7; Gaps 2;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKGLEWIGYIYSGSTY 60  
 Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKGLEWIGYIYSGSTY 60  
 Qy 61 YNPSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARGDGYKY-----WGQGLTVTV 115  
 Db 61 YNPSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCAR--DGYNWYFDLWGRGLTVTV 118  
 Qy 116 SS 117  
 ||  
 Db 119 SS 120

RESULT 14  
 AAB62775  
 ID AAB62775 standard; protein; 120 AA.  
 XX  
 AC AAB62775;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE Human HIV-1 monoclonal antibody SEQ ID NO: 74.  
 XX  
 KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;  
 KW envelope glycoprotein; gp120; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200100678-A1.  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 23-JUN-2000; 2000WO-US017327.  
 XX  
 PR 30-JUN-1999; 99US-0141701P.  
 XX  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Watkins BA, Reitz MS;  
 XX  
 DR WPI; 2001-112438/12.  
 DR N-PSDB; AAF29076.  
 XX  
 XX Novel human monoclonal antibody immunoreactive with human  
 PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1  
 PT in biological sample and providing passive immunotherapy to HIV-1  
 PT infected mammal.  
 XX  
 PS Claim 1; Page 69; 81pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences for the  
 CC variable regions of human monoclonal antibodies which are immunoreactive  
 CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.  
 CC These can be used in diagnosis and therapy of HIV-1 infection  
 XX  
 SQ Sequence 120 AA;

Query Match 89.8%; Score 561; DB 4; Length 120;  
 Best Local Similarity 91.6%; Pred. No. 4.8e-40;  
 Matches 109; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKGLEWIGYIYSGSTY 60  
 Db 2 EVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKGLEWIGYIYSGSTY 61  
 Qy 61 YNPSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARG--GDGKYWGQGLTVTVSS 117  
 Db 62 YNPSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARGVVVDWFDPMQSGTLTVTVSS 120

RESULT 15  
ADJ80377 standard; protein; 121 AA.  
XX AC ADJ80377;  
XX DT 06-MAY-2004 (first entry)  
XX DE Antibody variable heavy chain with homology to mouse anti-human antibody.  
XX KW hybrid antibody; antibody; framework region; homology; immunogenicity.  
XX OS Unidentified.  
XX PN WO2003048321-A2.  
XX PD 12-JUN-2003.  
XX PF 03-DEC-2002; 2002WO-US038450.  
XX PR 03-DEC-2001; 2001US-0336591P.  
XX PA (ALEX-) ALEXION PHARM INC.  
XX PI Rother R, Wu D;  
XX PS WPI; 2003-513753/48.  
XX PT Producing a hybrid antibody or hybrid antibody fragment by operatively  
PT linking the selected framework sequences to one or more complementarity  
PT determining regions of the initial antibody.  
XX Example 1; SEQ ID NO 137; 77pp; English.  
XX The invention relates to a method of producing a hybrid antibody or  
CC hybrid antibody fragment by: (i) providing an initial antibody having  
CC specificity for a target; (ii) determining the sequence of a variable  
CC region of the initial antibody; (iii) selecting a first component of the  
CC variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the  
CC sequence of the first component to sequences contained in a reference  
CC database of antibody sequences or antibody fragment sequences from a  
CC target species; (v) selecting a sequence from an antibody in the database  
CC which demonstrates a high degree of homology to the first component; (vi)  
CC selecting a second component of the variable region which is different  
CC than the first component, the second component selected from the group  
CC consisting of FR1, FR2, FR3 and FR4; (vii) comparing the sequence of the  
CC second component to sequences contained in a reference database of  
CC antibody sequences or antibody fragment sequences from the target species  
CC; (viii) selecting a sequence from the database which demonstrates a high  
CC degree of homology to the second component and which is from a different  
CC antibody than the selected antibody; and (ix) operatively linking the  
CC selected framework sequences to one or more complementarity determining  
CC regions (CDRs) of the initial antibody to produce a hybrid antibody or  
CC hybrid antibody fragment. The method is useful for producing a hybrid  
CC antibody or hybrid antibody fragment (claimed). The antibody and  
CC fragments are useful for therapeutic and diagnostic purposes. The method  
CC uses entire framework regions from a single antibody variable heavy or  
CC variable light chain to receive the CDRs. This produces antibodies that  
CC are highly homologous and exhibit reduced immunogenicity while  
CC maintaining an optimum binding profile. This sequence represents an  
CC antibody variable heavy chain which has good homology to an initial  
CC murine anti-human mannose binding lectin antibody (ADJ80371). The  
CC sequence was used to generate a hybrid antibody of the invention.  
XX Sequence 121 AA;  
SQ

Query Match 89.5%; Score 559.5; DB 7; Length 121;  
Best Local Similarity 89.3%; Pred. No. 6.5e-40;  
Matches 108; Conservative 3; Mismatches 5; Indels 5; Gaps 1;  
QY 2 VQLQESGPGLVKPSQTLSTCTVSGSISSSGGYYWNWIRQHPGKGLEWIGYIYSGSTYY 61  
||||| :||||| :|:|||||

Db 1 VQLQESGPGLVKPSQTLSTCTVSGSISSSGGYYWNWIRQHPGKGLEWIGYIYSGSTYY 60  
QY 62 NPSLKSRTIISVDTSKNQFSLKLSVTAADTAVYVCARG- - - - -GDGYKYWGQGLTAVTS 116  
DB ||||| :|||||  
61 NPSLKSRTIISVDTSKNQFSLKLSVTAADTAVYVCARGLKWGNSNHYFDYWGQGLTAVTS 120  
QY 117 S 117  
DB 121 S 121

Search completed: November 9, 2005, 12:55:24  
Job time : 73.1353 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55 ; Search time 18.1805 Seconds  
(without alignments)  
480.403 Million cell updates/sec

Title: US-10-660-357A-5

Perfect score: 625

Sequence: 1 QVQLQSGPGLVKPSTLSL.....ARGGDKYKYGQGLTVTSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pcp.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543	86.9	119	3	US-09-025-769B-39
2	543	86.9	119	3	US-09-025-769B-65
3	543	86.9	119	4	US-09-490-070A-39
4	543	86.9	119	4	US-09-490-070A-65
5	543	86.9	119	4	US-09-490-153-39
6	543	86.9	119	4	US-09-490-153-65
7	543	86.9	119	4	US-09-490-324-39
8	543	86.9	119	4	US-09-490-324-65
9	535	85.6	119	1	US-08-360-125-5
10	535	85.6	119	2	US-08-450-578-5
11	535	85.6	119	2	US-09-017-628-5
12	535	85.6	119	2	US-09-014-880-5
13	535	85.6	119	4	US-08-450-363-5
14	535	85.6	119	4	US-09-467-903-5
15	532.5	85.2	122	1	US-08-360-125-11
16	532.5	85.2	122	2	US-08-450-578-11
17	532.5	85.2	122	2	US-09-017-628-11
18	532.5	85.2	122	2	US-09-014-880-11
19	532.5	85.2	122	4	US-08-450-363-11
20	532.5	85.2	122	4	US-09-467-903-11
21	532.5	85.2	473	3	US-09-049-672A-4
22	525.5	84.1	487	4	US-09-800-729-145
23	524.5	83.9	118	3	US-09-025-769B-25
24	524.5	83.9	118	4	US-09-490-070A-25
25	524.5	83.9	118	4	US-09-490-153-25
26	524.5	83.9	118	4	US-09-490-324-25
27	516	82.6	117	4	US-09-720-493-2

28	511	81.8	118	3	US-08-545-809A-116	Sequence 116, App
29	509.5	81.5	172	4	US-09-472-087-7	Sequence 7, Appli
30	509.5	81.5	172	4	US-09-472-087-86	Sequence 86, Appl
31	507.5	81.2	120	4	US-09-424-840B-20	Sequence 20, Appl
32	502.5	80.4	244	3	US-08-918-148-79	Sequence 79, Appl
33	502.5	80.4	244	4	US-09-138-091A-77	Sequence 77, Appl
34	501	80.2	142	2	US-08-480-774A-2	Sequence 2, Appli
35	491	78.6	118	3	US-08-545-809A-142	Sequence 142, App
36	489.5	78.3	278	3	US-09-260-527-3	Sequence 3, Appli
37	488.5	78.2	139	4	US-09-471-276-837	Sequence 837, App
38	479.5	76.7	98	1	US-08-478-039-75	Sequence 75, Appl
39	479.5	76.7	98	1	US-08-476-349A-75	Sequence 75, Appl
40	479	76.6	118	3	US-08-545-809A-123	Sequence 123, App
41	476	76.0	119	2	US-08-652-816A-10	Sequence 10, Appl
42	475	76.0	155	4	US-09-471-276-888	Sequence 888, App
43	473	75.7	116	3	US-08-545-809A-140	Sequence 140, App
44	472	75.5	117	4	US-09-232-290-47	Sequence 47, Appl
45	470.5	75.3	150	4	US-09-582-337-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-09-025-769B-39  
; Sequence 39, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-39

Query Match 86.9%; Score 543; DB 3; Length 119;  
Best Local Similarity 90.1%; Pred. No. 7e-47;  
Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3;

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QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGIYYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYMSWIRQHPGKGLEWIGIYYSGSTN 58
QY 61 YNPISLSRVITISVDTSKNQFSLKSSVTAADTAIVYCAR--GGDGY---KYWGQGLTVTVS 116
Db 59 YNPISLSRVITISVDTSKNQFSLKSSVTAADTAIVYCARWGGDGFYAMDYWGQGLTVTVS 118
QY 117 S 117
Db 119 S 119

RESULT 2
US-09-025-769B-65
; Sequence 65, Application US/09025769B
; Patent No. 630064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-65

Query Match 86.9%; Score 543; DB 3; Length 119;
Best Local Similarity 90.1%; Pred. No. 7e-47;
Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGIYYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYMSWIRQHPGKGLEWIGIYYSGSTN 58
QY 61 YNPISLSRVITISVDTSKNQFSLKSSVTAADTAIVYCAR--GGDGY---KYWGQGLTVTVS 116
Db 59 YNPISLSRVITISVDTSKNQFSLKSSVTAADTAIVYCARWGGDGFYAMDYWGQGLTVTVS 118
QY 117 S 117
Db 119 S 119

RESULT 3
US-09-490-070A-39
; Sequence 39, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-490-070A-39

Query Match 86.9%; Score 543; DB 4; Length 119;
Best Local Similarity 90.1%; Pred. No. 7e-47;
Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGIYYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYMSWIRQHPGKGLEWIGIYYSGSTN 58
QY 61 YNPISLSRVITISVDTSKNQFSLKSSVTAADTAIVYCAR--GGDGY---KYWGQGLTVTVS 116
Db 59 YNPISLSRVITISVDTSKNQFSLKSSVTAADTAIVYCARWGGDGFYAMDYWGQGLTVTVS 118
QY 117 S 117
Db 119 S 119

RESULT 4
US-09-490-070A-65
; Sequence 65, Application US/09490070A
```









APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5837845Ihiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,578  
FILING DATE: May 25, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL TYPE: antibody GAH  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:

JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-578-5

Query Match 85.6%; Score 535; DB 2; Length 119;

Best Local Similarity 86.6%; Pred. No. 4.4e-46;  
Matches 103; Conservative 7; Mismatches 7; Indels 2; Gaps 1;

QY 1 QVQLQESGFLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGIYYSGSY 60  
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Db 1 QVQLQESGFLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGIYYSGSY 60  
|||  
QY 61 YNPISLKSRTVISVDTSKNQFSLKSSVTAADTAVVYCARGG--DGKYWGQGLTVTVSS 117  
|||  
Db 61 YNPISLKSRTVISVDTSKNQFSLKSSVTAADTAVVYCARSTRLRGADYWGQGLTVTVSS 119

## RESULT 11

US-09-017-628-5  
Sequence 5, Application US/09017628  
Patent No. 5930287

GENERAL INFORMATION:  
APPLICANT: HOSOKAWA, Saiko

APPLICANT: TAGAWA, Toshiaki  
APPLICANT: HIRAKAWA, Yoko

APPLICANT: NAGAIKE, Kazuhiro  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO

TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
FILE REFERENCE: 177/527361KH

CURRENT APPLICATION NUMBER: US/09/017,628  
CURRENT FILING DATE: 1998-02-02

EARLIER APPLICATION NUMBER: 08/360,125  
EARLIER FILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5  
LENGTH: 119

TYPE: PRT  
ORGANISM: Unknown

FEATURE:  
OTHER INFORMATION: Hybridoma producing human antibody GAH

US-09-017-628-5

Query Match 85.6%; Score 535; DB 2; Length 119;

Best Local Similarity 86.6%; Pred. No. 4.4e-46;  
Matches 103; Conservative 7; Mismatches 7; Indels 2; Gaps 1;

QY 1 QVQLQESGFLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGIYYSGSY 60  
|||  
Db 1 QVQLQESGFLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGIYYSGSY 60  
|||  
QY 61 YNPISLKSRTVISVDTSKNQFSLKSSVTAADTAVVYCARGG--DGKYWGQGLTVTVSS 117  
|||  
Db 61 YNPISLKSRTVISVDTSKNQFSLKSSVTAADTAVVYCARSTRLRGADYWGQGLTVTVSS 119

## RESULT 12

US-09-014-880-5  
Sequence 5, Application US/09014880  
Patent No. 5930297

GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA et al.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY  
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE

NUMBER OF SEQUENCES: 42

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
;; STREET: 2033 K Street, N.W., #800  
;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: U.S.A.  
;; ZIP: 20006  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: MS-DOS  
;; SOFTWARE: Wordperfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/014,880  
;; FILING DATE: January 28, 1998  
;; CLASSIFICATION: 536  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/450,578  
;; FILING DATE: May 25, 1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/360,125  
;; FILING DATE: December 20, 1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/905,534  
;; FILING DATE: June 29, 1992  
;; NAME: Warren M. Cheek, Jr.  
;; ATTORNEY/AGENT INFORMATION:  
;; REGISTRATION NUMBER: 33,367  
;; REFERENCE/DOCKET NUMBER:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-721-8200  
;; TELEFAX: 202-721-8250  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 119 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; ORIGINAL SOURCE:  
;; CELL TYPE: Hybridoma producing human  
;; CELL TYPE: antibody GAH  
US-09-014-880-5

Query Match 85.6%; Score 535; DB 2; Length 119;  
Best Local Similarity 86.6%; Fred. No. 4.4e-46;  
Matches 103; Conservative 7; Mismatches 7; Indels 2; Gaps 1;

Qy 1 QVQLQESGPGLVKPSQTLISLTCTVSGGSISSGYHWSWIROHPGKLEWIGYIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLISLTCTVSGGSISSCGFWNIROHPGKLEWIGYIYSGSTY 60

Qy 61 YNPSLKSRVTISVTSKRNQFSLKSSVTAADTAIVYCARGG--DGYKYWGQGTLLVTYSS 117  
Db 61 YNPSLKSRVTISLDTSKSQFSLKSLTAADTAIVYCARSTRLRGADYWGQGTMTVTYSS 119

RESULT 13  
US-08-450-363-5  
; Sequence 5, Application US/08450363  
; Patent No. 6436434  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA  
; APPLICANT: Toshiaki TAGAWA  
; APPLICANT: Yoko HIRAKAWA  
; APPLICANT: No. 6436434hiho ITO  
; APPLICANT: Kazuhiro NAGAIKE  
; TITLE OF INVENTION: Human Monoclonal Antibody  
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Wenderoth, Lind & Ponack  
;; STREET: 805 Fifteenth Street, N.W., #700  
;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: U.S.A.  
;; ZIP: 20005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: MS-DOS  
;; SOFTWARE: Wordperfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/450,363  
;; FILING DATE: May 25, 1995  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/360,125  
;; FILING DATE: December 20, 1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/905,534  
;; FILING DATE: June 29, 1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warren M. Cheek, Jr.  
;; REGISTRATION NUMBER: 33,367  
;; REFERENCE/DOCKET NUMBER:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-8850  
;; TELEFAX:  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 119 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL:  
;; ANTI-SENSE:  
;; FRAGMENT TYPE:  
;; ORIGINAL SOURCE:  
;; ORGANISM:  
;; STRAIN:  
;; INDIVIDUAL ISOLATE:  
;; DEVELOPMENTAL STAGE:  
;; HAPLOTYPE:  
;; TISSUE TYPE:  
;; CELL TYPE: Hybridoma producing human  
;; CELL TYPE: antibody GAH  
;; CELL LINE:  
;; ORGANELLE:  
;; IMMEDIATE SOURCE:  
;; LIBRARY:  
;; CLONE:  
;; POSITION IN GENOME:  
;; CHROMOSOME/SEGMENT:  
;; MAP POSITION:  
;; UNITS:  
;; FEATURE:  
;; NAME/KEY:  
;; LOCATION:  
;; IDENTIFICATION METHOD:  
;; OTHER INFORMATION:  
;; PUBLICATION INFORMATION:  
;; AUTHORS:  
;; TITLE:  
;; JOURNAL:  
;; VOLUME:  
;; ISSUE:  
;; PAGES:  
;; DATE:  
;; DOCUMENT NUMBER:  
;; FILING DATE:  
;; PUBLICATION DATE:



COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,125  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:

US-08-360-125-11

Query Match 85.2%; Score 532.5; DB 1; Length 122;  
Best Local Similarity 86.1%; Pred. No. 8e-46;  
Matches 105; Conservative 4; Mismatches 8; Indels 5; Gaps 2;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTVHMSWIRHPGKLEWICVYYSGSTY 60  
Db 1 QQLQESGPGLVKPSQTLSTCTVSGGSISSGTVHMSWIRHPGKLEWICVYYSGSTY 60  
Qy 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGG-DGYKY----WGQGTLLTV 115  
Db 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGSGYGYGMVWGQGTLLTV 120  
Qy 116 SS 117  
Db 121 SS 122

Search completed: November 9, 2005, 11:46:37  
Job time : 19.1805 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:40:37 ; Search time 65 Seconds  
(without alignments)  
753.137 Million cell updates/sec

Title: US-10-660-357A-5  
Perfect score: 625  
Sequence: 1 QVQLQSGPGGLVKPSQTLSTL.....ARGGDGYKYWGQTLTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09D\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10F\_PUBCOMB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	625	100.0	117	14	US-10-330-613-5
2	625	100.0	117	14	US-10-330-530-5
3	625	100.0	117	16	US-10-660-357-5
4	604	96.6	117	14	US-10-330-613-33
5	604	96.6	117	14	US-10-330-530-33
6	604	96.6	117	16	US-10-660-357-33
7	587	93.9	117	14	US-10-330-613-13
8	587	93.9	117	14	US-10-330-530-13
9	587	93.9	117	16	US-10-660-357-13
10	571.5	91.4	118	15	US-10-309-762-138
11	571	91.4	123	15	US-10-309-762-110
					Sequence 5, Appli
					Sequence 5, Appli
					Sequence 5, Appli
					Sequence 33, Appli
					Sequence 33, Appli
					Sequence 33, Appli
					Sequence 13, Appli
					Sequence 13, Appli
					Sequence 13, Appli
					Sequence 138, Appli
					Sequence 10, Appli

12	567.5	90.8	120	15	US-10-309-762-13	Sequence 13, Appli
13	567.5	90.8	120	15	US-10-309-762-144	Sequence 144, Appli
14	565.5	90.5	125	17	US-10-805-177-53	Sequence 53, Appli
15	564.5	90.3	122	18	US-10-984-960A-20	Sequence 20, Appli
16	564.5	90.3	149	17	US-10-910-901-22	Sequence 22, Appli
17	569.5	89.5	121	15	US-10-308-817-137	Sequence 137, Appli
18	559.5	89.5	121	15	US-10-453-698-137	Sequence 137, Appli
19	559.5	89.5	122	18	US-10-984-960A-56	Sequence 56, Appli
20	559	89.4	119	15	US-10-309-762-140	Sequence 140, Appli
21	556.5	89.0	120	17	US-10-706-689-40	Sequence 40, Appli
22	556.5	89.0	120	18	US-10-988-360-40	Sequence 40, Appli
23	556.5	89.0	124	15	US-10-309-762-75	Sequence 75, Appli
24	556.5	89.0	143	15	US-10-309-762-96	Sequence 96, Appli
25	555.5	88.9	110	15	US-10-309-762-74	Sequence 74, Appli
26	555.5	88.9	122	15	US-10-309-762-147	Sequence 147, Appli
27	555	88.8	121	15	US-10-309-762-151	Sequence 151, Appli
28	555	88.8	123	15	US-10-309-762-9	Sequence 9, Appli
29	553	88.5	125	15	US-10-309-762-8	Sequence 8, Appli
30	553	88.5	125	15	US-10-309-762-16	Sequence 16, Appli
31	552.5	88.4	122	15	US-10-309-762-15	Sequence 15, Appli
32	552	88.3	125	15	US-10-309-762-11	Sequence 11, Appli
33	552	88.3	129	16	US-10-312-316-48	Sequence 48, Appli
34	552	88.3	148	17	US-10-893-576-31	Sequence 31, Appli
35	552	88.2	480	17	US-10-910-901-6	Sequence 6, Appli
36	551	88.2	123	15	US-10-309-762-12	Sequence 12, Appli
37	551	88.2	142	17	US-10-893-576-37	Sequence 37, Appli
38	550.5	88.1	110	17	US-10-727-155-272	Sequence 272, Appli
39	550.5	88.1	136	20	US-11-131-648-15	Sequence 15, Appli
40	550.5	88.1	136	20	US-11-131-648-39	Sequence 39, Appli
41	550	88.0	121	15	US-10-309-762-152	Sequence 152, Appli
42	550	88.0	253	10	US-09-880-748-1619	Sequence 1619, Ap
43	550	88.0	253	15	US-10-293-418-1619	Sequence 1619, Ap
44	549.5	87.9	252	10	US-09-880-748-1994	Sequence 1994, Ap
45	549.5	87.9	252	15	US-10-293-418-1994	Sequence 1994, Ap

ALIGNMENTS

RESULT 1  
US-10-330-613-5  
; Sequence 5, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-5

Query Match 100.0%; Score 625; DB 14; Length 117;  
Best Local Similarity 100.0%; Pred. No. 1.7e-47;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60  
Db 1 QVQLQSGGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAAADTAVYICARGGDGYKYWGQTLTVSS 117  
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAAADTAVYICARGGDGYKYWGQTLTVSS 117

RESULT 2

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US-10-330-530-5
; Sequence 5, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-5

Query Match      100.0%; Score 625; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-47;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYCARGGDGYKYWGQGLTVTVSS 117
DB 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYCARGGDGYKYWGQGLTVTVSS 117

RESULT 3
US-10-660-357-5
; Sequence 5, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-5

Query Match      100.0%; Score 625; DB 16; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-47;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYCARGGDGYKYWGQGLTVTVSS 117
DB 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYCARGGDGYKYWGQGLTVTVSS 117

RESULT 4
US-10-330-613-33
; Sequence 33, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
```

---

```
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-33

Query Match      96.6%; Score 604; DB 14; Length 117;
Best Local Similarity 94.0%; Pred. No. 1.2e-45;
Matches 110; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYCARGGDGYKYWGQGLTVTVSS 117
DB 61 HNPFLKSRITISVDTSKNQFSLKSSVTAADTAIVYCARGGDGYKYWGQGLTVTVSS 117

RESULT 5
US-10-330-530-33
; Sequence 33, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-33

Query Match      96.6%; Score 604; DB 14; Length 117;
Best Local Similarity 94.0%; Pred. No. 1.2e-45;
Matches 110; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYCARGGDGYKYWGQGLTVTVSS 117
DB 61 HNPFLKSRITISVDTSKNQFSLKSSVTAADTAIVYCARGGDGYKYWGQGLTVTVSS 117

RESULT 6
US-10-660-357-33
; Sequence 33, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
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; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-33

Query Match          96.6%; Score 604; DB 16; Length 117;
Best Local Similarity 94.0%; Pred. No. 1.2e-45;
Matches 110; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYTCARGDGYKYWGQGLTVTSS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 HNPSLKSRITISVDTSKNQFSLKSSVTAADTAIVYTCARGDGYRYWGQGLTVTSS 117

RESULT 7
US-10-330-613-13
; Sequence 13, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-13

Query Match          93.9%; Score 587; DB 14; Length 117;
Best Local Similarity 94.0%; Pred. No. 3.8e-44;
Matches 110; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYTCARGDGYKYWGQGLTVTSS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYTCAREGDFYWGQGLTVTSS 117

RESULT 8
US-10-330-530-13
; Sequence 13, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-13

Query Match          93.9%; Score 587; DB 16; Length 117;
Best Local Similarity 94.0%; Pred. No. 3.8e-44;
Matches 110; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYTCARGDGYKYWGQGLTVTSS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYTCAREGDFYWGQGLTVTSS 117

RESULT 9
US-10-660-357-13
; Sequence 13, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-13

Query Match          93.9%; Score 587; DB 16; Length 117;
Best Local Similarity 94.0%; Pred. No. 3.8e-44;
Matches 110; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYTCARGDGYKYWGQGLTVTSS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYTCAREGDFYWGQGLTVTSS 117

RESULT 10
US-10-309-762-138
; Sequence 138, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-138
```

```
Query Match          91.4%; Score 571.5; DB 15; Length 118;
Best Local Similarity 94.1%; Pred. No. 8.8e-43;
Matches 111; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
  |||||
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
  |||||

QY 61 YNPISLSRVITISVDTSKNQFSLKSLSSVTAADTAIVYCAR--GGDGYKYWGQGLTLTVSS 117
  |||||
Db 61 YNPISLSRVITISVDTSKNQFSLKSLSSVTAADTAIVYCAR--GGDGYKYWGQGLTLTVSS 118

RESULT 11
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-10

Query Match          91.4%; Score 571; DB 15; Length 123;
Best Local Similarity 90.2%; Pred. No. 1e-42;
Matches 111; Conservative 1; Mismatches 5; Indels 6; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
  |||||
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
  |||||

QY 61 YNPISLSRVITISVDTSKNQFSLKSLSSVTAADTAIVYCAR--GGDGYKYWGQGLTLTV 114
  |||||
Db 61 YNPISLSRVITISVDTSKNQFSLKSLSSVTAADTAIVYCAR--GGDGYKYWGQGLTLTV 120

QY 115 VSS 117
  |||
Db 121 VSS 123

RESULT 12
US-10-309-762-13
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 13
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-13

Query Match          90.8%; Score 567.5; DB 15; Length 120;
Best Local Similarity 91.0%; Pred. No. 2e-42;
Matches 111; Conservative 2; Mismatches 2; Indels 7; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
  |||||
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
  |||||

QY 61 YNPISLSRVITISVDTSKNQFSLKSLSSVTAADTAIVYCAR--GGDGYKYWGQGLTLTV 115
  |||||
Db 61 YNPISLSRVITISVDTSKNQFSLKSLSSVTAADTAIVYCAR--GGDGYKYWGQGLTLTV 118

QY 116 SS 117
  ||
Db 119 SS 120

RESULT 13
US-10-309-762-144
; Sequence 144, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-144

Query Match          90.8%; Score 567.5; DB 15; Length 120;
Best Local Similarity 91.0%; Pred. No. 2e-42;
Matches 111; Conservative 2; Mismatches 2; Indels 7; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
  |||||
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
  |||||

QY 61 YNPISLSRVITISVDTSKNQFSLKSLSSVTAADTAIVYCAR--GGDGYKYWGQGLTLTV 115
  |||||
Db 61 YNPISLSRVITISVDTSKNQFSLKSLSSVTAADTAIVYCAR--GGDGYKYWGQGLTLTV 118

QY 116 SS 117
  ||
Db 119 SS 120

RESULT 14
US-10-805-177-53
; Sequence 53, Application US/10805177
; Publication No. US20050084449A1
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Chen, Francine
; APPLICANT: Bezabeh, Binyam
; APPLICANT: Foltz, Ian
```

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; APPLICANT: Tse, Kam Fai
; APPLICANT: Jeffers, Michael
; APPLICANT: Mesri, Mehdi
; APPLICANT: Starling, Gary
; APPLICANT: Mezes, Peter
; APPLICANT: Khrantsov, Nikolai
; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
; FILE REFERENCE: ABXCUR.006A
; CURRENT APPLICATION NUMBER: US/10/805,177
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/456,652
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-805-177-53
```

```
Query Match          90.5%; Score 565.5; DB 17; Length 125;
Best Local Similarity 87.9%; Pred. No. 3.2e-42;
Matches 109; Conservative 3; Mismatches 5; Indels 7; Gaps 1;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60

Qy 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGD-----DGKYWGQGLTV 113
Db 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARNNNSSWYNNFDYWGQGLTV 120

Qy 114 TVSS 117
Db 121 TVSS 124
```

```
RESULT 15
US-10-984-960A-20
; Sequence 20, Application US/10984960A
; Publication No. US20050142137A1
; GENERAL INFORMATION:
; APPLICANT: Gallo, Michael
; APPLICANT: Chui, Daniel
; APPLICANT: Zhong, Haihong
; APPLICANT: Ara, Gulshan
; APPLICANT: LaRoche, William J.
; TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
; FILE REFERENCE: Cura 970
; CURRENT APPLICATION NUMBER: US/10/984,960A
; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: 60/518,275
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 20
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-984-960A-20
```

```
Query Match          90.3%; Score 564.5; DB 18; Length 122;
Best Local Similarity 89.3%; Pred. No. 3.8e-42;
Matches 109; Conservative 4; Mismatches 4; Indels 5; Gaps 1;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60

Qy 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGD-----GYKYWGQGLTV 115
Db 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVFYCAREGEYDEGGFDYWGQGLTV 120
```

Qy 116 SS 117  
Db 121 SS 122

Search completed: November 9, 2005, 12:42:58  
Job time : 66 secs

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F;46-128/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 527; DB 2; Length 140;  
Best Local Similarity 86.2%; Pred. No. 4.1e-39;  
Matches 106; Conservative 3; Mismatches 6; Indels 8; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHNSWIRQHPGKGLEWIGYIYSGSY 60  
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGSISST--YYNSWIRQPPGKGLEWIGYIYSGSTN 77  
QY 61 YNPGLSRVTISVDTSKNQFSLKSSVTAADTAVYICARGD-----GDGKYKYGQGLT 114  
DB 78 YNPGLSRVTISVDTSKNQFSLKSSVTAADTAVYICARHNSSWGRFYDYGQGLT 137  
QY 115 VSS 117  
DB 138 VSS 140

## RESULT 3

S31690  
IG heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31690  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31690  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-130 <CU>  
A;Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;20-102/Domain: immunoglobulin homology <IMM>

Query Match 83.7%; Score 523; DB 2; Length 130;  
Best Local Similarity 82.7%; Pred. No. 8.4e-39;  
Matches 105; Conservative 3; Mismatches 7; Indels 12; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHNSWIRQHPGKGLEWIGYIYSGSY 60  
DB 6 QVQLQESGPGLVKPSQTLSTCTVSGSISST--YYNSWIRQPPGKGLEWIGYIYSGSTN 63  
QY 61 YNPGLSRVTISVDTSKNQFSLKSSVTAADTAVYICARGD-----GKYKYGQ 110  
DB 64 YNPGLSRVTISVDTSKNQFSLKSSVTAADTAVYICARGSSVLLWFGELLYYFDYWGQ 123  
QY 111 TLTVSS 117  
DB 124 TLTVSS 130

## RESULT 4

S37456  
IG mu chain - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S37456  
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.  
submitted to the EMBL Data Library, September 1993  
A;Description: Cloning and analysis of human IGM anti-Thyroglobulin autoantibodies from  
A;Reference number: S37453  
A;Accession: S37456  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-116 <MCI>  
A;Cross-references: EMBL:X75024; NID:g404313; PIDN:CAA52932.1; PID:g758095  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;6-90/Domain: immunoglobulin homology <IMM>

Query Match 83.5%; Score 522; DB 2; Length 116;  
Best Local Similarity 87.1%; Pred. No. 9.1e-39;  
Matches 101; Conservative 2; Mismatches 5; Indels 8; Gaps 1;

QY 10 GLVKPSQTLSTCTVSGSISSTGYHNSWIRQHPGKGLEWIGYIYSGSYNPSLSKSRV 69  
DB 1 GLVKPSQTLSTCTVSGSISSTGYHNSWIRQHPGKGLEWIGYIYSGSYNPSLSKSRV 60  
QY 70 TISVDTSKNQFSLKSSVTAADTAVYICARGDGDGKY-----WGQGLT 117  
DB 61 TISVDTSKNQFSLKSSVTAADTAVYICARGSYGYYYMYDMVGKGT 116

## RESULT 5

S78051  
IG heavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C;Accession: S78051; S23716  
R;Harindranath, N.  
submitted to the EMBL Data Library, August 1990  
A;Reference number: S78051  
A;Accession: S78051  
A;Molecule type: mRNA  
A;Residues: 1-135 <HAR>  
A;Cross-references: EMBL:X54437; NID:g37814; PIDN:CAA38306.1; PID:g930117  
R;Harindranath, N.; Goldfarb, I.S.; Ikenatsu, H.; Burastero, S.E.; Wilder, R.L.; Norkin  
Int. Immunol. 3, 865-875, 1991  
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and  
patient.  
A;Reference number: S23716; MUID:92031262; PMID:1718404  
A;Accession: S23716  
A;Molecule type: mRNA  
A;Residues: 13-111 <HAW>  
A;Cross-references: EMBL:X54437  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;1-13/Domain: signal sequence (fragment) #status predicted <SIG>  
F;14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>  
F;27-111/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 519; DB 2; Length 135;  
Best Local Similarity 82.1%; Pred. No. 1.9e-38;  
Matches 101; Conservative 7; Mismatches 9; Indels 6; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHNSWIRQHPGKGLEWIGYIYSGSY 60  
DB 13 QVQLQESGPGLVKPSQTLSTCTVSGSISRGSHYWGIRQPPGKGLEWIGSYIYSGNTY 72  
QY 61 YNPGLSRVTISVDTSKNQFSLKSSVTAADTAVYICARGD-----DGKYKYGQGLT 114  
DB 73 FNPGLSRVTISVDTSKNQFSLKSSVTAADTAVYICARLPGDDYTLDGMDVWGQGLT 132  
QY 115 VSS 117  
DB 133 VSS 135

## RESULT 6

S44113  
IG heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C;Accession: S44113  
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable  
A;Reference number: S44105  
A;Accession: S44113  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-121 <HAW>

R.; Tomlinson, I. M.; Walter, G.; Marks, J. D.; Llewellyn, M. B.; Winter, G. A.; Cross-References: EMBL:Z14237; NID:G37706; PIDN:CAA78506.1; PID:G1335372

A;Reference number: S31509  
A;Accession: S31512  
A;Status: preliminary

A:Molecule type: mRNA  
A:Residues: 1-155 <CHA>  
A:Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:47-129/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 509; DB 2; Length 155;  
Best Local Similarity 80.8%; Pred. No. 1.7e-37;  
Matches 101; Conservative 5; Mismatches 9; Indels 10; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
DB 33 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYWSWIRQHPGKGLEWIGYIYSGSAT 90  
QY 61 YNPPLSKSRVTISVDTSKNQFSLKSSVTAADTAIVYICARGGD-----GYKYWGQGTLL 112  
DB 91 YNPPIKSRVTISVDTSKNQFSLKSSVTAADTAIVYICARGGSISSWYVYVYGMVDWGQGT 150  
QY 113 VTVSS 117  
DB 151 VTVSS 155

RESULT 11  
S31586  
Ig heavy chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31586  
R:Quisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.  
Submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A:Reference number: S31585  
A:Accession: S31586  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-139 <CUI>  
A:Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 80.6%; Score 503.5; DB 2; Length 139;  
Best Local Similarity 83.6%; Pred. No. 4.5e-37;  
Matches 102; Conservative 5; Mismatches 8; Indels 7; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYWSWIRQHPGKGLEWIGRIYTSSTN 77  
QY 61 YNPPLSKSRVTISVDTSKNQFSLKSSVTAADTAIVYICARGGD-----YKYWGQGTLLTV 115  
DB 78 YNPPLSKSRVTISVDTSKNQFSLKSSVTAADTAIVYICARGGLIRRGAPDVGQGTMTV 137  
QY 116 SS 117  
DB 138 SS 139

RESULT 12  
S31514  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S31514  
R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
Submitted to the EMBL Data Library, December 1992  
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto  
A:Reference number: S31509  
A:Accession: S31514  
A>Status: preliminary  
A:Molecule type: mRNA

A:Residues: 1-128 <CHA>  
A:Cross-references: EMBL:X69862; NID:g33086; PIDN:CAA49496.1; PID:g33087  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:22-106/Domain: immunoglobulin homology <IMM>

Query Match 80.5%; Score 503; DB 2; Length 128;  
Best Local Similarity 80.2%; Pred. No. 4.6e-37;  
Matches 97; Conservative 9; Mismatches 11; Indels 4; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
DB 8 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGMALEWIAHYIFSGSTY 67  
QY 61 YNPPLSKSRVTISVDTSKNQFSLKSSVTAADTAIVYICARGGDGYKY----WGQGTLLTVTS 116  
DB 68 YNPPLSKSRVTISVDTSKNQFSLRLTSVTPADTAIVYICARIGYFVGFDPWGQGTLLTVTS 127  
QY 117 S 117  
DB 128 S 128

RESULT 13  
S26803  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S26803  
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.  
Eur. J. Immunol. 22, 1075-1082, 1992  
A:Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.  
A:Reference number: S26800; MUID:92201299; PMID:1348029  
A:Accession: S26803  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-99 <WEN>  
A:Cross-references: EMBL:Z14238; NID:g37710; PIDN:CAA78607.1; PID:g1335374  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 502; DB 2; Length 99;  
Best Local Similarity 97.0%; Pred. No. 4.2e-37;  
Matches 96; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
QY 61 YNPPLSKSRVTISVDTSKNQFSLKSSVTAADTAIVYICAR 99  
DB 61 YNPPLSKSRVTISVDTSKNQFSLKSSVTAADTAIVYICAR 99

RESULT 14  
S26802  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S26802  
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.  
Eur. J. Immunol. 22, 1075-1082, 1992  
A:Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.  
A:Reference number: S26800; MUID:92201299; PMID:1348029  
A:Accession: S26802  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-99 <WEN>  
A:Cross-references: EMBL:Z14239; NID:g37708; PIDN:CAA78608.1; PID:g1335373  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-99/Domain: immunoglobulin homology <IMM>



Query Match 79.5%; Score 497; DB 2; Length 99;  
Best Local Similarity 96.0%; Pred. No. 1.2e-36;  
Matches 95; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 QVQLQESGPGILVKPSQTLTCTVSGSISSGTYHMSWIRQHPGKGLEWIGYIYSGSTY 60  
Db 1 QVQLQESGPGILVKPSQTLTCTVSGSISSGTYHMSWIRQHPGKGLEWIGYIYSGSTY 60  
Qy 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR 99  
Db 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR 99

RESULT 15  
S44114  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C;Accession: S44114  
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r  
A;Reference number: S44105  
A;Accession: S44114  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-129 <HAW>  
A;Cross-references: EMBL:Z31579; NID:g472968; PIDN:CAA83451.1; PID:g940525  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 496.5; DB 2; Length 129;  
Best Local Similarity 80.0%; Pred. No. 1.7e-36;  
Matches 100; Conservative 6; Mismatches 10; Indels 9; Gaps 3;  
Qy 1 QVQLQESGPGILVKPSQTLTCTVSGSISSGTYHMSWIRQHPGKGLEWIGYIYSGSTY 60  
Db 1 QVQLQESGPGILVKPSGTLTCAVSGSISSSNW-NSWVRQPPGKGLEWIGEYHSGSTN 59  
Qy 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR-----GGDG-YKYWGQGTLL 112  
Db 60 YNPFKSRVTISADTSKNQFSLKNSVTAADTAVYCARNYDFWSGGDFDYWGQGTLL 119  
Qy 113 VTVSS 117  
Db 120 VTVSS 124

Search completed: November 9, 2005, 13:08:01  
Job time : 12.609 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: November 9, 2005, 11:46:52 ; Search time 60.406 Seconds  
(without alignments)  
991.843 Million cell updates/sec  
Title: US-10-660-357A-5  
Perfect score: 625  
Sequence: 1 QVQLQESGPGLVKPSQTLSL.....ARGGDGKYWGQGLTVTSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	551	88.2	476	2 Q6GMX1	Q6gm1 homo sapien
2	519.5	83.1	478	2 Q7Z379	Q7z379 homo sapien
3	500.5	80.1	465	2 Q6GMX6	Q6gm6 homo sapien
4	500	80.0	119	2 Q9UL73	Q9ul73 homo sapien
5	497.5	79.6	477	2 Q6GMX7	Q6gm7 homo sapien
6	489.5	78.3	150	2 Q95973	Q95973 homo sapien
7	488.5	78.2	496	2 Q96KX8	Q96kx8 homo sapien
8	488.5	78.2	576	2 Q6P418	Q6p418 homo sapien
9	486.5	77.8	620	2 Q96EY0	Q96ey0 homo sapien
10	478.5	76.6	130	2 Q81ZD7	Q81zd7 homo sapien
11	477	76.3	492	2 Q7Z374	Q7z374 homo sapien
12	474	75.8	139	2 Q86SX2	Q86sx2 homo sapien
13	453	72.5	129	1 HV2F_HUMAN	P01824 homo sapien
14	445	71.2	478	2 Q6NYH3	Q6nyh3 homo sapien
15	434	69.4	595	2 Q8WUX4	Q8wux4 homo sapien
16	434	69.4	597	2 Q6GMX5	Q6gm5 homo sapien
17	434	69.4	597	2 Q9BU10	Q9bu10 homo sapien
18	434	69.4	625	2 Q96AA6	Q96aa6 homo sapien
19	429.5	68.7	136	2 Q6LBQ5	Q6lbq5 mus musculus
20	429.5	68.7	146	1 HV21_HUMAN	P06331 homo sapien
21	428	68.5	597	2 Q9BQ58	Q9bq58 homo sapien
22	425.5	68.1	473	2 Q8TC53	Q8tc53 homo sapien
23	425	68.0	479	2 Q99M22	Q99m22 mus musculus
24	413.5	66.2	122	2 Q9UL75	Q9ul75 homo sapien
25	413	66.1	137	1 HV46_MOUSE	P01822 mus musculus
26	410	65.6	262	2 Q65Z11	Q65z11 mus musculus
27	404	64.6	116	2 Q7Z3Y6	Q7z3y6 homo sapien
28	403	64.5	113	1 HV47_MOUSE	P01823 mus musculus
29	403	64.5	117	1 HV2G_HUMAN	P01825 homo sapien
30	401	64.2	476	2 Q6MZX7	Q6mzx7 homo sapien
31	387	61.9	117	1 HV62_MOUSE	P18533 mus musculus

32	380.5	60.9	116	1 HV61_MOUSE	P18532 mus musculus
33	379.5	60.7	116	1 HV60_MOUSE	P18531 mus musculus
34	356	57.0	121	2 Q9UL96	Q9ul96 homo sapien
35	352.5	56.4	118	2 Q811U5	Q811u5 mus musculus
36	351.5	56.2	482	2 Q91X92	Q91x92 mus musculus
37	350	56.0	144	1 HV43_MOUSE	P01819 mus musculus
38	345.5	55.3	135	1 HV02_XENLA	P20957 xenopus lae
39	343.5	55.0	121	2 Q99NG4	Q99ng4 mus musculus
40	330	52.8	118	2 Q9UL74	Q9ul74 homo sapien
41	330	52.8	119	1 HV2C_HUMAN	P01816 homo sapien
42	330	52.8	466	2 Q6IN78	Q6in78 homo sapien
43	326.5	52.2	606	2 Q6GMX2	Q6gm2 homo sapien
44	325	52.0	116	2 Q9UL93	Q9ul93 homo sapien
45	324.5	51.9	147	2 Q9Y509	Q9y509 homo sapien

ALIGNMENTS

RESULT 1  
Q6GMX1 PRELIMINARY; PRT; 476 AA.  
AC Q6GMX1;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MDLLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RS Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
EMBL; BC073773; AAH73773.1; -  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00047; ig; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.

```
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABASC62DDE9D CRC64;

Query Match      88.2%; Score 551; DB 2; Length 476;
Best Local Similarity 82.7%; Pred. No. 3.8e-46;
Matches 105; Conservative 7; Mismatches 5; Indels 10; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPKGLIEWIGYIYSGSTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPKGLIEWIGYIYSGSTY 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAATVAVYCARGG-----DGKYGQG 110
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 YNPSLKSRVTISLDTSKNQFSLKLSVTAADTAATVAVYCARAGVWGSRFSAIDGFIWQGG 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 111 TLTVSS 117
   |||||
Db 140 TMTVSS 146

RESULT 2
Q72379 PRELIMINARY; PRT; 478 AA.
AC Q72379;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein (KDFZp686K04218)
GN Name=DKFZp686K04218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Human rectum tumor;
RA Bloecker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538066; CAD97996.1; -.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match      83.1%; Score 519.5; DB 2; Length 478;
Best Local Similarity 80.8%; Pred. No. 5e-43;
Matches 97; Conservative 12; Mismatches 8; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPKGLIEWIGYIYSGSTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 19 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPKGLIEWIGYIYSGSTY 78
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAATVAVYCARG---GDGKYGQGTLTVSS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 79 YNPFLSRLSISIDTSKNQFSLRLNSLTAADTAATVAVYCARGVGLGTAPDINGQGTIVTVSS 138
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
```

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DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match      80.1%; Score 500.5; DB 2; Length 465;
Best Local Similarity 86.4%; Pred. No. 3.7e-41;
Matches 102; Conservative 3; Mismatches 10; Indels 3; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPKGLIEWIGYIYSGSTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPKGLIEWIGYIYSGSTN 77
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 YNPFLKSRVTISVDTSKNQFSLKLSVTAADTAATVAVYCARGGDGY-KYWGQGLTVTVSS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 78 YNPFLKSRVTISVDTSKNQFSLKLSVTAADTAATVAVYCARGRFTYFDYWGQGLTVTVSS 135
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
Q9UL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN NCBI\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 EX MEDLINE=92277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
 DR EMBL; AF035041; AAD56277.1; -.  
 DR PIR; PH0876; PH0876.  
 DR HIS; S12416; S12416.  
 DR HSSP; P01820; IGTJ.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON TER 1  
 FT NON TER 119  
 SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;  
 Query Match 80.0%; Score 500; DB 2; Length 119;  
 Best Local Similarity 82.6%; Pred. No. 9.9e-42;  
 Matches 100; Conservative 6; Mismatches 9; Indels 6; Gaps 2;  
 Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHNSWIRQHPKGLGIEWIGYIYSGSTY 60  
 Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHNSWIRQHPKGLGIEWIGYIYSGSTN 58  
 Qy 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYVCAR---GGDGVKYGQGLTVTVS 116  
 Db 59 YTPSLKSRVVISVDTSKNQFSLKLSVTAADTAVYFCARLSNWPYFDYWGQGLTVTVS 118  
 Qy 117 S 117  
 Db 119 S 119  
 RESULT 5  
 Q6GMX7 PRELIMINARY; PRT; 477 AA.  
 AC Q6GMX7  
 -DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Primary B-Cells;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Aramanci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073765; AAH73765.1; -.  
 DR InterPro; IPR003599; Ig-like.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 2.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00409; IG; 4.  
 DR SMART; SM00407; IGV; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;  
 Query Match 79.6%; Score 497.5; DB 2; Length 477;  
 Best Local Similarity 81.7%; Pred. No. 7.6e-41;  
 Matches 98; Conservative 8; Mismatches 9; Indels 5; Gaps 2;  
 Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHNSWIRQHPKGLGIEWIGYIYSGSTY 60  
 Db 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHNSWIRQHPKGLGIEWIGYIYSGSTT 77  
 Qy 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYVCARGD---GVKYGQGLTVTVS 117  
 Db 78 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYVCARGSSWDFADYWGQGLTVTVS 137  
 RESULT 6  
 O95973 PRELIMINARY; PRT; 150 AA.  
 AC O95973  
 -DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE VH4 heavy chain variable region precursor (Fragment).  
 GN Name=IGH;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF103795; AAC79084.1; -.  
 DR PIR; S31673; S31673.  
 DR HSSP; P01820; IGTJ.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Signal.  
 FT SIGNAL 1 19 Potential.  
 FT CHAIN 20 >150 VH4 heavy chain variable region.  
 FT NON TER 150  
 SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;  
 Query Match 78.3%; Score 489.5; DB 2; Length 150;  
 Best Local Similarity 80.5%; Pred. No. 1.4e-40;  
 Matches 95; Conservative 10; Mismatches 12; Indels 1; Gaps 1;  
 Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHNSWIRQHPKGLGIEWIGYIYSGSTY 60



86 YNPGLKSRVTISVDTSKNQFSLKLSVTAADTAVVYCASLGDIYYGYMDVWGQGTTLTV 145

117 S 117

146 S 146

## RESULT 9

Q96EY0 PRELIMINARY; PRT; 620 AA.  
AC Q96EY0  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE IGHM protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Zhang C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011857; ANH11857.2; -;  
DR PIR; S15590; S15590.  
DR HSP; P01820; 1G7J.  
DR InterPro; IPR003599; Ig-like.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig-MHC.  
DR Pfam; PF07654; C1-set; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 5.  
DR PROSITE; PS00290; IG-MHC; UNKNOWN 3.  
SQ SEQUENCE 620 AA; 68125 MW; 950A1A4A6E8FF27B CRC64;

Query Match 77.8%; Score 486.5; DB 2; Length 620;  
Best Local Similarity 82.8%; Pred. No. 1.2e-39;  
Matches 101; Conservative 3; Mismatches 11; Indels 7; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYVHWSWIRHPKGLGWIGYVYSGSTY 60  
DB 27 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYWSWIRHPKGLGWIGYVYSGSTN 84  
QY 61 YNPGLKSRVTISVDTSKNQFSLKLSVTAADTAVVYCAR-----GGDGKYWGQGTTLTV 115

85 YNPGLKSRVTISVDTSKNQFSLKLSVTAADTAVVYCASQWELPTVGLFYWGQGTTLTV 144

116 SS 117

145 SS 146

## RESULT 10

Q81ZD7 PRELIMINARY; PRT; 130 AA.  
AC Q81ZD7;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Anti-thyroglobulin heavy chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Jang Y.-J., Chung J., Park J.-Y.;  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY145445; AAN64329.1; -;  
DR HSP; P01820; 1G7J.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig-v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
FT NON TER 1  
FT NON TER 130  
SQ SEQUENCE 130 AA; 13901 MW; 036131FC6EC1551E CRC64;  
Query Match 76.6%; Score 478.5; DB 2; Length 130;  
Best Local Similarity 74.6%; Pred. No. 1.5e-39;  
Matches 97; Conservative 9; Mismatches 11; Indels 13; Gaps 3;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYVHWSWIRHPKGLGWIGYVYSGST- 59  
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSSSYYWGWIRHPKGLGWIGYVYSGSTY 60  
QY 60 ----YNPGLKSRVTISVDTSKNQFSLKLSVTAADTAVVYCA-----RGDDGY---KYW 107  
DB 61 SGSPYAPSLRSRVIIISVDTSKNQLSLSSVTAADTAVVYCASPHCSGGGCVAFQHW 120  
QY 108 QGGLTVTVSS 117  
DB 121 QGGLTVTVSS 130  
QY PRELIMINARY; PRT; 492 AA.  
ID Q72374  
AC Q72374;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein DKF2p686C02218 (Fragment).  
GN Name=DKF2p686C02218;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RA Bloeker H., Boecker M., Meves H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX538077; CAD98001.1; -;  
DR HSP; P01820; 1G7J.  
DR InterPro; IPR007110; Ig-like.

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DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760FOCA74B CRC64;

Query Match 76.3%; Score 477; DB 2; Length 492;
Best Local Similarity 75.8%; Pred. No. 8.4e-39;
Matches 91; Conservative 13; Mismatches 13; Indels 4; Gaps 1;

QY 1 QVQLQESGPGCLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYVSGSTY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 32 QLQLQESGPGCLVKPSETLSLTCTVSGGSVSNRYWGWIRQPPGKGLEWIGSIYNYNTY 91
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 YNPSLKSRVTISVDTSKNQFSLKSLSVTAADTAVYYCARGGDG---YKYGQGLTVTVS 116
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 92 YPSLKSRLTIFVDTSKNHFSLRLTSVTAADTAVYYCVRHVEGPGYGFDPWGQGLTVTVS 151
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 117 S 117
Db 152 S 152

RESULT 12
Q84SX2 PRELIMINARY; PRT; 139 AA.
AC Q86SX2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line) of
DE Homo sapiens (human) (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
QY 1 QVQLQESGPGCLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYVSGSTY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 33 QLQLQESGPGCLVKPSETLSLTCTVSGGSISS--YWSWIRQPPGKGLEWIGIYVSGSTN 90
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 YNPSLKSRVTISVDTSKNQFSLKSLSVTAADTAVYYCAR 99
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 91 YNPSLKSRVTISVDTSKNQFSLKSLSVTAADTAVYYCAR 129
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Query Match 75.8%; Score 474; DB 2; Length 139;
Best Local Similarity 93.9%; Pred. No. 4.4e-39;
Matches 93; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 QVQLQESGPGCLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYVSGSTY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 33 QVQLQESGPGCLVKPSETLSLTCTVSGGSISS--YWSWIRQPPGKGLEWIGIYVSGSTN 90
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 YNPSLKSRVTISVDTSKNQFSLKSLSVTAADTAVYYCAR 99
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 91 YNPSLKSRVTISVDTSKNQFSLKSLSVTAADTAVYYCAR 129
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 13
HV2F HUMAN STANDARD; PRT; 129 AA.
ID P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-II region WAH.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=8222235; PubMed=6806818;
RX Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
RT immunoglobulin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
CC -!- MISCELLANEOUS: This chain was isolated from an IgD myeloma
CC protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02099; D2HUWA.
DR HSSP; P01820; IG7J.
DR GlycoSuiteDB; P01824; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 113
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 72.5%; Score 453; DB 1; Length 129;
Best Local Similarity 67.4%; Pred. No. 4.9e-37;
Matches 87; Conservative 11; Mismatches 19; Indels 12; Gaps 1;

QY 1 QVQLQESGPGCLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYVSGSTY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 RLQLQESGPGCLVKPSETLSLTCTVSGGPIRRTGYWGWIRQPPGKGLEWIGYVYTGSIY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 YNPSLKSRVTISVDTSKNQFSLKSLSVTAADTAVYYCARGG-----DGKYYWG 108
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YNPSLGRVTISVDTSRNQFSLNLSMSAADIATMYTCARGNPPYYDITGSDGDDIDVWG 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 109 QGTLTVTVSS 117
   :|||:|||||
Db 121 QGTVTVSS 129
   :|||:|||||

RESULT 14
Q6NYH3 PRELIMINARY; PRT; 478 AA.
AC Q6NVH3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC066594; AA66594.1; -.
DR HSSP; P01820; IA7N.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig ci.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-set; 2.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00407; IGV; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 51856 MW; 5F8B98F60F077256 CRC64;

Query Match 71.2%; Score 445; DB 2; Length 478;
Best Local Similarity 71.1%; Pred. No. 1.2e-35;
Matches 86; Conservative 17; Mismatches 12; Indels 6; Gaps 2;

QY 1 QVQLQSGGPGLVKPSQTLSTCTVSGSGSISSGYTHMSWIRQHPGKGLWIGIYYSGSTY 60
Db 20 QVQLQSGGPGLVKPSQTLSTCTVSGSGSISSGYTHMSWIRQHPGKGLWIGIYYSGSTL 77
QY 61 YNPFLSKSRVTISVDTSKNQPSLKLSSVTAADTAIVYCARGGDG-----YKTWGGGTLVTVS 116
Db 78 YNPFLSKSRVTISVDTSKNQPSLKLSSVTAADTAIVYCARGGDG-----YKTWGGGTLVTVS 137
QY 117 S 117
Db 138 S 138

RESULT 15
Q8WUX4 PRELIMINARY; PRT; 595 AA.
AC Q8WUX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.2; -.
DR PIR; G34964; G34964.
DR HSSP; P01861; IADO.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;

Query Match 69.4%; Score 434; DB 2; Length 595;
Best Local Similarity 71.7%; Pred. No. 1.9e-34;
Matches 91; Conservative 5; Mismatches 19; Indels 12; Gaps 2;

QY 1 QVQLQSGGPGLVKPSQTLSTCTVSGSGSISSGYTHMSWIRQHPGKGLWIGIYYSGSTY 60
Db 27 QVQLQSGGPGLVKPSQTLSTCTVSGSGSISSGYTHMSWIRQHPGKGLWIGIYYSGSTN 84
QY 61 YNPFLSKSRVTISVDTSKNQPSLKLSSVTAADTAIVYCAR-----GGDGKYWGGG 110
Db 85 YNPFLSKSRVTISVDTSKNQPSLKLSSVTAADTAIVYCARVITRASPGTDGRYGDVWGGG 144
QY 111 TLVTSS 117
Db 145 TTVTVSS 151

Search completed: November 9, 2005, 13:05:47
Job time : 61.406 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model  
Run on: November 9, 2005, 11:43:32 ; Search time 74.6015 Seconds  
(without alignment)  
627.306 Million cell updates/sec

Title: US-10-660-357A-9  
Perfect score: 650  
Sequence: 1 QVQLQESGPGLVKPSSETLSL.....WLLPDAFDINGQGTMTVTS 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	650	100.0	121	7 ADC99780	Adc99780 Anti-huma
2	650	100.0	121	7 ADD05384	Add05384 Anti-MUC1
3	650	100.0	121	7 ADF09822	Adf09822 Human ant
4	643	98.9	121	7 ADC99772	Adc99772 Anti-huma
5	643	98.9	121	7 ADC99788	Adc99788 Anti-huma
6	643	98.9	121	7 ADD05376	Add05376 Anti-MUC1
7	643	98.9	121	7 ADD05392	Add05392 Anti-MUC1
8	643	98.9	121	7 ADF09814	Adf09814 Human ant
9	643	98.9	121	7 ADF09830	Adf09830 Human ant
10	598	92.0	121	7 ADC99808	Adc99808 Anti-huma
11	598	92.0	121	7 ADD05412	Add05412 Anti-MUC1
12	598	92.0	121	7 ADF09850	Adf09850 Human ant
13	566.5	87.2	243	8 ADO58076	Ado58076 S9 cell d
14	548	84.3	121	5 ABG92884	Abg92884 Human imm
15	546.5	84.1	121	5 ABB07171	Abb07171 ebvHigM M
16	546.5	84.1	121	8 ADI26658	Adi26658 Human ant
17	546.5	84.1	122	7 ADP03887	Adp03887 Murine-ex
18	546.5	84.1	122	7 ADP03884	Adp03884 Murine-ex
19	545.5	83.9	122	7 ADP03885	Adp03885 Murine-ex
20	545.5	83.9	122	7 ADP03889	Adp03889 Murine-ex
21	541	83.2	119	2 AA27554	Aaw27554 Human Ab
22	541	83.2	119	6 ABJ18676	Abj18676 Antibody
23	540.5	83.2	118	8 ADP22272	Adp22272 Human ant
24	540	83.1	123	6 ADA89258	Ada89258 Human ant
25	539.5	83.0	122	7 ADP03931	Adp03931 Murine-ex

# ALIGNMENTS

RESULT 1

ADC99780  
ID ADC99780 standard; protein; 121 AA.

XX AC ADC99780;

XX AC  
DT 01-JAN-2004 (first entry)

XX DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 9.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.

XX OS Homo sapiens.

XX PN WO2003057838-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041581.

XX PR 28-DEC-2001; 2001US-0346299P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J;

XX DR WPI; 2003-587113/55.

XX N-PSDB; ADC99782.

XX PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
or condition associated with expression of MUC18 in a patient, e.g.  
tumors, cancers, and other malignancies.

XX PS Claim 1; SEQ ID NO 9; 78pp; English.

XX CC The invention relates to a novel isolated monoclonal antibody comprising  
a heavy or light chain amino acid or a heavy or light chain variable  
domain where the antibody binds to MUC18. The monoclonal antibody of the  
invention demonstrates cytostatic activity and may be useful for treating  
a disease or condition associated with the expression of MUC18 on the  
cell surface such as tumours, specifically melanoma, oesophageal,  
pancreatic or colorectal tumours, carcinomas, particularly cervical  
carcinomas and cervical intraepithelial neoplasia and cancers including  
colorectal, breast or lung cancer, as well as other malignancies. The  
current sequence is that of the anti-human MUC18 monoclonal antibody

Adp03864 Murine-ex  
Adp03862 Murine-ex  
Adp03984 Murine-ex  
Adp03973 Murine-ex  
Adp03871 Murine-ex  
Aay15126 Anti-muri  
Adp03886 Murine-ex  
Adp03933 Murine-ex  
Adp03886 Murine-ex  
Abp43199 Human ova  
Adp19313 Heavy cha  
Aaw90287 Human ant  
Abg92888 Human imm  
Adp03868 Murine-ex  
Adp03876 Murine-ex  
Abg97827 Human MPL  
Abg35304 Thrombopo  
Abg97829 Mouse 12E  
Abg35331 Thrombopo  
Aay06718 Antibody  
Ado39737 Human C-m

26 537.5 82.7 120 7 ADP03864  
27 537.5 82.7 120 7 ADP03862  
28 537.5 82.7 121 7 ADP03984  
29 537 82.6 119 7 ADP03973  
30 537 82.6 125 7 ADP03871  
31 536.5 82.5 246 3 AAY15126  
32 535.5 82.4 122 7 ADP03933  
33 534.5 82.2 124 7 ADP03886  
34 534.5 82.2 193 5 ABP43199  
35 533.5 82.1 128 8 ADS19313  
36 532.5 81.9 120 2 AAW90287  
37 532.5 81.9 126 5 ABG92888  
38 532 81.8 125 7 ADP03868  
39 532 81.8 125 7 ADP03876  
40 530.5 81.6 114 5 ABG97827  
41 530.5 81.6 114 5 ABG35304  
42 530.5 81.6 133 5 ABG97829  
43 530.5 81.6 133 5 ABG35331  
44 530.5 81.6 244 2 AAY06718  
45 530.5 81.6 244 8 ADO39737

```
CC heavy chain protein of the invention.
XX
SQ Sequence 121 AA;
    Query Match 100.0%; Score 650; DB 7; Length 121;
    Best Local Similarity 100.0%; Pred. No. 1.5e-47;
    Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGIYYTWTN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGIYYTWTN 60
QY 61 PSLSKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGQ 120
Db 61 PSLSKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGQ 120
QY 121 S 121
Db 121 S 121

RESULT 2
ADD05384
ID ADD05384 standard; protein; 121 AA.
XX
AC ADD05384;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 9.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
XX
OS Homo sapiens.
XX
PN W02003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
WPI; 2003-577496/54.
XX
N-PSDB; ADD05386.

XX
PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
PS Claim 1; SEQ ID NO 9; 87pp; English.
XX
CC The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC sequence represents an anti-MUC18 antibody heavy chain, variable region,
CC protein of the invention.

XX
SQ Sequence 121 AA;
    Query Match 100.0%; Score 650; DB 7; Length 121;
    Best Local Similarity 100.0%; Pred. No. 1.5e-47;
    Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGIYYTWTN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGIYYTWTN 60
QY 61 PSLSKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGQ 120
Db 61 PSLSKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGQ 120
QY 121 S 121
Db 121 S 121

RESULT 3
ADF09822
ID ADF09822 standard; protein; 121 AA.
XX
AC ADF09822;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human anti-MUC18 monoclonal antibody heavy chain #3.
XX
KW cell proliferation inhibition; MUC18 tumour antigen;
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; heavy chain; human.
XX
OS Homo sapiens.
XX
PN W02003057837-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041580.
XX
PR 28-DEC-2001; 2001US-0346414P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
WPI; 2003-598367/56.
XX
N-PSDB; ADF09824.

XX
PT Inhibiting cell proliferation associated with expression of MUC18 tumor
PT antigen, involves incubating and inhibiting cell by administering anti-
PT MUC18 monoclonal antibody.
XX
PS Claim 1; SEQ ID NO 9; 83pp; English.
XX
CC The invention comprises a method for inhibiting cell proliferation
CC associated with expression of MUC18 tumour antigen. The method involves
CC administering anti-MUC18 monoclonal antibody. The method of the invention
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
CC proliferation associated with the expression of MUC18 tumour antigen, the
CC method is preferably useful for inhibiting tumour metastasis. The method
CC is useful for inhibiting cell proliferation in patients with tumours,
CC carcinomas, cancer and other malignancies. The present amino acid
CC sequence represents a heavy chain from an MUC18 tumour antigen-specific
CC monoclonal antibody.
XX
SQ Sequence 121 AA;
    Query Match 100.0%; Score 650; DB 7; Length 121;
    Best Local Similarity 100.0%; Pred. No. 1.5e-47;
    Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	QVQLQESGFLVKPSETLSLTCTVSGGSISSYYWWSWIRQPPGKGLEWIGIYYTWTNNY	60
Db	1	QVQLQESGFLVKPSETLSLTCTVSGGSISSYYWWSWIRQPPGKGLEWIGIYYTWTNNY	60
Qy	61	PSLKSRTVISVDTSKNQFSRLSSVTAADTALYYCARDQGGWLLPDAFDIWGGTWTWYS	120
Db	61	PSLKSRTVISVDTSKNQFSRLSSVTAADTALYYCARDQGGWLLPDAFDIWGGTWTWYS	120
Qy	121	S 121	
Db	121	S 121	
RESULT 4			
ID	ADC99772		
AD	ADC99772	standard; protein; 121 AA.	
XX	AC		
XX	ADC99772;		
XX			
DT	01-JAN-2004	(first entry)	
XX			
DE	Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 1.		
XX			
KW	anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;		
KW	cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;		
KW	cervical carcinoma; intraepithelial neoplasia; colorectal; breast;		
KW	lung cancer; human.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2003057838-A2.		
XX			
PD	17-JUL-2003.		
XX			
PF	26-DEC-2002; 2002WO-US041581.		
XX			
PR	28-DEC-2001; 2001US-0346299P.		
XX			
PA	(ABGE-) ARGENTX INC.		
XX			
PI	Gudas J;		
XX			
DR	WPI; 2003-587113/55.		
XX			
DR	N-PSDB; ADC99774.		
XX			
PT	New human anti-MUC18 monoclonal antibodies, useful for treating a disease		
PT	or condition associated with expression of MUC18 in a patient, e.g.		
PT	tumors, cancers, and other malignancies.		
XX			
PS	Claim 1; SEQ ID NO 1; 78pp; English.		
XX			
CC	The invention relates to a novel isolated monoclonal antibody comprising		
CC	a heavy or light chain amino acid or a heavy or light chain variable		
CC	domain where the antibody binds to MUC18. The monoclonal antibody of the		
CC	invention demonstrates cytostatic activity and may be useful for treating		
CC	a disease or condition associated with the expression of MUC18 on the		
CC	cell surface such as tumours, specifically melanoma, oesophageal,		
CC	pancreatic or colorectal tumours, carcinomas, particularly cervical		
CC	carcinomas and cervical intraepithelial neoplasia and cancers including		
CC	colorectal, breast or lung cancer, as well as other malignancies. The		
CC	current sequence is that of the anti-human MUC18 monoclonal antibody		
CC	heavy chain protein of the invention.		
XX			
SQ	Sequence 121 AA;		
Query Match	98.9%;	Score 643;	DB 7; Length 121;
Best Local Similarity	98.3%;	Pred. No. 5.8e-47;	
Matches 119;	Conservative	2; Mismatches	0; Indels 0; Gaps 0;
Qy	1	QVQLQESGFLVKPSETLSLTCTVSGGSISSYYWWSWIRQPPGKGLEWIGIYYTWTNNY	60
Db	1	QVQLQESGFLVKPSETLSLTCTVSGGSISSYYWWSWIRQPPGKGLEWIGIYYTWTNNY	60

QY	61	PSLSRVITISVDTSKNOFSLRLSSVTAADTALYYCARDQGOWLLPDAFDIWGGGTWTVTS	120
Dd	61	PSLSRVITISVDTSKNOFSLRLSSVTAADTAVYYCARDQGOWLLPDAFDIWGGGTWTVTS	120
QY	121	S	121
Dd	121	S	121
 RESULT 5 ADC99788			
ID	ADC99788	standard; protein; 121 AA.	
XX	AC	ADC99788;	
XX	DT	01-JAN-2004 (first entry)	
XX	DE	Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 17.	
XX	KW	anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;	
KW	KW	cystostatic; melanoma; oesophageal; pancreatic; colorectal tumour;	
KW	KW	cervical carcinoma; intraepithelial neoplasia; colorectal; breast;	
XX	XX	lung cancer; human.	
OS		Homo sapiens.	
XX	XX	WO2003057838-A2.	
PD	PD	17-JUL-2003.	
XX	PF	26-DEC-2002; 2002WO-US041581.	
XX	PR	28-DEC-2001; 2001US-0346299P.	
XX	PA	(ABGE-) ABGENIX INC.	
XX	PI	Gudas J;	
DR	DR	WPI; 2003-587113/55.	
XX	N-	PSDB; ADC99790.	
PT	PT	New human anti-MUC18 monoclonal antibodies, useful for treating a disease	
PT	PT	or condition associated with expression of MUC18 in a patient, e.g.	
FT	FT	tumors, cancers, and other malignancies.	
XX	FS	Claim 1; SEQ ID NO 17; 78pp; English.	
XX	CC	The invention relates to a novel isolated monoclonal antibody comprising	
CC	CC	a heavy or light chain amino acid or a heavy or light chain variable	
CC	CC	domain where the antibody binds to MUC18. The monoclonal antibody of the	
CC	CC	invention demonstrates cytostatic activity and may be useful for treating	
CC	CC	a disease or condition associated with the expression of MUC18 on the	
CC	CC	cell surface such as tumors, specifically melanoma, oesophageal,	
CC	CC	pancreatic or colorectal tumors, carcinomas, particularly cervical	
CC	CC	carcinomas and cervical intraepithelial neoplasia and cancers including	
CC	CC	colorectal, breast or lung cancer, as well as other malignancies. The	
CC	CC	current sequence is that of the anti-human MUC18 monoclonal antibody	
XX	XX	heavy chain protein of the invention.	
SQ		Sequence 121 AA;	
 Query Match                      98.9%; Score 643; DB 7; Length 121; Best Local Similarity    98.3%; Pred. No. 5.8e-47; Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0			
Qy	1	QVQLQESGPGLVKPSETLSLTCTVSGGSISYYWSWIROPKKGLEWIGIYYTWTNYN	60
Dd	1	QVQLQESGPGLVKPSETLSLTCTVSGGSISYYWSWIROPKKGLEWIGIYYTWTNYN	60
Qy	61	PSLSRVITISVDTSKNOFSLRLSSVTAADTALYYCARDQGOWLLPDAFDIWGGGTWTVTS	120
Dd	61	PSLSRVITISVDTSKNOFSLRLSSVTAADTAVYYCARDQGOWLLPDAFDIWGGGTWTVTS	120

QY	61	PSLSRVITISVDTSKNOFSLRLSSVTAADTALYYCARDQGOWLLPDAFDIWGGGTWTVTS	120
Db	61	PSLSRVITISVDTSKNOFSLRLSSVTAADTALYYCARDQGOWLLPDAFDIWGGGTWTVTS	120
QY	121	S	121
Db	121	S	121
 RESULT 5 ADC99788			
ID	ADC99788	standard; protein; 121 AA.	
XX	AC	ADC99788;	
XX	DT	01-JAN-2004 (first entry)	
XX	DE	Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 17.	
XX	KW	anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;	
KW	KW	cystostatic; melanoma; oesophageal; pancreatic; colorectal tumour;	
KW	KW	cervical carcinoma; intraepithelial neoplasia; colorectal; breast;	
XX	XX	lung cancer; human.	
OS	Homo sapiens.		
XX	WO	2003057838-A2.	
PD	17-JUL-2003.		
XX	PF	26-DEC-2002; 2002WO-US041581.	
XX	PR	28-DEC-2001; 2001US-0346299P.	
XX	PA	(ABGE-) ABGENIX INC.	
PI	Gudas J;		
DR	WPI; 2003-587113/55.		
N-PSDB; ADC99790.			
PT	New human anti-MUC18 monoclonal antibodies, useful for treating a disease		
PT	or condition associated with expression of MUC18 in a patient, e.g.		
FT	tumors, cancers, and other malignancies.		
XX	Claim 1; SEQ ID NO 17; 78pp; English.		
CC	The invention relates to a novel isolated monoclonal antibody comprising		
CC	a heavy or light chain amino acid or a heavy or light chain variable		
CC	domain where the antibody binds to MUC18. The monoclonal antibody of the		
CC	invention demonstrates cytostatic activity and may be useful for treating		
CC	a disease or condition associated with the expression of MUC18 on the		
CC	cell surface such as tumors, specifically melanoma, oesophageal,		
CC	pancreatic or colorectal tumors, carcinomas, particularly cervical		
CC	carcinomas and cervical intraepithelial neoplasia and cancers including		
CC	colorectal, breast or lung cancer, as well as other malignancies. The		
CC	current sequence is that of the anti-human MUC18 monoclonal antibody		
CC	heavy chain protein of the invention.		
XX	Sequence 121 AA;		
 Query Match                      98.9%; Score 643; DB 7; Length 121; Best Local Similarity    98.3%; Pred. No. 5.8e-47; Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0			
QY	1	QVQLQESGPGLVKPSETLSLTCTVSGGSISYSYWIRQPPKGLEWIGIYYTWTNYN	60
Db	1	QVQLQESGPGLVKPSETLSLTCTVSGGSISYSYWIRQPPKGLEWIGIYYTWTNYN	60
QY	61	PSLSRVITISVDTSKNOFSLRLSSVTAADTALYYCARDQGOWLLPDAFDIWGGGTWTVTS	120
Db	61	PSLSRVITISVDTSKNOFSLRLSSVTAADTALYYCARDQGOWLLPDAFDIWGGGTWTVTS	120

QY 121 S 121  
Db 121 S 121

## RESULT 6

ADD05376  
ID ADD05376 standard; protein; 121 AA.

XX  
AC ADD05376;

DT 01-JAN-2004 (first entry)

XX Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 1.

XX monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.

XX Homo sapiens.

XX WO2003057006-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041582.

XX 28-DEC-2001; 2001US-0346460P.

XX (ABGE-) ABGENIX INC.

XX Gudas J, Bar-Eli M;

XX WPI; 2003-577496/54.

DR N-PSDB; ADD05378.

XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
PT associated with melanoma, or increasing survival of an animal having a  
PT metastatic tumor.

XX Claim 1; SEQ ID NO 1; 87pp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting  
CC tumour growth in an animal. The tumour inhibition process comprises  
CC selecting an animal in need of treatment for a tumour, providing a  
CC monoclonal antibody comprising a heavy chain amino acid, where the  
CC antibody consists of any one of 10 fully defined sequences of 117-123  
CC amino acids given in the specification, and where the monoclonal antibody  
CC binds MUC18, and contacting the tumour with the antibody resulting in  
CC inhibited proliferation of the cells. The monoclonal antibody has  
CC cytostatic and can be used in the production of a vaccine. The monoclonal  
CC antibodies against the MUC18 antigen are useful for diagnosing and  
CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or  
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
CC increasing survival of an animal having a metastatic tumour. This  
CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
CC protein of the invention.

XX Sequence 121 AA;

Query Match 98.9%; Score 643; DB 7; Length 121;  
Best Local Similarity 98.3%; Pred. No. 5.8e-47;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKLEWIGYIYTTNTYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKLEWIGYIYTTNTYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGGGTWTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGGTWTVTS 120

QY 121 S 121  
Db 121 S 121

## RESULT 7

ADD05392  
ID ADD05392 standard; protein; 121 AA.

XX  
AC ADD05392;

DT 01-JAN-2004 (first entry)

XX Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 17.

XX monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.

XX Homo sapiens.

XX WO2003057006-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041582.

XX 28-DEC-2001; 2001US-0346460P.

XX (ABGE-) ABGENIX INC.

XX Gudas J, Bar-Eli M;

XX WPI; 2003-577496/54.

DR N-PSDB; ADD05394.

XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
PT associated with melanoma, or increasing survival of an animal having a  
PT metastatic tumor.

XX Claim 1; SEQ ID NO 17; 87pp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting  
CC tumour growth in an animal. The tumour inhibition process comprises  
CC selecting an animal in need of treatment for a tumour, providing a  
CC monoclonal antibody comprising a heavy chain amino acid, where the  
CC antibody consists of any one of 10 fully defined sequences of 117-123  
CC amino acids given in the specification, and where the monoclonal antibody  
CC binds MUC18, and contacting the tumour with the antibody resulting in  
CC inhibited proliferation of the cells. The monoclonal antibody has  
CC cytostatic and can be used in the production of a vaccine. The monoclonal  
CC antibodies against the MUC18 antigen are useful for diagnosing and  
CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or  
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
CC increasing survival of an animal having a metastatic tumour. This  
CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
CC protein of the invention.

XX Sequence 121 AA;

Query Match 98.9%; Score 643; DB 7; Length 121;  
Best Local Similarity 98.3%; Pred. No. 5.8e-47;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKLEWIGYIYTTNTYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKLEWIGYIYTTNTYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGGGTWTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGGTWTVTS 120

QY 121 S 121

```

Db      121 S 121
RESULT 8
ADF09814
ID      ADF09814 standard; protein; 121 AA.
XX
AC
XX      ADF09814;
XX
AC
XX      12-FEB-2004 (first entry)
XX
DT
DE
XX      Human anti-MUC18 monoclonal antibody heavy chain #1.
XX
DE
XX      cell proliferation inhibition; MUC18 tumour antigen;
XX      anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
XX      carcinoma; cancer; malignancy; heavy chain; human.
XX
OS      Homo sapiens.
XX
XX      WO2003057837-A2.
XX
PN
XX
XX      17-JUL-2003.
XX
PD
XX
XX      26-DEC-2002; 2002WO-US041580.
XX
XX      28-DEC-2001; 2001US-0346414P.
XX
PR
XX
XX      (ABGE-) ABGENIX INC.
XX
PA
XX
XX      Gudas J;
XX
PI
XX
XX      WPI; 2003-598367/56.
XX
DR
XX      N-PSDB; ADF09816.
XX
XX
XX      Inhibiting cell proliferation associated with expression of MUC18 tumor
XX      antigen, involves incubating and inhibiting cell by administering anti-
XX      MUC18 monoclonal antibody.
XX
PS      Claim 1; SEQ ID NO 1; 83pp; English.
XX
XX      The invention comprises a method for inhibiting cell proliferation
XX      associated with expression of MUC18 tumour antigen. The method involves
XX      administering anti-MUC18 monoclonal antibody. The method of the invention
XX      is useful for inhibiting cell (e.g. melanoma or tumour cell)
XX      proliferation associated with the expression of MUC18 tumour antigen, the
XX      method is preferably useful for inhibiting tumour metastasis. The method
XX      is useful for inhibiting cell proliferation in patients with tumours,
XX      carcinomas, cancer and other malignancies. The present amino acid
XX      sequence represents a heavy chain from an MUC18 tumour antigen-specific
XX      monoclonal antibody.
XX
SQ      Sequence 121 AA;
Query Match      98.9%; Score 643; DB 7; Length 121;
Best Local Similarity 98.3%; Pred. No. 5.8e-47;
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYVTTNYN 60
      |||
Db      1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYVTTNYN 60
      |||
QY      61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDWGGTMTVTS 120
      |||
Db      61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDWGGTMTVTS 120
      |||
QY      121 S 121
      |||
Db      121 S 121
      |||
RESULT 10
ADC99808
ID      ADC99808 standard; protein; 121 AA.
XX
AC
XX      ADC99808;
XX
AC
XX      01-JAN-2004 (first entry)
XX
DT
DE
XX

```

DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 37.  
 XX  
 KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
 KW cytotatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
 KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
 KW lung cancer; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003057838-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 26-DEC-2002; 2002WO-US041581.  
 XX  
 PR 28-DEC-2001; 2001US-0346299P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas J;  
 XX  
 DR WPI; 2003-587113/55.  
 DR N-PSDB; ADC99810.  
 XX  
 XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
 PT or condition associated with expression of MUC18 in a patient, e.g.  
 PT tumors, cancers, and other malignancies.  
 PT  
 XX  
 PS Claim 1; SEQ ID NO 37; 78pp; English.  
 XX  
 CC The invention relates to a novel isolated monoclonal antibody comprising  
 CC a heavy or light chain amino acid or a heavy or light chain variable  
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
 CC invention demonstrates cytostatic activity and may be useful for treating  
 CC a disease or condition associated with the expression of MUC18 on the  
 CC cell surface such as tumours, specifically melanoma, oesophageal,  
 CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
 CC carcinomas and cervical intraepithelial neoplasia and cancers including  
 CC colorectal, breast or lung cancer, as well as other malignancies. The  
 CC current sequence is that of the anti-human MUC18 monoclonal antibody  
 CC heavy chain protein of the invention.  
 CC  
 XX  
 SQ Sequence 121 AA;  
 Query Match 92.0%; Score 598; DB 7; Length 121;  
 Best Local Similarity 90.9%; Pred. No. 3.8e-43;  
 Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISISSYVWSWIROPKGLWIGVYYTWTNYYN 60  
 DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISISSYVWSWIROPKGLWIGVYYTWTNYYN 60  
 QY 61 PSLKSRVTISVDTSKNQFSLRLSVTAADTALYYCARDQGWLLPDAFDIWGGTVMVTVS 120  
 DB 61 PSLKSRVTISVDTSKNQFSLRLSVTAADTALYYCARDQGWLLPDAFDIWGGTVMVTVS 120  
 QY 121 S 121  
 DB 121 S 121  
 RESULT 11  
 ADD05412  
 ID ADD05412 standard; protein; 121 AA.  
 XX  
 AC ADD05412;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 37.  
 DE  
 KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
 KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.

XX Homo sapiens.  
 XX  
 PN WO2003057006-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 26-DEC-2002; 2002WO-US041582.  
 XX  
 PR 28-DEC-2001; 2001US-0346460P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas J, Bar-Eli M;  
 XX  
 DR WPI; 2003-577496/54.  
 DR N-PSDB; ADD05414.  
 XX  
 XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
 PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
 PT associated with melanoma, or increasing survival of an animal having a  
 PT metastatic tumor.  
 PT  
 XX  
 PS Claim 1; SEQ ID NO 37; 87pp; English.  
 XX  
 CC The invention relates to a novel monoclonal antibody used for inhibiting  
 CC tumor growth in an animal. The tumor inhibition process comprises  
 CC selecting an animal in need of treatment for a tumour, providing a  
 CC monoclonal antibody comprising a heavy chain amino acid, where the  
 CC antibody consists of any one of 10 fully defined sequences of 117-123  
 CC amino acids given in the specification, and where the monoclonal antibody  
 CC binds MUC18, and contacting the tumour with the antibody resulting in  
 CC inhibited proliferation of the cells. The monoclonal antibody has  
 CC cytostatic and can be used in the production of a vaccine. The monoclonal  
 CC antibodies against the MUC18 antigen are useful for diagnosing and  
 CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or  
 CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
 CC increasing survival of an animal having a metastatic tumour. This  
 CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
 CC protein of the invention.  
 CC  
 XX  
 SQ Sequence 121 AA;  
 Query Match 92.0%; Score 598; DB 7; Length 121;  
 Best Local Similarity 90.9%; Pred. No. 3.8e-43;  
 Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISISSYVWSWIROPKGLWIGVYYTWTNYYN 60  
 DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISISSYVWSWIROPKGLWIGVYYTWTNYYN 60  
 QY 61 PSLKSRVTISVDTSKNQFSLRLSVTAADTALYYCARDQGWLLPDAFDIWGGTVMVTVS 120  
 DB 61 PSLKSRVTISVDTSKNQFSLRLSVTAADTALYYCARDQGWLLPDAFDIWGGTVMVTVS 120  
 QY 121 S 121  
 DB 121 S 121  
 RESULT 12  
 ADF09850  
 ID ADF09850 standard; protein; 121 AA.  
 XX  
 AC ADF09850;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human anti-MUC18 monoclonal antibody heavy chain #10.  
 DE  
 KW cell proliferation inhibition; MUC18 tumour antigen;  
 KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
 KW carcinoma; cancer; malignancy; heavy chain; human.



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XX OS Homo sapiens.
XX PN WO2003057837-A2.
XX PD 17-JUL-2003.
XX PF 26-DEC-2002; 2002WO-US041580.
XX PR 28-DEC-2001; 2001US-0346414P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas J;
XX PT WPI; 2003-598367/56.
XX DR N-PSDB; ADF09852.
XX PT Inhibiting cell proliferation associated with expression of MUC18 tumor
XX PT antigen, involves incubating and inhibiting cell by administering anti-
XX PT MUC18 monoclonal antibody.
XX PS Claim 1; SEQ ID NO 37; 83pp; English.
XX CC The invention comprises a method for inhibiting cell proliferation
XX CC associated with expression of MUC18 tumour antigen. The method involves
XX CC administering anti-MUC18 monoclonal antibody. The method of the invention
XX CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
XX CC proliferation associated with the expression of MUC18 tumour antigen, the
XX CC method is preferably useful for inhibiting tumour metastasis. The method
XX CC is useful for inhibiting cell proliferation in patients with tumours,
XX CC carcinomas, cancer and other malignancies. The present amino acid
XX CC sequence represents a heavy chain from an MUC18 tumour antigen-specific
XX CC monoclonal antibody.
XX SQ Sequence 121 AA;
Query Match 92.0%; Score 598; DB 7; Length 121;
Best Local Similarity 90.9%; Pred. No. 3.8e-43;
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISSTYWSMIROPPGKLEWIGYIYTTNTYN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISSTYWSMIROPPGKLEWIGYIYTTNTYN 60
QY 61 PSLKSRVTISVDTSKNQPSRLSSVTAADTALYYCARDQGWLLPDAFDIWGGTWTVS 120
Db 61 PSLKSRVTISVDTSKNQPSRLSSVTAADTALYYCARDQGWLLPDAFDIWGGTWTVS 120
QY 121 S 121
Db 121 S 121
RESULT 13
ADO58076
ID ADO58076 standard; protein; 243 AA.
XX AC ADO58076;
XX DT 12-AUG-2004 (first entry)
XX DE S9 cell derived human scFVVL-VH protein.
XX KW B cell; surface immunoglobulin; Ig; binding site; antigen; human CD28;
XX KW closed system; detection laser-beam; catcher tube;
XX KW electrochemical device; fluorescence activated cell sorter; FACS;
XX KW antibody variable region; human.
XX OS Homo sapiens.
XX PN WO2004044584-A1.
XX
```

```
PD 27-MAY-2004.
XX 12-NOV-2003; 2003WO-EP012664.
XX PR 13-NOV-2002; 2002EP-00025335.
XX PA (MICR-) MICROMET AG.
XX PI Baeuerle P, Hoffmann P, Weinberger S, Kischel R;
XX PT WPI; 2004-449579/42.
XX DR N-PSDB; ADO58077.
XX PT Identifying a B cell carrying a surface immunoglobulin molecule having a
XX PT binding site for an antigen of interest, useful for constructing
XX PT therapeutic antibodies, comprises contacting a sample with the antigen
XX PT and a receptor.
XX PS Claim 22; SEQ ID NO 76; 156pp; English.
XX CC The invention relates to a novel method for identifying a B cell carrying
XX CC a surface immunoglobulin (Ig) molecule having a binding site for an
XX CC antigen of interest. The method comprises contacting a sample putatively
XX CC specifically binding to the Ig molecule, and assessing the presence of
XX CC the detectable signal. The invention further comprises: an antibody
XX CC generated by the method above which is specific for human CD28 or
XX CC comprising an amino acid(s) sequence(s) given in the specification,
XX CC and/or are encoded by a nucleic acid sequence(s) also given in the
XX CC specification; and a device for assessing the presence of a detectable
XX CC signal defined above, where the device comprises a closed system for the
XX CC detection laser-beam and a catcher tube, and where the B cell of interest
XX CC can be collected as a single cell by means of an electrochemical device,
XX CC which is triggered by an electric signal generated by the fluorescence
XX CC activated cell sorter (FACS) device, where the electrochemical device
XX CC moves the nozzle of the steady catcher tube liquid stream for a
XX CC programmed time over a collecting tube, microtiter plate or other
XX CC container after a B cell is sorted. The method is useful for identifying
XX CC a B cell carrying a surface Ig molecule having a binding site for an
XX CC antigen of interest. The method is also useful for cloning of antibody
XX CC variable regions from the identified B cells, which may subsequently be
XX CC employed in the construction of proteins such as antibodies or its
XX CC fragments or derivatives useful in therapeutic approaches. The method is
XX CC useful as an alternative to phage display for the gain of antibodies or
XX CC its fragments. This sequence represents an S2 cell derived human
XX CC polypeptide of the invention.
XX SQ Sequence 243 AA;
Query Match 87.2%; Score 566.5; DB 8; Length 243;
Best Local Similarity 90.1%; Pred. No. 3.6e-40;
Matches 109; Conservative 6; Mismatches 5; Indels 1; Gaps 1;
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISSTYWSMIROPPGKLEWIGYIYTTNTYN 60
Db 124 QVQLQESGPGLVKPSSETLSLTCTVSGSISSTYWSMIROPPGKLEWIGYIYTTNTYN 183
QY 61 PSLKSRVTISVDTSKNQPSRLSSVTAADTALYYCARDQGWLLPDAFDIWGGTWTVS 120
Db 184 PSLKSRVTISVDTSKNQPSRLSSVTAADTALYYCARDQGWLLPDAFDIWGGTWTVS 242
QY 121 S 121
Db 243 S 243
RESULT 14
AEG92884
ID AEG92884 standard; protein; 121 AA.
XX AC AEG92884;
XX DT 19-NOV-2002 (first entry)
XX
```

XX	Human immunoglobulin variable light domain #1.
DE	Immunoglobulin; variable heavy chain; variable light chain; human;
XX	G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;
KW	immunologic deficiency syndrome; blood protein disorder; nephritis;
KW	ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
KW	histiocytosis; chemotaxis; infectious disease; autoimmune disease;
KW	Addison's disease; dermatitis; rheumatoid arthritis; allergy;
KW	neurodegenerative disorder; viral infection; poxvirus infection; HIV;
KW	human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
KW	Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;
KW	Lymphocytopenia.
XX	Homo sapiens.
OS	WO200264612-A2.
PN	22-AUG-2002.
XX	08-FEB-2002; 2002WO-US003634.
PF	09-FEB-2001; 2001US-00779880.
PR	09-FEB-2001; 2001WO-US004155.
PR	12-JUN-2001; 2001US-0297257P.
PR	08-AUG-2001; 2001US-0310458P.
PR	12-OCT-2001; 2001US-0328447P.
PR	21-DEC-2001; 2001US-0341725P.
XX	(HUMA-) HUMAN GENOME SCI INC.
PA	Roschke V, Rosen CA, Ruben SW;
PI	WPI; 2002-643455/69.
DR	N-PDSB; ABS68607.
XX	New human G-protein Chemokine Receptor gene (HDGNR10) useful for
PT	treating, preventing, ameliorating or monitoring diseases or disorders
PT	associated with aberrant expression of HDGNR10 e.g. cancer.
PT	Example 55; Fig 4; 562pp; English.
PS	The invention describes an isolated polynucleotide encoding a first
XX	antibody at least 95-100% identical to a second antibody consisting of an
CC	amino acid sequence comprising at least one, two or three CDR regions of
CC	a variable heavy (VH) or variable light (VL) domain of the antibody
CC	expressed by a hybridoma cell line consisting of XF3.5f1, XF11.f1f8,
CC	XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9B6, XF27/28.7D5, XF27/28.1B85,
CC	XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
CC	is useful treating, preventing, ameliorating, prognosing or monitoring
CC	cancers or other diseases or disorders e.g. immunologic deficiency
CC	syndromes such as blood protein disorders and ataxia telangiectasia,
CC	inflammation associated disorders such as endotoxin lethality, nephritis
CC	and inflammatory bowel disease, conditions associated with an increase in
CC	certain haematopoietic cells such as histiocytosis, defective or aberrant
CC	chemotaxis of immune cells or T-cell antigen presenting cell interaction,
CC	an infectious disease, an autoimmune disease such as Addison's disease,
CC	dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
CC	disorder, a viral infection e.g. HIV infection, cytomegalovirus or
CC	poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,
CC	cardiovascular disorders such as atherosclerosis, lymphocytopenia, or a
CC	disease or disorder associated with aberrant expression of novel human G-
CC	protein chemokine receptor (CCR5) HDGNR10. This is the amino acid
CC	sequence of human immunoglobulin sequence associated with the antibodies
CC	against HDGNR10
XX	Sequence 121 AA;
SQ	Query Match 84.3%; Score 548; DB 5; Length 121;
	Best Local Similarity 86.0%; Pred. No. 6.6e-39;
	Matches 104; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
QY	1 QVQLQESGPGLVKPESETLSLTCTVSGGISISFYMSWIROPAGKGLDWIGRIYTSNTNYYN 60

CC damaged as by trauma. The present sequence represents the ebvHgm  
CC MS19D10 heavy chain variable region amino acid sequence

XX  
SQ Sequence 121 AA;

Query Match 84.1%; Score 546.5; DB 5; Length 121;  
Best Local Similarity 87.6%; Pred. No. 8.8e-39;  
Matches 106; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGYIYYTWTNIN 60

Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGYIYYGGININ 60

Qy 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVS 120

Db 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARSAQQQLV-YFVDYWGQGLVTVS 119

Qy 121 S 121

Db 120 S 120

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Job time : 75.6015 secs

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OM protein - protein search, using sw model

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480.403 Million cell updates/sec

Title: US-10-660-357A-9

Perfect score: 650

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	541	83.2	119	3	US-09-025-769B-39
2	541	83.2	119	3	US-09-025-769B-65
3	541	83.2	119	4	US-09-490-070A-39
4	541	83.2	119	4	US-09-490-070A-65
5	541	83.2	119	4	US-09-490-153-39
6	541	83.2	119	4	US-09-490-153-65
7	541	83.2	119	4	US-09-490-324-39
8	541	83.2	119	4	US-09-490-324-65
9	532.5	81.9	118	3	US-09-025-769B-25
10	532.5	81.9	118	4	US-09-490-070A-25
11	532.5	81.9	118	4	US-09-490-153-25
12	532.5	81.9	118	4	US-09-490-324-25
13	532.5	81.9	120	4	US-09-424-840B-20
14	530.5	81.6	244	3	US-08-918-148-79
15	530.5	81.6	244	4	US-09-138-091A-77
16	516.5	79.5	473	3	US-09-049-672A-4
17	503	77.4	142	2	US-08-480-774A-2
18	501	77.1	117	4	US-09-720-493-2
19	500.5	77.0	139	4	US-09-471-276-837
20	499.5	76.8	122	1	US-08-360-125-11
21	499.5	76.8	122	2	US-08-450-578-11
22	499.5	76.8	122	2	US-09-017-628-11
23	499.5	76.8	122	2	US-09-014-880-11
24	499.5	76.8	122	4	US-08-450-363-11
25	499.5	76.8	122	4	US-09-467-903-11
26	495.5	76.2	487	4	US-09-800-729-145
27	489	75.2	116	3	US-08-545-809A-140

28	486	74.8	119	1	US-08-360-125-5
29	486	74.8	119	2	US-08-450-578-5
30	486	74.8	119	2	US-09-017-628-5
31	486	74.8	119	2	US-09-014-880-5
32	486	74.8	119	4	US-08-450-363-5
33	486	74.8	119	4	US-09-467-903-5
34	485	73.9	172	4	US-08-652-816A-10
35	480.5	73.9	172	4	US-09-472-087-7
36	480.5	73.9	172	4	US-09-472-087-86
37	480	73.8	123	3	US-08-793-450-4
38	478	73.5	118	3	US-08-545-809A-142
39	477	73.4	472	3	US-08-793-450-8
40	473.5	72.8	139	4	US-09-203-768A-2
41	472	72.6	155	4	US-09-471-276-888
42	471.5	72.5	118	4	US-09-343-698-6
43	471.5	72.5	118	4	US-08-325-955-6
44	470.5	72.4	832	3	US-08-630-820-7
45	470.5	72.4	832	4	US-09-273-453-7

ALIGNMENTS

RESULT 1  
US-09-025-769B-39  
; Sequence 39, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-39

Query Match 83.2%; Score 541, DB 3; Length 119;  
Best Local Similarity 86.8%; Pred. No. 5.2e-46;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;



Patent No. 6696248  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-070A-65  
Query Match 83.2%; Score 541; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 5.2e-46;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGYIYYTWTN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGYIYYSGT 60  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDADFQGWGTW 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARWGGDGFY--AMDYWGQGT 118  
QY 121 S 121  
Db 119 S 119  
RESULT 5  
US-09-490-153-39  
Sequence 39, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-153-39  
Query Match 83.2%; Score 541; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 5.2e-46;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGYIYYTWTN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGYIYYSGT 60  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDADFQGWGTW 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARWGGDGFY--AMDYWGQGT 118  
QY 121 S 121  
Db 119 S 119  
RESULT 6  
US-09-490-153-65  
Sequence 65, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York





; FILING DATE: 18-FEB-1998  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-324-65  
  
Query Match 83.2%; Score 541; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 5.2e-46;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;  
  
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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGIYYTWTNYYN 60  
  
Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGQGTWTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARWGGDGFY--ANDYWGQGTWTVTS 118  
  
Qy 121 S 121  
Db 119 S 119  
  
RESULT 9  
US-09-025-769B-25  
; Sequence 25, Application US/09025769B  
; Patent No. 630064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000

; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 118 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-025-769B-25  
  
Query Match 81.9%; Score 532.5; DB 3; Length 118;  
Best Local Similarity 85.1%; Pred. No. 3.5e-45;  
Matches 103; Conservative 7; Mismatches 8; Indels 3; Gaps 1;  
  
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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGIYYTWTNYYN 60  
  
Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGQGTWTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARGRG--GGVFDYWGQGTWTVTS 117  
  
Qy 121 S 121  
Db 118 S 118  
  
RESULT 10  
US-09-490-070A-25  
; Sequence 25, Application US/09490070A  
; Patent No. 6696248  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
; White & McAuliffe  
; STREET: 1666 K Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,070A  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Colin G. Sandercock, Esq.  
; REGISTRATION NUMBER: 31,298  
; REFERENCE/DOCKET NUMBER: 37629-0005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 912-2000  
; TELEFAX: (202) 912-2020  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 118 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:40:37 ; Search time 67.2222 Seconds  
(without alignments)  
753.137 Million cell updates/sec

Title: US-10-660-357A-9

Perfect score: 650

Sequence: 1 QVQLQESGPGLVKPSSTLSL.....WLLPDAFDIGQGTWMTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
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- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	650	100.0	121	14	US-10-330-613-9
2	650	100.0	121	14	US-10-330-530-9
3	650	100.0	121	16	US-10-660-357-9
4	643	98.9	121	14	US-10-330-613-1
5	643	98.9	121	14	US-10-330-613-17
6	643	98.9	121	14	US-10-330-530-1
7	643	98.9	121	14	US-10-330-530-17
8	643	98.9	121	16	US-10-660-357-1
9	643	98.9	121	16	US-10-660-357-17
10	598	92.0	121	14	US-10-330-613-37
11	598	92.0	121	14	US-10-330-530-37
Sequence 9, Appli					
Sequence 9, Appli					
Sequence 9, Appli					
Sequence 1, Appli					
Sequence 17, Appli					
Sequence 17, Appli					
Sequence 1, Appli					
Sequence 17, Appli					
Sequence 37, Appli					

ALIGNMENTS

RESULT 1  
US-10-330-613-9  
; Sequence 9, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-9

Query Match 100.0%; Score 650; DB 14; Length 121;  
Best Local Similarity 100.0%; Pred. No. 3.5e-49;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 QVQLQESGPGLVKPSSTLSLTCTVSGGSISSYVSWIRQPPGKLEWIGYIYTTWNTYN 60  
QY 61 PSLSKRVTTISVDTSKNQFSLRSSVTAADTALYYCARDQOGWLLPDAFDIGQGTWMTVS 120  
Db 61 PSLSKRVTTISVDTSKNQFSLRSSVTAADTALYYCARDQOGWLLPDAFDIGQGTWMTVS 120  
QY 121 \$ 121

Sequence 37, Appli  
Sequence 142, App  
Sequence 109, App  
Sequence 60, Appl  
Sequence 60, Appl  
Sequence 11, Appl  
Sequence 24, Appl  
Sequence 27, Appl  
Sequence 23, Appl  
Sequence 25, Appl  
Sequence 29, Appl  
Sequence 5, Appli  
Sequence 178, App  
Sequence 102, App  
Sequence 71, Appl  
Sequence 90, Appl  
Sequence 4, Appli  
Sequence 154, App  
Sequence 143, App  
Sequence 11, Appl  
Sequence 37, Appl  
Sequence 73, Appl  
Sequence 94, Appl  
Sequence 5, Appli  
Sequence 26, Appl  
Sequence 4331, Ap  
Sequence 10, Appl  
Sequence 10, Appl  
Sequence 24, Appl  
Sequence 20, Appl  
Sequence 56, Appl  
Sequence 68, Appl

D**b** 121 S 121

## RESULT 2

US-10-330-530-9  
; Sequence 9, Application US/10330530  
; Publication No. US20030152514A1

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, GENERAL INFORMATION:
, APPLICANT: Gudgas, Jean
, TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
, FILE REFERENCE: AEGENIX.031A
, CURRENT APPLICATION NUMBER: US/10/330,530
, CURRENT FILING DATE: 2002-12-26
, PRIOR APPLICATION NUMBER: US 60/346414
, PRIOR FILING DATE: 2001-12-18
, NUMBER OF SEQ ID NOS: 40
, SOFTWARE: FastSEQ for Windows Version 4.0
, SEQ ID NO 9
, LENGTH: 121
, TYPE: PRT
, ORGANISM: Homo Sapiens
, US-10-330-530-9

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Query Match      100.0%; Score 650; DB 14; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.5e-49;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	QVQLQESGGGLVQPKSETISLTCTVSSGGSSSYVNSWITROPQKGLEWIGVYVYTWNTYN	60
Db	1	QVQLQESGGGLVQPKSETISLTCTVSSGGSSSYVNSWITROPQKGLEWIGVYVYTWNTYN	60
Qy	61	PSLKSRTVISDVTSKNQFSLRLSSVTAADTALYYCARDQGGWLLPDAFDIWGGQTVVTS	120
Db	61	PSLKSRTVISDVTSKNQFSLRLSSVTAADTALYYCARDQGGWLLPDAFDIWGGQTVVTS	120

Ov 121 S 121

D<sup>b</sup> 121 S 121

### RESULT 3

US-10-660-357-9  
; Sequence 9, Application US/10660357  
; Publication No. US20040115205A1

```

? GENERAL INFORMATION:
? APPLICANT: Bar-Eli, Menashe
? APPLICANT: Green, Larry L.
? TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
? TITLE OF INVENTION: ANTIGEN
? FILE REFERENCE: ABGENIX.030C1
? CURRENT APPLICATION NUMBER: US/10/660,357
? CURRENT FILING DATE: 2003-09-10
? PRIOR APPLICATION NUMBER: 10/330,580
? PRIOR FILING DATE: 2002-12-26
? NUMBER OF SEQ ID NOS: 40
? SOFTWARE: FastSEQ for Windows Version 4.0
? SEQ ID NO 9
? LENGTH: 121
? TYPE: PRT
? ORGANISM: Homo Sapiens
? US-10-660-357-9

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Best Local Similarity 100.0%; Pred. No. 3.5e-49;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	1	QVQLQESGGGLVQPKSETLSLTCTVGGSGIS	SSVYHSWIRPPKGLGLEWIGIYYTWTN	60
Qy	61	PSLKSRTVISDVTSKNQFSLRLSSVYTAADTAL	YYCARDQGGWLLPDAFDINGQGTWTVTS	120
Db	61	PSLKSRTVISDVTSKNQFSLRLSSVYTAADTAL	YYCARDQGGWLLPDAFDINGQGTWTVTS	120

Ov 121 S 121

Db 121 S 121

## RESULT 4

US-10-330-613-1  
; Sequence 1, Application US/10330613  
; Publication No. US20030147809A1

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; GENERAL INFORMATION:
; APPLICANT: Gudás, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-330-613-1

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Query Match 98.9%; Score 643; DB 14; Length 121;  
Best Local Similarity 98.3%; Pred. NO. 1.4e-48;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0

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Db	1	OYQOESGPGLVKPKETLSLCTCTSGGSISSYVMSWIRQPPGKCLEWIGVLYVTWTNNY	60
Qy	61	PSLGRVTISVDTSKNOFSLRLSSVTAADTALYYCARDQCGWLLPDAFDIWGGGTWVTVS	120
Db	61	PSLGRVTISVDTSKNOFSLRLSSVTAADTALYYCARDQCGWLLPDAFDIWGGGTWVTVS	120

Qy 121 S 121L

Db 121 S 121

## RESULT 5

US-10-330-613-17  
; Sequence 17, Application US/10330613  
; Publication No. US20030147809A1

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; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: AGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-17

```

Query Match 98.9%; Score 643; DB 14; Length 121;  
Best Local Similarity 98.3%; Pred. NO. 1.4e-48;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0

1 QVQLQESGPGLVKPSETLSLTCTVSGSISYYKSWIRPPGKGLEWIGIYYTWTNYN 60  
Qy  
1 QVQLQESGPGLVKPSETLSLTCTVSGSISYYKSWIRPPGKGLEWIGIYYTWTNYN 60  
Db  
61 PSIKGRVTISVDTSKNQSFSLSSVTAADTALYVCARDQGWLPPDAFDITWGOGTWTVS 120  
Qy

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQMTWTVS 120  
121 S 121  
|  
Db 121 S 121

## RESULT 6

US-10-330-530-1  
; Sequence 1, Application US/10330530  
; Publication No. US20030152514A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
; FILE REFERENCE: ABGENIX.031A  
; CURRENT APPLICATION NUMBER: US/10/330,530  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: US 60/346414  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-530-1

Query Match 98.9%; Score 643; DB 14; Length 121;  
Best Local Similarity 98.3%; Pred. No. 1.4e-48;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGPGLVFPSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTN 60  
|  
Db 1 QVQLQSGPGLVFPSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTN 60  
|  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGGQMTWTVS 120  
|  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQMTWTVS 120  
121 S 121  
|  
Db 121 S 121

## RESULT 7

US-10-330-530-17  
; Sequence 17, Application US/10330530  
; Publication No. US20030152514A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
; FILE REFERENCE: ABGENIX.031A  
; CURRENT APPLICATION NUMBER: US/10/330,530  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: US 60/346414  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-530-17

Query Match 98.9%; Score 643; DB 14; Length 121;  
Best Local Similarity 98.3%; Pred. No. 1.4e-48;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGPGLVFPSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTN 60  
|  
Db 1 QVQLQSGPGLVFPSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTN 60  
|  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGGQMTWTVS 120

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQMTWTVS 120  
121 S 121  
|  
Db 121 S 121

## RESULT 8

US-10-660-357-1  
; Sequence 1, Application US/10660357  
; Publication No. US20040115205A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Eli, Menashe  
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
; TITLE OF INVENTION: ANTIGEN  
; FILE REFERENCE: ABGENIX.030C1  
; CURRENT APPLICATION NUMBER: US/10/660,357  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 10/330,580  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-1

Query Match 98.9%; Score 643; DB 16; Length 121;  
Best Local Similarity 98.3%; Pred. No. 1.4e-48;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGPGLVFPSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTN 60  
|  
Db 1 QVQLQSGPGLVFPSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTN 60  
|  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGGQMTWTVS 120  
|  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQMTWTVS 120  
121 S 121  
|  
Db 121 S 121

## RESULT 9

US-10-660-357-17  
; Sequence 17, Application US/10660357  
; Publication No. US20040115205A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Eli, Menashe  
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
; TITLE OF INVENTION: ANTIGEN  
; FILE REFERENCE: ABGENIX.030C1  
; CURRENT APPLICATION NUMBER: US/10/660,357  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 10/330,580  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-17

Query Match 98.9%; Score 643; DB 16; Length 121;  
Best Local Similarity 98.3%; Pred. No. 1.4e-48;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QVQLQESGPGELVKPSETSLCTCTVSGGSISSYVSWNRPPGKGLGWIGIYYTWTNN	60
Db	1	QVQLQESGPGELVKPSETSLCTCTVSGGSISSYVSWNRPPGKGLGWIGIYYTWTNN	60
Qy	61	PSLKSRTVTSVDTSKNQSRLRSSVTAADTALYTCARDQGWLLPDAFDIWGGTWTWVS	120
Db	61	PSLKSRTVTSVDTSKNQSRLRSSVTAADTALYTCARDQGWLLPDAFDIWGGTWTWVS	120

```

RESULT 10
US-10-330-613-37
; Sequence 37, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.02ZA
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-37

```

```

RESULT 11
US-10-330-530-37
; Sequence 37, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCES: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-37

```

Qy	1	QVQLQESGPGLVKPSSETLSLTCTVS	GSGISSTYSYFWSWIRQPPGKGLEWIGIYYTWTNTYN	60
		:	:	
D <sub>B</sub>	1	QVQLQESGPGLVKPSSETLSLTCTVS	GSGISTSYFWSWIRQPPGKGLEWIGIYYVTGNTYN	60
		:	:	
Qy	61	PSLKSRTVISVDTSKNQFSRLSSVAADP	ALYYCARDQGQWLPLPAFDITWGOGTMVTVS	120
		:	:	
D <sub>B</sub>	61	PSLKSRTVISVDTSKNQFSRLKLNSVAAD	PVAVYYCARDPGQWLVPDAFDITWGOGTMVSVS	120
Qy	121	S	121	
D <sub>B</sub>	121	S	121	

```

RESULT 12
US-10-660-357-37
; Sequence 37, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menaehe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: AEGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: fastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-37

```

RESULT 13  
US-10-292-088-142  
; Sequence 142, Application US/10292088  
; Publication No. US20030211100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-Pf/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 142  
; LENGTH: 118





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 12:25:58 ; Search time 13.0401 Seconds  
(without alignments)  
892.802 Million cell updates/sec

Title: US-10-660-357A-9

Perfect score: 650

Sequence: 1 QVQLQSGGPGLVKPSSETLSL.....WLLPDAFDIWGQGMVTVS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: pir1.\*
- 2: pir2.\*
- 3: pir3.\*
- 4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	544	83.7	140	2 I37782	Ig variable region
2	534	82.2	130	2 S31690	Ig heavy chain V r
3	532	81.8	155	2 S31512	Ig heavy chain - h
4	529	81.4	155	2 S31511	Ig heavy chain - h
5	527.5	81.2	139	2 S31586	Ig heavy chain V r
6	519.5	79.9	130	2 S30534	Ig heavy chain V r
7	513.5	79.0	137	2 S31676	Ig heavy chain V r
8	510.5	78.5	118	2 S20780	Ig heavy chain V r
9	506	77.8	147	2 S31519	Ig heavy chain V r
10	499.5	76.8	140	2 S78052	Ig heavy chain pre
11	496	76.3	135	2 S78051	Ig heavy chain pre
12	491	75.5	105	2 S44125	Ig lambda chain V
13	490	75.4	97	2 S26906	Ig heavy chain V r
14	490	75.4	146	2 S09711	Ig heavy chain V r
15	489	75.2	116	2 B26340	Ig heavy chain pre
16	487	74.9	97	2 S12416	Ig heavy chain V r
17	487	74.9	121	2 S44113	Ig heavy chain V r
18	486	74.8	140	2 A49045	Ig heavy chain V r
19	482	74.2	139	2 S31696	Ig heavy chain V r
20	478	73.5	118	2 A26340	Ig heavy chain pre
21	475.5	73.2	129	2 S44114	Ig heavy chain V r
22	475	73.1	123	2 S30530	Ig heavy chain V r
23	474.5	73.0	126	2 S47010	Ig heavy chain V4
24	474.5	73.0	145	2 S78055	Ig heavy chain pre
25	469.5	72.2	118	2 S24443	Ig heavy chain V r
26	468	72.0	99	2 S26802	Ig heavy chain V r
27	468	72.0	99	2 S26803	Ig heavy chain V r
28	468	72.0	220	2 A49444	Ig gamma-1 heavy c
29	467	71.8	97	2 PH0876	Ig heavy chain V r

ALIGNMENTS

RESULT 1

I37782

Ig variable region (VDJ) (clone T23-9) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999

C;Accession: I37782; S25476

R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A;Title: Somatic diversification in the heavy chain variable region genes expressed by

A;Reference number: A36876; MUID:94119917; PMID:8290556

A;Accession: I37782

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140 <RES>

A;Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;46-128/Domain: immunoglobulin homology <IMM>

Query Match 83.7%; Score 544; DB 2; Length 140;

Best Local Similarity 86.0%; Pred. No. 6.4e-42;

Matches 104; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 1 QVQLQSGGPGLVKPSSETLSLTCVSGSISYVSWIRQPPGKLEWIGVYTTWTNYN 60

Db 20 QVQLQSGGPGLVKPSSETLSLTCVSGSISYVSWIRQPPGKLEWIGVYTTWTNYN 79

Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGQGMVTVS 120

Db 80 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARHNSSSWVGRYFDYWGQGLTVTS 139

Qy 121 S 121

Db 140 S 140

RESULT 2

S31690

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C;Accession: S31690

R;Quisnier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the

A;Reference number: S31585

A;Accession: S31690

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-130 <CUI>

A;Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;20-102/Domain: immunoglobulin homology <IMM>

Query Match 82.2%; Score 534; DB 2; Length 130;  
Best Local Similarity 84.0%; Pred. No. 4.7e-41;  
Matches 105; Conservative 5; Mismatches 11; Indels 4; Gaps 1;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYVTWNTYN 60  
DB 6 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYVTGNTYN 65  
  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWL- ---LPDAFDIWGQGTMT 116  
DB 66 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARGSSVLLWFGLLYYFDYWGQGT 125  
  
QY 117 VTVSS 121  
DB 126 VTVSS 130

RESULT 3  
S31512  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S31512  
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto  
A:Reference number: S31509  
A:Accession: S31512  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <CHA>  
A:Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 532; DB 2; Length 155;  
Best Local Similarity 82.1%; Pred. No. 8.5e-41;  
Matches 101; Conservative 7; Mismatches 13; Indels 2; Gaps 1;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYVTWNTYN 60  
DB 33 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYVTGNTYN 92  
  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWL- ---QWLLPDAFDIWGQGTMT 118  
DB 93 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARGGSISSYYWWSWIROPKGLGWIGYIYVTGNTYN 152  
  
QY 119 VSS 121  
DB 153 VSS 155

RESULT 4  
S31511  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S31511  
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto  
A:Reference number: S31509  
A:Accession: S31511  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <CHA>  
A:Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 529; DB 2; Length 155;  
Best Local Similarity 82.9%; Pred. No. 1.6e-40;  
Matches 102; Conservative 5; Mismatches 14; Indels 2; Gaps 1;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYVTWNTYN 60  
DB 33 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYVTGNTYN 92  
  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWL- ---QWLLPDAFDIWGQGTMT 118  
DB 93 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARGGSISSYYWWSWIROPKGLGWIGYIYVTGNTYN 152  
  
QY 119 VSS 121  
DB 153 VSS 155

RESULT 5  
S31586  
Ig heavy chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31586  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.  
submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A:Reference number: S31585  
A:Accession: S31586  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-139 <CU1>  
A:Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 527.5; DB 2; Length 139;  
Best Local Similarity 86.0%; Pred. No. 1.9e-40;  
Matches 104; Conservative 6; Mismatches 10; Indels 1; Gaps 1;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYVTWNTYN 60  
DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYVTGNTYN 79  
  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWL- ---QWLLPDAFDIWGQGTMT 120  
DB 80 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARG-GLGIRRGAFDIWGQGTMT 138  
  
QY 121 S 121  
DB 139 S 139

RESULT 6  
S30534  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Aug-1996  
C:Accession: S30534  
R;Mariette, X.  
submitted to the EMBL Data Library, October 1992  
A:Reference number: S30520  
A:Accession: S30534  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-130 <MAR>  
A:Cross-references: EMBL:Z18320  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>  
  
Query Match 79.9%; Score 519.5; DB 2; Length 130;

Best Local Similarity 81.5%; Pred. No. 9.4e-40;  
Matches 106; Conservative 6; Mismatches 9; Indels 9; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYSWMIROPPGKLEWIGYIYYTWTN 58  
DB 1 QVQLQESGPGLVKPSQTLSTLTCTVSGGSISSGYYSWMIROPPGKLEWIGRIYTSGSTN 60

QY 59 YNPSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGO-WL-----LPDAFDIW 111  
DB 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARDKGGFWSGYYTRNSRAAFDIW 120

QY 112 GQGTMTVTSS 121  
DB 121 GQGTMTVTSS 130

RESULT 7  
S31676  
Ig heavy chain V region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S31676  
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
Submitted to the EMBL Data Library, June 1992  
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A/Reference number: S31585  
A/Accession: S31676  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-137 <CUI>  
A/Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 513.5; DB 2; Length 137;  
Best Local Similarity 83.5%; Pred. No. 3.4e-39;  
Matches 101; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYSWMIROPPGKLEWIGYIYYTWTN 60  
DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYSWMIROPPGKLEWIGRIYTSGSTN 79

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGOQLLPDAFDIWGQGTMTVTS 120  
DB 80 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARDAP--LTYGMDVWGQGTMTVTS 136

QY 121 S 121  
DB 137 S 137

RESULT 8  
S20780  
Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C/Accession: S20780  
R/Mortari, F.; Wang, J.; Schroeder, H.W.  
Submitted to the EMBL Data Library, April 1992  
A/Description: Analysis of human cord blood Ig heavy chain Iga and Igg repertoire.  
A/Reference number: S20764  
A/Accession: S20780  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-118 <MOR>  
A/Cross-references: EMBL:Z11958; NID:g33893; PIDN:CAA78015.1; PID:g33894  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 78.5%; Score 510.5; DB 2; Length 118;  
Best Local Similarity 81.0%; Pred. No. 5.4e-39;

Matches 98; Conservative 11; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYSWMIROPPGKLEWIGYIYYTWTN 60  
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISGHTWSWIRQPPGKLEWIAFIRYTGSTHYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGOQLLPDAFDIWGQGTMTVTS 120  
DB 61 PSLKSRVTISVDTSKNQFSLKMTSVTAADTAVYSCARDGR---DGGFDIWGQGTMTVTS 117

QY 121 S 121  
DB 118 S 118

RESULT 9  
S13519  
Ig heavy chain V region precursor - human  
C/Species: Homo sapiens (man)  
C/Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S13519  
R/Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.  
Nucleic Acids Res. 19, 673, 1991  
A/Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked  
A/Reference number: S13519; MUID:91187691; PMID:2011536  
A/Accession: S13519  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-147 <MOR>  
A/Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;41-125/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 506; DB 2; Length 147;  
Best Local Similarity 82.1%; Pred. No. 1.7e-38;  
Matches 101; Conservative 7; Mismatches 11; Indels 4; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSI--SSYYSWMIROPPGKLEWIGYIYYTWTN 58  
DB 27 QQLQESGPGLVKPSSETLSLTCTVSGSISSSSYWGWIRQPPGKLEWISYISGSTY 86

QY 59 YNPSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGOQLLPDAFDIWGQGTMTV 118  
DB 87 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARPL-LW-FGEELFDYWGGTTLVT 144

QY 119 VSS 121  
DB 145 VSS 147

RESULT 10  
S78052  
Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C/Accession: S78052; S23717  
R/Harindranath, N.  
Submitted to the EMBL Data Library, August 1990  
A/Reference number: S78051  
A/Accession: S78052  
A/Molecule type: mRNA  
A/Residues: 1-140 <HAR>  
A/Cross-references: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118  
R/Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin  
Int. Immunol. 3, 865-875, 1991  
A/Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and  
patient.  
A/Reference number: S23716; MUID:92031262; PMID:1718404  
A/Accession: S23717  
A/Molecule type: mRNA  
A/Residues: 15-111 <HAW>  
A/Cross-references: EMBL:X54441



Search completed: November 9, 2005, 13:08:02  
Job time : 14.0401 secs

## RESULT 14

S09711  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C:Accession: S09711  
R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.  
Biochem. J. 268, 135-140, 1990  
A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of human immunoglobulin V region; immunoglobulin homology  
A:Reference number: S09710; MUID:90262535; PMID:2111699  
A:Accession: S09711  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-146 <HUG>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 75.4%; Score 490; DB 2; Length 146;  
Best Local Similarity 74.0%; Pred. No. 4.7e-37;  
Matches 97; Conservative 11; Mismatches 9; Indels 14; Gaps 3;

Qy 1 QVQLQSGPGLVXPSETLSLTCTVSGGSISS--YYMSWIRQPPKGLGWIGYIYYTWTN 58  
Db 20 QVQLQSGPGLVXPSETLSLTCTVSGGSSVSSGLYMSWIRQPPKGLGWIGYIYYSGTN 79  
Qy 59 YNPSLRSRVTVISVDTSKNQFSLRSSVTAADTALYYCAR-----DQGWLLPDAFDI 110  
Db 80 YNPSLRSRVTVISVDTSKNQFSLKGLSVTAADTAVYYCARVLVSRVTSISQSYTNM----DV 135

Qy 111 WGQGTWTVTVSS 121  
Db 136 WKGTTVTVSS 146

## RESULT 15

B26340  
Ig heavy chain precursor V-II region (71-4) - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Jun-1998 #sequence\_revision 30-Jun-1991 #text\_change 23-Jul-1999  
C:Accession: B26340  
R:Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo, T.  
J. Mol. Biol. 190, 529-541, 1986  
A:Title: Organization and evolution of variable region genes of the human immunoglobulin  
A:Reference number: A26340; MUID:87061007; PMID:3097326  
A:Accession: B26340  
A:Molecule type: DNA  
A:Residues: 1-116 <KOD>  
A:Cross-references: GB:X05711; NID:933602; PIDN:CAA29183.1; PID:q296660  
A:Note: the authors translated the codon GAG for residue 25 as Gln  
C:Genetics:  
A:Introns: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-116/Product: Ig heavy chain V region 71-4 #status predicted <MAT>  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 75.2%; Score 489; DB 2; Length 116;  
Best Local Similarity 93.0%; Pred. No. 4.5e-37;  
Matches 91; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVQLQSGPGLVXPSETLSLTCTVSGGSISSYVSWIRQPPKGLGWIGYIYYTWTN 60  
Db 20 QVQLQSGPGLVXPSETLSLTCTVSGSVSSVYVSWIRQPPKGLGWIGYIYYSGTN 79  
Qy 61 PSLKSRVTISVDTSKNQFSLRSSVTAADTALYYCAR 97  
Db 80 PSLKSRVTISVDTSKNQFSLKGLSVTAADTAVYYCAR 116

CLASS >100 10 2000 5000



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:46:52 ; Search time 62.4712 Seconds  
(without alignments)  
991.843 Million cell updates/sec

Title: US-10-660-357A-9  
Perfect score: 650  
Sequence: 1 QVQLQESGPGLVKPSFTLSL.....WLLPDADFIMGQGMVTVSS 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	517	79.5	476	2	Q6GMX1	Q6gm1 homo sapien
2	516	79.4	119	2	Q9UL73	Q9ul73 homo sapien
3	509.5	78.4	465	2	Q6GMX6	Q6gm6 homo sapien
4	502.5	77.3	620	2	Q6GEY0	Q6gey0 homo sapien
5	499.5	76.8	477	2	Q6GMX7	Q6gm7 homo sapien
6	496	76.3	139	2	Q86SX2	Q86sx2 homo sapien
7	494.5	76.1	478	2	Q72379	Q72379 homo sapien
8	478.5	73.6	150	2	Q95973	Q95973 homo sapien
9	473.5	72.8	576	2	Q6P418	Q6p418 homo sapien
10	473	72.8	492	2	Q72374	Q72374 homo sapien
11	461.5	71.0	496	2	Q96KX8	Q96kx8 homo sapien
12	455.5	70.1	146	1	HV21 HUMAN	P06331 homo sapien
13	453	69.7	478	2	Q6NYH3	Q6nyh3 homo sapien
14	452	69.5	595	2	Q8WUX4	Q8wux4 homo sapien
15	452	69.5	597	2	Q6GMX5	Q6gm5 homo sapien
16	452	69.5	597	2	Q9BU10	Q9bu10 homo sapien
17	452	69.5	625	2	Q96AA6	Q96aa6 homo sapien
18	450	69.2	597	2	Q9BQ88	Q9bq88 homo sapien
19	446	68.6	129	1	HV2F HUMAN	P01824 homo sapien
20	439	67.5	117	1	HV2G HUMAN	P01825 homo sapien
21	436.5	67.2	130	2	Q81ZD7	Q81zd7 homo sapien
22	417.5	64.2	116	2	Q723V6	Q723v6 homo sapien
23	407.5	62.7	122	2	Q9UL75	Q9ul75 homo sapien
24	405	62.3	479	2	Q9NM22	Q9nm22 mus musculus
25	395	60.8	476	2	Q6MZX7	Q6mzx7 homo sapien
26	392.5	60.4	136	2	Q6LBQ5	Q6lbq5 mus musculus
27	392	60.3	137	1	HV45 MOUSE	P01822 mus musculus
28	387.5	59.6	473	2	Q8TC63	Q8tc63 homo sapien
29	378	58.2	113	1	HV47 MOUSE	P01823 mus musculus
30	375	57.7	262	2	Q65Z11	Q65z11 mus musculus
31	374.5	57.6	482	2	Q91X92	Q91x92 mus musculus

RESULT 1

ID	Q6GMX1	PRELIMINARY;	PRT;	476 AA.
AC	Q6GMX1;			
DT	05-JUL-2004 (Tremblrel. 27, Created)			
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)			
DE	05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RC	Strausberg R.;			
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC073773; AAH73773.1; -.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG-cl.			
DR	InterPro; IPR003006; IG_MHC.			
DR	Pfam; PF07654; C1-set; 3.			
DR	Pfam; PF00047; ig; 4.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00407; IGcl; 3.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG LIKE; 4.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.			

P18531 mus musculus  
P18532 mus musculus  
P18533 mus musculus  
P01819 mus musculus  
Q99094 mus musculus  
P20957 xenopus lae  
Q81105 mus musculus  
Q9ul74 homo sapien  
Q6p1a4 homo sapien  
Q6p1a4 homo sapien  
Q9ul91 homo sapien  
Q8wuk1 homo sapien  
Q6gm12 homo sapien  
Q6in78 homo sapien

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KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match
Best Local Similarity 79.5%; Score 517; DB 2; Length 476;
Matches 102; Conservative 10; Mismatches 8; Indels 8; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYTTN 58
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWSWIRQPPGKGLEWIGYIYSGSTY 79
|||
QY 59 YNPISKSRVTISVDTSKNQFSLRSSVTAADTALYYCARDQGW-----LLDPADFIWGQ 113
Db 80 YNPISKSRVTISLDTSKNQFSLKXNSVTAADTAVYFCAR-AGVWGSRFSAIDGFNIWGQ 138
|||
QY 114 GTMVTVSS 121
Db 139 GTMVTVSS 146
|||

RESULT 2
ID Q9UL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035041; AAD56277.1; -.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSP; P01820; IG7J.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BD886B6420EAOBE CRC64;

Query Match
Best Local Similarity 79.4%; Score 516; DB 2; Length 119;
Matches 100; Conservative 8; Mismatches 11; Indels 2; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYTTN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYSGSTNT 60
|||
QY 61 PSLKSRVTISVDTSKNQFSLRSSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTISVDRSKNQFSLKLTSLTAADTAVYFCAR-LSNW-GPYFDYWGQGLTIVTS 118
|||
QY 121 S 121
Db 119 S 119

RESULT 3
Q6GMX6 PRELIMINARY; PRT; 465 AA.
ID Q6GMX6
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AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388357; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match
Best Local Similarity 78.4%; Score 509.5; DB 2; Length 465;
Matches 99; Conservative 8; Mismatches 9; Indels 5; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGYIYTTN 60
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGRIYSGSTN 79
|||
QY 61 PSLKSRVTISVDTSKNQFSLRSSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVTS 120
Db 80 PSLKSRVTSMVDSKTNQFSLKSLSSVTAADTAVYFCARGFTY-----FDYWGGTIVTS 134
|||
QY 121 S 121
Db 135 S 135

RESULT 4
Q96EY0
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Q96EY0 PRELIMINARY; PRT; 620 AA.  
 AC Q96EY0; 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE IGHM protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Primary B-Cells;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Primary B-Cells;  
 RC Strausberg R.;  
 RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: BC011857; AHH1857.2; -.  
 DR PIR: S15590; S15590.  
 DR HSP: P01820; IGTJ.  
 DR InterPro: IPR003599; IG.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003597; IG cl.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam: PF07654; Cl-set; 4.  
 DR Pfam: PF00047; IG; 3.  
 DR SMART: SM00409; IG; 4.  
 DR SMART: SM00407; IGV; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS00835; IG LIKE; 5.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN 3.  
 SQ SEQUENCE 620 AA; 68125 MW; 950A1A4A6E8F27B CRC64;  
 Query Match 77.3%; Score 502.5; DB 2; Length 620;  
 Best Local Similarity 82.0%; Pred. No. 6.4e-42;  
 Matches 100; Conservative 6; Mismatches 13; Indels 3; Gaps 2;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVMSWIRQPPGKLEWIGYIYTWNTYN 60  
 DB 27 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVMSWIRQPPGKLEWIGYIYTSN 86  
 QY 61 PSLSKRVITSDVTSKQFSLRLSSVTAADTALYYCARDQGWLLPD-APDIWGQGTWTV 119  
 DB 87 PSLSKRVITSDVTSKQFSLRLSSVTAADTALYYCARDQGWLLPD-APDIWGQGTWTV 144  
 QY 120 SS 121  
 DB 145 SS 146

RESULT 5

Q6GMX7 PRELIMINARY; PRT; 477 AA.  
 AC Q6GMX7; 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Primary B-Cells;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Primary B-Cells;  
 RC Strausberg R.;  
 RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: BC073765; AAH73765.1; -.  
 DR InterPro: IPR003599; IG.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003597; IG cl.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam: PF07654; Cl-set; 2.  
 DR Pfam: PF00047; IG; 3.  
 DR SMART: SM00409; IG; 4.  
 DR SMART: SM00407; IGV; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS00835; IG LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFE85 CRC64;  
 Query Match 76.8%; Score 499.5; DB 2; Length 477;  
 Best Local Similarity 81.0%; Pred. No. 9.7e-42;  
 Matches 99; Conservative 8; Mismatches 12; Indels 3; Gaps 2;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVMSWIRQPPGKLEWIGYIYTWNTYN 60  
 DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVMSWIRQPPGKLEWIGYIYTSN 79  
 QY 61 PSLSKRVITSDVTSKQFSLRLSSVTAADTALYYCARDQGWLLPD-APDIWGQGTWTV 120  
 DB 80 PSLSKRVITSDVTSKQFSLRLSSVTAADTALYYCARDQGWLLPD-APDIWGQGTWTV 136  
 QY 121 S 121  
 DB 137 S 137

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RESULT 6
Q86SX2
ID Q86SX2 PRELIMINARY; PRT; 139 AA.
AC Q86SX2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CSODL004YM19 of B cells (Ramos cell line) of
DE Homo sapiens (human) (Fragment).
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Genoscope;
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BX248300; CAD62627.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 76.3%; Score 496; DB 2; Length 139;
Best Local Similarity 94.9%; Pred. No. 5.8e-42;
Matches 93; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYMSWIRQPPGKLEWIGYIYYTWTN 60
DB 33 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYMSWIRQPPGKLEWIGYIYYTWTN 92
QY 61 PSLKSRVTISVDTSKQFSLRLSVTAADTALYYCARD 98
DB 93 PSLKSRVTISVDTSKQFSLRLSVTAADTAVYYCARD 130

RESULT 7
Q72379
ID Q72379 PRELIMINARY; PRT; 478 AA.
AC Q72379;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFp686K04218 (Fragment).
GN Name=DKFp686K04218;
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538066; CAD97996.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
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DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match 76.1%; Score 494.5; DB 2; Length 478;
Best Local Similarity 77.2%; Pred. No. 3.1e-41;
Matches 95; Conservative 15; Mismatches 8; Indels 5; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISS--YYMSWIRQPPGKLEWIGYIYYTWTN 58
DB 19 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSGGDYFMSWIRQPPGKLEWIGYIYSGSTY 78
QY 59 YNPSLKSRVTISVDTSKQFSLRLSVTAADTALYYCARDQGWLLPDAFDIWGQGTMYT 118
DB 79 YNPSLKSRVTISVDTSKQFSLRLSVTAADTAVYYCARDG---LGTAFDIWGQGTMYT 135
QY 119 VSS 121
DB 136 VSS 138

RESULT 8
Q95973
ID Q95973 PRELIMINARY; PRT; 150 AA.
AC Q95973;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE VH4 heavy chain variable region precursor (Fragment).
GN Name=IGM;
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RA Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF103795; AAC79084.1; -.
DR PIR; S31673; S31673.
DR PIR; S78056; S78056.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 >150 VH4 heavy chain variable region.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 73.6%; Score 478.5; DB 2; Length 150;
Best Local Similarity 78.9%; Pred. No. 3.6e-40;
Matches 97; Conservative 7; Mismatches 12; Indels 7; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISS--YYMSWIRQPPGKLEWIGYIYYTWTN 58
DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWGWIRQPPGKLEWIGSLHNSGSDY 79
QY 59 YNPSLKSRVTISVDTSKQFSLRLSVTAADTALYYCARDQGWLLPDAFDIWGQGTMYT 118
DB 80 YNPSLKSRVTISVDTSKQFSLRLSVTAADTAVYYCAR-----LGMGAPDFWGHGTMVT 134
QY 119 VSS 121
DB 135 VSS 137

RESULT 9
Q6P4I8
ID Q6P4I8 PRELIMINARY; PRT; 576 AA.
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AC Q69418; 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE IGHD protein.  
 GN Name=IGHD;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Glimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smillius D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC063384; AAH63384.1; -  
 DR HSSP; P01820; 1A7N.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 2.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00407; IGI; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 SQ SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;  
 Query Match 72.8%; Score 473.5; DB 2; Length 576;  
 Best Local Similarity 76.2%; Pred. No. 4.9e-39;  
 Matches 96; Conservative 9; Mismatches 10; Indels 11; Gaps 3;  
 QY 1 QVQLQESGPGLVKPSSTLTCTVSGGSI--SSYWSWIRQPPGKLEWIGYIYYTWTN 59  
 DB 27 QVQLQESGPGLVKPSSTLTCTVSGGSISSSNWSVQPPGKLEWIGYIYHSGSTNY 86  
 QY 60 NPSLKSRTVISVDTSKNQFSLRLSSVTAADTALYICARDQGWLLDPAP-----DIWQGT 115  
 DB 87 NPSLKSRTVISVDTSKNQFSLRLSSVTAADTALYICARDQGWLLDPAP-----DIWQGT 140  
 QY 116 MVTVSS 121  
 DB 141 TVTVSS 146  
 RESULT 10

Q72374  
 ID Q72374 PRELIMINARY; PRT; 492 AA.  
 AC Q72374;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein DKFZp686C02218 (Fragment).  
 GN Names=DKFZp686C02218;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human rectum tumor;  
 RA Bloecker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobo G., Han M., Wiemann S.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX538077; CAD98001.1; -  
 DR HSSP; P01820; 1G7J.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760FOCA74B CRC64;  
 Query Match 72.8%; Score 473; DB 2; Length 492;  
 Best Local Similarity 75.4%; Pred. No. 4.6e-39;  
 Matches 95; Conservative 9; Mismatches 12; Indels 10; Gaps 4;  
 QY 1 QVQLQESGPGLVKPSSTLTCTVSGGSI--SSYWSWIRQPPGKLEWIGYIYYTWTN 58  
 DB 32 QLQLQESGPGLVKPSSTLTCTVSGSVSNRYWGWIRQPPGKLEWIGSIYYNNTY 91  
 QY 59 YNPSLKSRTVISVDTSKNQFSLRLSSVTAADTALYICARD-QGQ--WLLPDAFDIWQGT 115  
 DB 92 YSPSLKSLRTIFVDTSKNHFSLRLTSTAADTAVYICVRHVEGPGYGV-----FDPWQGT 146  
 QY 116 MVTVSS 121  
 DB 147 LVTVSS 152  
 RESULT 11  
 ID Q96KX8 PRELIMINARY; PRT; 496 AA.  
 AC Q96KX8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE MGC27165 protein.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,



DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; C1-set; 2.  
DR SMART; SM00409; IG; 4.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG MHC; UNKNOWN\_2.  
KW Hypothetical protein\_  
SQ SEQUENCE 478 AA; 51856 MW; 5F8B98F60F077256 CRC64;  
  
Query Match 69.7%; Score 453; DB 2; Length 478;  
Best Local Similarity 71.9%; Pred. No. 4.6e-37;  
Matches 87; Conservative 16; Mismatches 16; Indels 2; Gaps 1;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYKWSIRQPPGKLEWIGYIYYTWTNYN 60  
DB 20 QVDLQESGPGLVKPSSETLSLTCTVSGGSISSYYKWSIRQPPGKLEWIGYIYYTWTNYN 79  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWDGQWTVTS 120  
DB 80 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWDGQWTVTS 137  
QY 121 S 121  
DB 138 S 138

RESULT 14  
Q8WUX4 PRELIMINARY; PRT; 595 AA.  
AC Q8WUX4  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Lymph;  
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Whiting M., Madan A., Young A.C., Rodriguez S., Sanchez A.,  
Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Jones S.J., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Lymph;  
RC Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC019235; AAH19235.2; -.  
DR InterPro; IPR003597; Ig.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig MHC.  
DR PIR; G34964; G34964.

DR HSP; P01861; IADQ.  
DR Pfam; PF07654; C1-set; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 5.  
DR PROSITE; PS00290; IG MHC; UNKNOWN\_3.  
KW Hypothetical protein\_  
SQ SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;  
  
Query Match 69.5%; Score 452; DB 2; Length 595;  
Best Local Similarity 69.8%; Pred. No. 7.4e-37;  
Matches 90; Conservative 10; Mismatches 17; Indels 12; Gaps 2;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYKWSIRQPPGKLEWIGYIYYTWTNYN 60  
DB 27 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYKWSIRQPPGKLEWIGYIYYTWTNYN 86  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCAR-----DQGWLLPDAFDIWDG 112  
DB 87 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARVITRASPTDGRY----GMDVWG 142  
QY 113 QGTWTVTS 121  
DB 143 QGTWTVTS 151  
  
RESULT 15  
Q6GMX5 PRELIMINARY; PRT; 597 AA.  
AC Q6GMX5  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Lymph;  
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Whiting M., Madan A., Young A.C., Rodriguez S., Sanchez A.,  
Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Jones S.J., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Lymph;  
RC Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC073767; AAH73767.1; -.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig MHC.





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:43:32 ; Search time 72.1353 Seconds  
(without alignments)  
627.306 Million cell updates/sec

Title: US-10-660-357A-13

Perfect score: 624

Sequence: 1 QVQLQSGPGLVFPSTLSL.....AREGDFYWGQGLTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	624	100.0	117	7 ADC99784	Adc99784 Anti-huma
2	624	100.0	117	7 ADD05388	Add05388 Anti-MUC1
3	624	100.0	117	7 ADF09826	Adf09826 Human ant
4	587	94.1	117	7 ADC99776	Adc99776 Anti-huma
5	587	94.1	117	7 ADD05380	Add05380 Anti-MUC1
6	587	94.1	117	7 ADF09818	Adf09818 Human ant
7	585.5	93.8	118	7 ADC93968	Adp03968 Murine-ex
8	579	92.8	123	7 ADC93870	Adp03870 Murine-ex
9	575.5	92.2	120	7 ADC93974	Adp03974 Murine-ex
10	575.5	92.2	120	7 ADC93873	Adp03873 Murine-ex
11	574.5	92.1	124	7 ADC93935	Adp03935 Murine-ex
12	572	91.7	125	7 ADC93868	Adp03868 Murine-ex
13	572	91.7	125	7 ADC93876	Adp03876 Murine-ex
14	571.5	91.6	121	7 ADJ80377	Adj80377 Antibody
15	570.5	91.4	122	7 ADC93977	Adp03977 Murine-ex
16	570	91.3	121	7 ADC93981	Adp03981 Murine-ex
17	569	91.2	120	4 AAB62775	Aab62775 Human HIV
18	569	91.2	125	7 ADC93871	Adp03871 Murine-ex
19	568	91.0	117	7 ADC99804	Adc99804 Anti-huma
20	568	91.0	117	7 ADD05408	Add05408 Anti-MUC1
21	568	91.0	117	7 ADF09845	Adf09845 Human ant
22	567	90.9	121	7 ADC93982	Adp03982 Murine-ex
23	567	90.9	122	4 AAB62765	Aab62765 Human HIV
24	566	90.7	119	7 ADC93970	Adp03970 Murine-ex
25	566	90.7	253	5 ABP45608	Abp45608 Human Bly

## ALIGNMENTS

## RESULT 1

ADC99784  
ID ADC99784 standard; protein; 117 AA.

XX AC ADC99784;

XX AC  
DT 01-JAN-2004 (first entry)

DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 13.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.

XX Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

PI WPI; 2003-587113/55.

DR N-PSDB; ADC99786.

DR New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
PT or condition associated with expression of MUC18 in a patient, e.g.  
PT tumors, cancers, and other malignancies.

XX Claim 1; SEQ ID NO 13; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising  
CC a heavy or light chain amino acid or a heavy or light chain variable  
CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
CC invention demonstrates cytostatic activity and may be useful for treating  
CC a disease or condition associated with the expression of MUC18 on the  
CC cell surface such as tumours, specifically melanoma, oesophageal,  
CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
CC carcinomas and cervical intraepithelial neoplasia and cancers including  
CC colorectal, breast or lung cancer, as well as other malignancies. The  
CC current sequence is that of the anti-human MUC18 monoclonal antibody

Adg96435 Single ch  
Adk52356 Human ant  
Aab62745 Human HIV  
Adp03872 Murine-ex  
Adp03983 Murine-ex  
Aaw78433 Antibody  
Abb97976 Heavy cha  
Adg88414 Anti-Ob-R  
Adp03869 Murine-ex  
Adp03969 Murine-ex  
Adp22124 Human ant  
Adp22104 Human ant  
Adp22096 Human ant  
Adp03961 Murine-ex  
Adp03934 Murine-ex  
Adc99796 Anti-huma  
Add05400 Anti-MUC1  
Adf09838 Human ant  
Adp03877 Murine-ex  
Adp03874 Murine-ex

26 566 90.7 253 7 ADG96435  
27 566 90.7 446 8 ADK52356  
28 565.5 90.6 123 4 AAB62745  
29 565 90.5 123 7 ADP03872  
30 565 90.5 125 7 ADP03983  
31 563 90.2 123 2 AAW78433  
32 563 90.2 123 5 ABB97976  
33 563 90.2 123 7 ADG88414  
34 563 90.2 123 7 ADP03869  
35 562.5 90.1 120 7 ADP03969  
36 562.5 90.1 128 8 ADP22124  
37 562.5 90.1 128 8 ADP22104  
38 562.5 90.1 128 8 ADP22096  
39 562 90.1 119 7 ADP03961  
40 561.5 90.0 110 7 ADP03934  
41 561 89.9 119 7 ADC99796  
42 561 89.9 119 7 ADD05400  
43 561 89.9 119 7 ADF09838  
44 559 89.6 123 7 ADP03877  
45 559 89.6 127 7 ADP03874

```
CC heavy chain protein of the invention.
XX Sequence 117 AA;
SQ

Query Match      100.0%; Score 624; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.1e-48;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGSYWTWIRQHPGKLEWIGFIYSGSTY 60
   |||||
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGSYWTWIRQHPGKLEWIGFIYSGSTY 60
   |||||

QY 61 YNPISLKSRTVISVDTSKNQFSLKSSVTAADTAVYYCAREGDFYWGQGLTVTVSS 117
   |||||
Db 61 YNPISLKSRTVISVDTSKNQFSLKSSVTAADTAVYYCAREGDFYWGQGLTVTVSS 117
   |||||

RESULT 2
ADP09826
ID ADF09826 standard; protein; 117 AA.
XX
AC ADF09826;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human anti-MUC18 monoclonal antibody heavy chain #4.
XX
KW cell proliferation inhibition; MUC18 tumour antigen;
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; heavy chain; human.
XX
OS Homo sapiens.
XX
PN WO2003057837-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041580.
XX
PR 28-DEC-2001; 2001US-0346414P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
DR WPI; 2003-598367/56.
XX
DR N-PSDB; ADF09828.
XX
PT Inhibiting cell proliferation associated with expression of MUC18 tumor
PT antigen, involves incubating and inhibiting cell by administering anti-
PT MUC18 monoclonal antibody.
XX
PS Claim 1; SEQ ID NO 13; 87pp; English.
XX
CC The invention comprises a method for inhibiting cell proliferation
CC associated with expression of MUC18 tumour antigen. The method involves
CC administering anti-MUC18 monoclonal antibody. The method of the invention
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
CC proliferation associated with the expression of MUC18 tumour antigen, the
CC method is preferably useful for inhibiting tumour metastasis. The method
CC is useful for inhibiting cell proliferation in patients with tumours,
CC carcinomas, cancer and other malignancies. The present amino acid
CC sequence represents a heavy chain from an MUC18 tumour antigen-specific
CC monoclonal antibody.
XX
SQ Sequence 117 AA;

Query Match      100.0%; Score 624; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.1e-48;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGSYWTWIRQHPGKLEWIGFIYSGSTY 60
   |||||
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGSYWTWIRQHPGKLEWIGFIYSGSTY 60
   |||||

QY 61 YNPISLKSRTVISVDTSKNQFSLKSSVTAADTAVYYCAREGDFYWGQGLTVTVSS 117
   |||||
Db 61 YNPISLKSRTVISVDTSKNQFSLKSSVTAADTAVYYCAREGDFYWGQGLTVTVSS 117
   |||||

RESULT 2
ADD05388
ID ADD05388 standard; protein; 117 AA.
XX
AC ADD05388;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 13.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
XX
OS Homo sapiens.
XX
PN WO2003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
DR WPI; 2003-577496/54.
XX
DR N-PSDB; ADD05390.
XX
PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
PS Claim 1; SEQ ID NO 13; 87pp; English.
XX
CC The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC sequence represents an anti-MUC18 antibody heavy chain, variable region,
CC protein of the invention.
XX
SQ Sequence 117 AA;

Query Match      100.0%; Score 624; DB 7; Length 117;
```

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RESULT 4
ID ADC99776 standard; protein; 117 AA.
XX AC ADC99776;
XX DT 01-JAN-2004 (first entry)
XX DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 5.
XX KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
XX KW cytosolic; melanoma; oesophageal; pancreatic; colorectal tumour;
XX KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
XX KW lung cancer; human.
XX OS Homo sapiens.
XX PN WO2003057838-A2.
XX PD 17-JUL-2003.
XX PF 26-DEC-2002; 2002WO-US041581.
XX PR 28-DEC-2001; 2001US-0346299P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas J;
XX DR WPI; 2003-587113/55.
XX DR N-PSDB; ADC99778.
XX PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease
XX PT or condition associated with expression of MUC18 in a patient, e.g.
XX PT tumors, cancers, and other malignancies.
XX PS Claim 1; SEQ ID NO 5; 78pp; English.
XX CC The invention relates to a novel isolated monoclonal antibody comprising
XX CC a heavy or light chain amino acid or a heavy or light chain variable
XX CC domain where the antibody binds to MUC18. The monoclonal antibody of the
XX CC invention demonstrates cytostatic activity and may be useful for treating
XX CC a disease or condition associated with the expression of MUC18 on the
XX CC cell surface such as tumours, specifically melanoma, oesophageal,
XX CC pancreatic or colorectal tumours, carcinomas, particularly cervical
XX CC carcinomas and cervical intraepithelial neoplasia and cancers including
XX CC colorectal, breast or lung cancer, as well as other malignancies. The
XX CC current sequence is that of the anti-human MUC18 monoclonal antibody
XX CC heavy chain protein of the invention.
XX SQ Sequence 117 AA;
Query Match 94.1%; Score 587; DB 7; Length 117;
Best Local Similarity 94.0%; Pred. No. 6.4e-45;
Matches 110; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYWTWIRQHPKGLGWIGFIYSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYWTWIRQHPKGLGWIGFIYSGSTY 60
QY 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARGDGFYWGQGLTVTVSS 117
DB 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARGDGFYWGQGLTVTVSS 117
RESULT 5
ID ADD05380 standard; protein; 117 AA.
XX AC ADD05380;
XX DT 12-FEB-2004 (first entry)
XX DE Human anti-MUC18 monoclonal antibody heavy chain #2.
XX DE cell proliferation inhibition; MUC18 tumour antigen;
XX KW

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DT 01-JAN-2004 (first entry)
XX Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 5.
XX monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
XX antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
XX OS Homo sapiens.
XX PN WO2003057006-A2.
XX PD 17-JUL-2003.
XX PF 26-DEC-2002; 2002WO-US041582.
XX PR 28-DEC-2001; 2001US-0346460P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas J, Bar-Eli M;
XX DR WPI; 2003-577496/54.
XX DR N-PSDB; ADD05382.
XX PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
XX PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
XX PT associated with melanoma, or increasing survival of an animal having a
XX PT metastatic tumor.
XX PS Claim 1; SEQ ID NO 5; 87pp; English.
XX CC The invention relates to a novel monoclonal antibody used for inhibiting
XX CC tumour growth in an animal. The tumour inhibition process comprises
XX CC selecting an animal in need of treatment for a tumour, providing a
XX CC monoclonal antibody comprising a heavy chain amino acid, where the
XX CC antibody consists of any one of 10 fully defined sequences of 117-123
XX CC amino acids given in the specification, and where the monoclonal antibody
XX CC binds MUC18, and contacting the tumour with the antibody resulting in
XX CC inhibited proliferation of the cells. The monoclonal antibody has
XX CC cytostatic and can be used in the production of a vaccine. The monoclonal
XX CC antibodies against the MUC18 antigen are useful for diagnosing and
XX CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
XX CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
XX CC increasing survival of an animal having a metastatic tumour. This
XX CC sequence represents an anti-MUC18 antibody heavy chain, variable region,
XX CC protein of the invention.
XX SQ Sequence 117 AA;
Query Match 94.1%; Score 587; DB 7; Length 117;
Best Local Similarity 94.0%; Pred. No. 6.4e-45;
Matches 110; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYWTWIRQHPKGLGWIGFIYSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYWTWIRQHPKGLGWIGFIYSGSTY 60
QY 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARGDGFYWGQGLTVTVSS 117
DB 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARGDGFYWGQGLTVTVSS 117
RESULT 6
ADF09818
ID ADF09818 standard; protein; 117 AA.
XX AC ADF09818;
XX DT 12-FEB-2004 (first entry)
XX DE Human anti-MUC18 monoclonal antibody heavy chain #2.
XX KW cell proliferation inhibition; MUC18 tumour antigen;

```



XX PI Gudas J, Foltz I, Handa M, Gallo M;  
 XX DR WPI; 2003-523295/49.  
 XX PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 XX PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 XX PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX PS Claim 1; SEQ ID NO 10; 89pp; English.  
 XX CC The invention relates to a novel isolated monoclonal antibody (mAb)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytostatic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.  
 XX SQ Sequence 123 AA;  
 Query Match 92.8%; Score 579; DB 7; Length 123;  
 Best Local Similarity 90.2%; Pred. No. 3.5e-44;  
 Matches 111; Conservative 3; Mismatches 3; Indels 6; Gaps 1;  
 Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVYTWIRQHPKGLGWIGFIYSGSTY 60  
 Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVYTWIRQHPKGLGWIGFIYSGSTY 60  
 Qy 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVYYCAREGDG- - - - -DYWGQGLT 114  
 Db 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVYYCAREGDG- - - - -DYWGQGLT 120  
 Qy 115 VSS 117  
 Db 121 VSS 123  
 RESULT 9  
 ADP03974  
 ID ADP03974 standard; protein; 120 AA.  
 XX AC ADP03974;  
 XX DT 29-JUL-2004 (first entry)  
 XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.  
 XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytosstatic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX OS Unidentified.  
 XX PN W02003048328-A2.  
 XX PD 12-JUN-2003.  
 XX PF 02-DEC-2002; 2002WO-US038550.  
 XX PR 03-DEC-2001; 2001US-0337275P.  
 XX PA (ABGE-) ABGENIX INC.  
 XX PI Gudas J, Foltz I, Handa M, Gallo M;

XX DR WPI; 2003-523295/49.  
 XX PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 XX PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 XX PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX PS Example 2; SEQ ID NO 144; 89pp; English.  
 XX CC The invention relates to a novel isolated monoclonal antibody (mAb)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytostatic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.  
 XX SQ Sequence 120 AA;  
 Query Match 92.2%; Score 575.5; DB 7; Length 120;  
 Best Local Similarity 91.7%; Pred. No. 7e-44;  
 Matches 110; Conservative 4; Mismatches 3; Indels 3; Gaps 1;  
 Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVYTWIRQHPKGLGWIGFIYSGSTY 60  
 Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVYTWIRQHPKGLGWIGFIYSGSTY 60  
 Qy 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVYYCAREGDG- - - - -FDYWGQGLT 117  
 Db 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVYYCAREGDG- - - - -FDYWGQGLT 120  
 RESULT 10  
 ADP03873  
 ID ADP03873 standard; protein; 120 AA.  
 XX AC ADP03873;  
 XX DT 29-JUL-2004 (first entry)  
 XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.  
 XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytosstatic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX OS Unidentified.  
 XX PN W02003048328-A2.  
 XX PD 12-JUN-2003.  
 XX PF 02-DEC-2002; 2002WO-US038550.  
 XX PR 03-DEC-2001; 2001US-0337275P.  
 XX PA (ABGE-) ABGENIX INC.  
 XX PI Gudas J, Foltz I, Handa M, Gallo M;  
 XX DR WPI; 2003-523295/49.  
 XX PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 XX PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 XX PT intraepithelial squamous and glandular neoplasia or esophageal tumors.



CC demonstrates cytostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.  
XX  
SQ Sequence 125 AA;

Query Match 91.7%; Score 572; DB 7; Length 125;  
Best Local Similarity 88.0%; Pred. No. 1.5e-43;  
Matches 110; Conservative 2; Mismatches 5; Indels 8; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWIRQHPGKGLGWIGFIYSGSTY 60  
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWIRQHPGKGLGWIGFIYSGSTY 60  
QY 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARE-----GSGFDYWGQGTLL 112  
DB 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARTYYDILTGYPDADFINGQGT 120  
QY 113 VTVSS 117  
DB 121 VTVSS 125

## RESULT 13

ADP03876  
ID ADP03876 standard; protein; 125 AA.

XX AC ADP03876;

XX DT 29-JUL-2004 (first entry)

XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 16.

XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
XX KW cytostatic; colorectal neoplasm; renal cell carcinoma;  
XX KW cervical intraepithelial squamous neoplasia;  
XX KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
XX KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX OS Unidentified.

XX PN W02003048328-A2.

XX PD 12-JUN-2003.

XX PF 02-DEC-2002; 2002WO-US038550.

XX PR 03-DEC-2001; 2001US-0337275P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J, Foltz I, Handa M, Gallo M;

XX DR WPI; 2003-523295/49.

XX PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
XX PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
XX PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX PS Claim 1; SEQ ID NO 16; 89pp; English.

XX CC The invention relates to a novel isolated monoclonal antibody (mAb)  
XX CC comprising a heavy chain polypeptide and light chain polypeptide having a  
XX CC sequence chosen from one of 53 fully defined amino acid sequences given  
XX CC in the specification, where the antibody specifically binds carbonic  
XX CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
XX CC demonstrates cytostatic activity and may be useful for treating a tumour,  
XX CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,

CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.  
XX  
SQ Sequence 125 AA;

Query Match 91.7%; Score 572; DB 7; Length 125;  
Best Local Similarity 88.0%; Pred. No. 1.5e-43;  
Matches 110; Conservative 2; Mismatches 5; Indels 8; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWIRQHPGKGLGWIGFIYSGSTY 60  
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWIRQHPGKGLGWIGFIYSGSTY 60  
QY 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARE-----GSGFDYWGQGTLL 112  
DB 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARTYYDILTGYPDADFINGQGT 120  
QY 113 VTVSS 117  
DB 121 VTVSS 125

## RESULT 14

ADJ80377  
ID ADJ80377 standard; protein; 121 AA.

XX AC ADJ80377;

XX DT 06-MAY-2004 (first entry)

XX DE Antibody variable heavy chain with homology to mouse anti-human antibody.

XX KW hybrid antibody; antibody; framework region; homology; immunogenicity.

XX OS Unidentified.

XX PN W02003048321-A2.

XX PD 12-JUN-2003.

XX PF 03-DEC-2002; 2002WO-US038450.

XX PR 03-DEC-2001; 2001US-0336591P.

XX PA (ALEX-) ALEXION PHARM INC.

XX PI Rother R, Wu D;

XX DR WPI; 2003-513753/48.

XX PT Producing a hybrid antibody or hybrid antibody fragment by operatively  
XX PT linking the selected framework sequences to one or more complementarity  
XX PT determining regions of the initial antibody.

XX PS Example 1; SEQ ID NO 137; 77pp; English.

XX CC The invention relates to a method of producing a hybrid antibody or  
XX CC hybrid antibody fragment by: (i) providing an initial antibody having  
XX CC specificity for a target; (ii) determining the sequence of a variable  
XX CC region of the initial antibody; (iii) selecting a first component of the  
XX CC variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the  
XX CC sequence of the first component to sequences contained in a reference  
XX CC database of antibody sequences or antibody fragment sequences from a  
XX CC target species; (v) selecting a sequence from an antibody in the database  
XX CC which demonstrates a high degree of homology to the first component; (vi)  
XX CC selecting a second component of the variable region which is different  
XX CC than the first component, the second component selected from the group  
XX CC consisting of FR1, FR2, FR3 and FR4; (vii) comparing the sequence of the  
XX CC second component to sequences contained in a reference database of

CC antibody sequences or antibody fragment sequences from the target species  
CC ; (viii) selecting a sequence from the database which demonstrates a high  
CC degree of homology to the second component and which is from a different  
CC antibody than the selected antibody; and (ix) operatively linking the  
CC selected framework sequences to one or more complementarity determining  
CC regions (CDRs) of the initial antibody to produce a hybrid antibody or  
CC hybrid antibody fragment. The method is useful for producing a hybrid  
CC antibody or hybrid antibody fragment (claimed). The antibody and  
CC fragments are useful for therapeutic and diagnostic purposes. The method  
CC uses entire framework regions from a single antibody variable heavy or  
CC variable light chain to receive the CDRs. This produces antibodies that  
CC are highly homologous and exhibit reduced immunogenicity while  
CC maintaining an optimum binding profile. This sequence represents an  
CC antibody variable heavy chain which has good homology to an initial  
CC murine anti-human mannose binding lectin antibody (ADJ80371). The  
CC sequence was used to generate a hybrid antibody of the invention.

XX SQ Sequence 121 AA;  
Query Match 91.6%; Score 571.5; DB 7; Length 121;  
Best Local Similarity 90.9%; Pred. No. 1.6e-43;  
Matches 110; Conservative 1; Mismatches 5; Indels 5; Gaps 1;  
QY 2 VQLQESGPGLVKPSQTLSLTCTVSGGSISGGYVWIRQHPGKGLEWIGFYISGSTYY 61  
DB 1 VQLQESGPGLVKPSQTLSLTCTVSGGSISGGYVWIRQHPGKGLEWIGFYISGSTYY 60  
QY 62 NPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCAR-----EGDGFYWGQGLTVTVS 116  
DB 61 NPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARGLKWGSNHVFDYWGQGLTVTVS 120  
QY 117 S 117  
DB 121 S 121

RESULT 15  
ADP03977  
ID ADP03977 standard; protein; 122 AA.  
XX AC ADP03977;  
XX DT 29-JUL-2004 (first entry)  
XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 147.  
XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KW cytosstatic; colorectal neoplasm; renal cell carcinoma;  
KW cervical intraepithelial squamous neoplasia;  
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KW gene therapy; murine; mouse; human; heavy chain variable domain.  
XX Unidentified.  
XX WO2003048328-A2.  
XX PD 12-JUN-2003.  
XX PF 02-DEC-2002; 2002WO-US038550.  
XX PR 03-DEC-2001; 2001US-0337275P.  
XX PA (ABGE-) ABGENIX INC.  
XX Gudas J, Foltz I, Handa M, Gallo M;  
XX WPI; 2003-523295/49.  
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.;  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX Example 2; SEQ ID NO 147; 89pp; English.

XX CC The invention relates to a novel isolated monoclonal antibody (mAb)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cytostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.

XX SQ Sequence 122 AA;  
Query Match 91.4%; Score 570.5; DB 7; Length 122;  
Best Local Similarity 90.2%; Pred. No. 2e-43;  
Matches 110; Conservative 2; Mismatches 5; Indels 5; Gaps 1;  
QY 1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISGGYVWIRQHPGKGLEWIGFYISGSTY 60  
DB 1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISGGYVWIRQHPGKGLEWIGFYISGSTY 60  
QY 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCAR-----EGDGFYWGQGLTVTV 115  
DB 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARYYDILTGYGMDVWGQGLTVTV 120  
QY 116 SS 117  
DB 121 SS 122

Search completed: November 9, 2005, 12:55:25  
Job time : 72.1353 secs



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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55 ; Search time 18.1805 Seconds  
(without alignments)  
480.403 Million cell updates/sec

Title: US-10-660-357A-13  
Perfect score: 624  
Sequence: 1 QVQLQESGPGLVKPSQTSL.....AREGDFYWGQGLTVTSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	550	88.1	119	1	US-08-360-125-5
2	550	88.1	119	2	US-08-450-578-5
3	550	88.1	119	2	US-09-017-628-5
4	550	88.1	119	2	US-09-014-880-5
5	550	88.1	119	4	US-08-450-363-5
6	550	88.1	119	4	US-09-467-903-5
7	543	87.0	119	3	US-09-025-769B-39
8	543	87.0	119	3	US-09-025-769B-65
9	543	87.0	119	4	US-09-490-070A-39
10	543	87.0	119	4	US-09-490-070A-65
11	543	87.0	119	4	US-09-490-153-39
12	543	87.0	119	4	US-09-490-153-65
13	543	87.0	119	4	US-09-490-324-39
14	543	87.0	119	4	US-09-490-324-65
15	542.5	86.9	473	3	US-09-049-672A-4
16	542.5	86.9	487	4	US-09-800-729-145
17	537.5	84.5	118	3	US-09-025-769B-25
18	527.5	84.5	118	4	US-09-490-070A-25
19	527.5	84.5	118	4	US-09-490-153-25
20	527.5	84.5	118	4	US-09-490-324-25
21	527.5	84.5	122	1	US-08-360-125-11
22	527.5	84.5	122	2	US-08-450-578-11
23	527.5	84.5	122	2	US-09-017-628-11
24	527.5	84.5	122	2	US-09-014-880-11
25	527.5	84.5	122	4	US-08-450-363-11
26	527.5	84.5	122	4	US-09-467-903-11
27	525.5	84.2	172	4	US-09-472-087-7

28	525.5	84.2	172	4	US-09-472-087-86	Sequence 86, Appl
29	524	84.0	117	4	US-09-720-493-2	Sequence 2, Appli
30	517	82.9	118	3	US-08-545-809A-116	Sequence 116, App
31	511.5	82.0	120	4	US-09-424-840B-20	Sequence 20, Appl
32	510.5	81.8	244	3	US-08-918-148-79	Sequence 79, Appl
33	510.5	81.8	244	4	US-09-138-091A-77	Sequence 77, Appl
34	500	80.1	155	4	US-09-471-276-888	Sequence 888, App
35	495.5	79.4	139	4	US-09-471-276-837	Sequence 837, App
36	495	79.3	142	2	US-08-480-774A-2	Sequence 2, Appli
37	488	78.2	118	3	US-08-545-809A-142	Sequence 142, App
38	482.5	77.3	278	3	US-09-260-527-3	Sequence 3, Appli
39	482	77.2	119	2	US-08-652-816A-10	Sequence 10, Appl
40	481.5	77.2	139	4	US-09-203-768A-2	Sequence 2, Appli
41	481	77.1	118	3	US-08-545-809A-123	Sequence 123, App
42	480.5	77.0	150	4	US-09-582-337-14	Sequence 14, Appl
43	478	76.6	123	3	US-08-793-450-4	Sequence 4, Appli
44	476.5	76.4	98	1	US-08-478-039-75	Sequence 75, Appl
45	476.5	76.4	98	1	US-08-476-349A-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1  
US-08-360-125-5  
; Sequence 5, Application US/08360125  
; Patent No. 5767246  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA  
; APPLICANT: Toshiaki TAGAWA  
; APPLICANT: Yoko HIRAKAWA  
; APPLICANT: No. 5767246biko ITO  
; APPLICANT: Kazuhiro NAGAIKE  
; TITLE OF INVENTION: Human Monoclonal Antibody  
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
; TITLE OF INVENTION: Cell Membrane  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/360,125  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/905,534  
; FILING DATE: June 29, 1992  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

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; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
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; US-08-360-125-5
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; Query Match 88.1%; Score 550; DB 1; Length 119;
; Best Local Similarity 88.2%; Pred. No. 1.3e-48;
; Matches 105; Conservative 6; Mismatches 6; Indels 2; Gaps 1;
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; Db 1 QVQLQSGGCLVKPSQTLSTCTVSGGSISSCGFYNNWIRQHPGKGLWIGFIYSGSY 60
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; QY 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVVYCAREG--DGFYWGQGLTVTVSS 117
; Db 61 YNPSLKSRVTISLDTSKQFSLKLSLTAADTAVVYCARSRLRGADYWGQGLTVTVSS 119
;
; RESULT 2
; US-08-450-578-5
; Sequence 5, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5837845hiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
;
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,578
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
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; US-08-450-578-5
;
; Query Match 88.1%; Score 550; DB 2; Length 119;
; Best Local Similarity 88.2%; Pred. No. 1.3e-48;
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IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-467-903-5

Query Match 88.1%; Score 550; DB 4; Length 119;  
Best Local Similarity 88.2%; Pred. No. 1.3e-48;  
Matches 105; Conservative 6; Mismatches 6; Indels 2; Gaps 1;  
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKGLWIGFIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSCGFYNNWIRQHPGKGLWIGFIYSGSTY 60  
Qy 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCAREG--DGFYWGQGTLTVTSS 117  
Db 61 YNPSLKSRTVISLDTSKNQFSLKLSLTAADTAVYYCARSTRLRGADYWGQGTMTVTSS 119

RESULT 7  
US-09-025-769B-39  
Sequence 39, Application US/09025769B  
Patent No. 6300064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION NUMBER: EP 95 11 3021.0  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-39

Query Match 87.0%; Score 543; DB 3; Length 119;  
Best Local Similarity 90.1%; Pred. No. 6.6e-48;  
Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3;  
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKGLWIGFIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYNSWIRQPPGKGLWIGFIYSGSTN 58  
Qy 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCAR-EGDGF---DYWGQGTLTVTVS 116  
Db 59 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARWGGDGFYAMDYWGQGTLTVTVS 118  
Qy 117 S 117  
Db 119 S 119

RESULT 8  
US-09-025-769B-65  
Sequence 65, Application US/09025769B  
Patent No. 6300064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION NUMBER: EP 95 11 3021.0  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids



Db 59 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARWGGDGFYAMDYWGQGLTVTS 118

Qy 117 S 117

Db 119 S 119

## RESULT 11

US-09-490-153-39

; Sequence 39, Application US/09490153

; Patent No. 6706484

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; Pack, Peter

; Ilag, Vic

; Ge, Liming

; Moroney, Simon

; Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10021

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/490,153

; FILING DATE: 24-Jan-2000

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/025,769B

; FILING DATE: 18-FEB-1998

; APPLICATION NUMBER: EP 95 11 3021.0

; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: James F. Haley, Jr., Esq.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: MORPHO/5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)596-9000

; TELEFAX: (212)596-9090

; INFORMATION FOR SEQ ID NO: 39:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 119 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-09-490-153-39

Query Match

Best Local Similarity 87.08; Score 543; DB 4; Length 119;

Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYVTWIRQHPGKGLIEWIGFIYSGSTY 60

Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYNSWIRQPPGKGLIEWIGFIYSGSTN 58

Qy 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCAR-EGDGF---DYWGQGLTVTS 116

Db 59 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARWGGDGFYAMDYWGQGLTVTS 118

Qy 117 S 117

Db 119 S 119

## RESULT 12

US-09-490-153-65

; Sequence 65, Application US/09490153

; Patent No. 6706484

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; Pack, Peter

; Ilag, Vic

; Ge, Liming

; Moroney, Simon

; Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10021

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/490,153

; FILING DATE: 24-Jan-2000

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/025,769B

; FILING DATE: 18-FEB-1998

; APPLICATION NUMBER: EP 95 11 3021.0

; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: James F. Haley, Jr., Esq.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: MORPHO/5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)596-9000

; TELEFAX: (212)596-9090

; INFORMATION FOR SEQ ID NO: 65:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 119 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 65:

US-09-490-153-65

Query Match

Best Local Similarity 87.08; Score 543; DB 4; Length 119;

Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYVTWIRQHPGKGLIEWIGFIYSGSTY 60

Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYNSWIRQPPGKGLIEWIGFIYSGSTN 58

Qy 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCAR-EGDGF---DYWGQGLTVTS 116

Db 59 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARWGGDGFYAMDYWGQGLTVTS 118

Qy 117 S 117

Db 119 S 119

## RESULT 13

US-09-490-324-39

; Sequence 39, Application US/09490324

; Patent No. 6828422

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

;;  
;; Pack, Peter  
;; Ilag, Vic  
;; Ge, Liming  
;; Moroney, Simon  
;; Plueckthun, Andreas  
;;  
;; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
;;  
;; NUMBER OF SEQUENCES: 373  
;;  
;; CORRESPONDENCE ADDRESS:  
;;  
;; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
;; STREET: 1251 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10021

;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
;;  
;; CURRENT APPLICATION DATA: US/09/490,324  
;; FILING DATE: 24-Jan-2000

;;  
;; PRIOR APPLICATION NUMBER: US/09/025,769

;;  
;; FILING DATE: 18-FEB-1998  
;; APPLICATION NUMBER: EP 95 11 3021.0  
;; FILING DATE: 18-AUG-1995

;;  
;; ATTORNEY/AGENT INFORMATION:

;; NAME: James F. Haley, Jr., Esq.  
;; REGISTRATION NUMBER: 27,794  
;; REFERENCE/DOCKET NUMBER: MORPHO/5  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212)596-9000  
;; TELEFAX: (212)596-9090

;;  
;; INFORMATION FOR SEQ ID NO: 39:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 119 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: <Unknown>

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-09-490-324-39  
  
Query Match 87.0%; Score 543; DB 4; Length 119;  
Best Local Similarity 90.1%; Pred. No. 6.6e-48;  
Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3;

QY 1 QVQLQESGPGLVKPSOTLSLTCTVSGGSISGGYYWTWIRHPGKGLEWIGFIYSGSTY 60  
|||||  
Db 1 QVQLQESGPGLVKPSOTLSLTCTVSGGSISGGYYWTWIRHPGKGLEWIGFIYSGSTN 58  
|||||

QY 61 YNPISLKSRTVISVDTSKNQFSLKSSVTAADTAATVAVYCAR-EGDGF---DYWGQGTILVTYS 116  
|||||  
Db 59 YNPISLKSRTVISVDTSKNQFSLKSSVTAADTAATVAVYCARWGSDGFYAMDYWGQGTILVTYS 118  
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QY 117 S 117  
Db 119 S 119

RESULT 14  
US-09-490-324-65  
; Sequence 65, Application US/09490324  
; Patent No. 6828422  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Moroney, Simon  
; Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries

;;  
;; NUMBER OF SEQUENCES: 373  
;;  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
;; STREET: 1251 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10021

;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
;;  
;; CURRENT APPLICATION DATA: US/09/490,324  
;; FILING DATE: 24-Jan-2000

;;  
;; PRIOR APPLICATION NUMBER: US/09/025,769

;;  
;; FILING DATE: 18-FEB-1998  
;; APPLICATION NUMBER: EP 95 11 3021.0  
;; FILING DATE: 18-AUG-1995

;;  
;; ATTORNEY/AGENT INFORMATION:

;; NAME: James F. Haley, Jr., Esq.  
;; REGISTRATION NUMBER: 27,794  
;; REFERENCE/DOCKET NUMBER: MORPHO/5  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212)596-9000  
;; TELEFAX: (212)596-9090

;;  
;; INFORMATION FOR SEQ ID NO: 65:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 119 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; SEQUENCE DESCRIPTION: SEQ ID NO: 65:

US-09-490-324-65

Query Match 87.0%; Score 543; DB 4; Length 119;  
Best Local Similarity 90.1%; Pred. No. 6.6e-48;  
Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3;

QY 1 QVQLQESGPGLVKPSOTLSLTCTVSGGSISGGYYWTWIRHPGKGLEWIGFIYSGSTY 60  
|||||  
Db 1 QVQLQESGPGLVKPSOTLSLTCTVSGGSISGGYYWTWIRHPGKGLEWIGFIYSGSTN 58  
|||||

QY 61 YNPISLKSRTVISVDTSKNQFSLKSSVTAADTAATVAVYCAR-EGDGF---DYWGQGTILVTYS 116  
|||||  
Db 59 YNPISLKSRTVISVDTSKNQFSLKSSVTAADTAATVAVYCARWGSDGFYAMDYWGQGTILVTYS 118  
|||||

QY 117 S 117  
Db 119 S 119

RESULT 15  
US-09-490-672A-4  
; Sequence 4, Application US/09049672A  
; Patent No. 6135941  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Yue, Henry  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Baughn, Mariah R.  
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto



STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049,672A  
FILING DATE: HEREWITH  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cerrone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0497 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 473 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: PANTUT01  
CLONE: 1513264  
US-09-049-672A-4

Query Match 86.9%; Score 542.5; DB 3; Length 473;  
Best Local Similarity 84.7%; Pred. No. 3.9e-47;  
Matches 105; Conservative 5; Mismatches 7; Indels 7; Gaps 1;  
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Db |||||  
QY 20 QVQLQESGPGLVKPSOTLSLCTVSGGSISSGGYYWTWIRQHPKGLGWIGFIYSGSTL 79  
Db |||||  
QY 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVYYCARE-----GDGFDYWGQGTLLV 113  
Db |||||  
QY 80 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVYYCARE-----GDGFDYWGQGTLLV 139  
Db |||||  
QY 114 TVSS 117  
Db |||||  
QY 140 TVSS 143

Search completed: November 9, 2005, 11:46:38  
Job time : 19.1805 secs

RECEIVED 10/10/1964

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2005, 11:40:37 ; Search time 65 Seconds  
(without alignments)  
753.137 Million cell update/sec

Title: US-10-660-357A-13  
Perfect score: 624  
Sequence: 1 QVQLQSGPGLVKPSQTLSTLCTCTVSGGSISSGGYYVTWIRQHPGKGLGWIGFYISGSTY 60

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues  
Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	624	100.0	117	14	US-10-330-613-13
2	624	100.0	117	14	US-10-330-530-13
3	624	100.0	117	16	US-10-660-357-13
4	587.5	94.2	122	18	US-10-984-960A-20
5	587	94.1	117	14	US-10-330-613-5
6	587	94.1	117	14	US-10-330-530-5
7	587	94.1	117	16	US-10-660-357-5
8	585.5	93.8	118	15	US-10-309-762-138
9	581.5	93.2	125	17	US-10-805-177-53
10	579	92.8	123	15	US-10-309-762-10
11	575.5	92.2	120	15	US-10-309-762-13
12	575.5	92.2	120	15	US-10-309-762-144
13	574.5	92.1	122	18	US-10-984-960A-56
14	574.5	92.1	124	15	US-10-309-762-75
15	574.5	92.1	143	15	US-10-309-762-96
16	572	91.7	125	15	US-10-309-762-8
17	572	91.7	125	15	US-10-309-763-16
18	571.5	91.6	121	15	US-10-308-817-137
19	571.5	91.6	121	15	US-10-453-698-137
20	570.5	91.4	122	15	US-10-309-762-147
21	570	91.3	121	15	US-10-309-762-151
22	569	91.2	125	15	US-10-309-762-11
23	569	91.2	480	17	US-10-910-901-6
24	568	91.0	117	14	US-10-330-613-33
25	568	91.0	117	14	US-10-330-530-33
26	568	91.0	117	16	US-10-660-357-33
27	567	90.9	121	15	US-10-309-762-152
28	567	90.9	140	17	US-10-893-576-41
29	566	90.7	119	15	US-10-309-762-140
30	566	90.7	148	17	US-10-893-576-31
31	566	90.7	253	10	US-09-880-748-1619
32	566	90.7	253	15	US-10-293-418-1619
33	566	90.7	446	17	US-10-644-277-62
34	565.5	90.6	149	17	US-10-910-901-22
35	565	90.5	121	17	US-10-706-689-8
36	565	90.5	121	18	US-10-988-360-8
37	565	90.5	123	15	US-10-309-762-12
38	565	90.5	125	15	US-10-309-762-153
39	564.5	90.5	120	17	US-10-706-689-40
40	564.5	90.5	120	18	US-10-988-360-40
41	564	90.4	144	17	US-10-893-576-35
42	563	90.2	123	15	US-10-309-762-9
43	562.5	90.1	120	15	US-10-309-762-139
44	562.5	90.1	128	17	US-10-727-155-2
45	562.5	90.1	128	17	US-10-727-155-10

ALIGNMENTS

RESULT 1  
US-10-330-613-13  
; Sequence 13, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; US-10-330-613-13

Query Match	100.0%;	Score 624;	DB 14;	Length 117;
Best Local Similarity	100.0%;	Pred. No. 1e-47;		
Matches 117;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	QVQLQSGPGLVKPSQTLSTLCTVSGGSISSGGYYVTWIRQHPGKGLGWIGFYISGSTY	60	
Db	1	QVQLQSGPGLVKPSQTLSTLCTVSGGSISSGGYYVTWIRQHPGKGLGWIGFYISGSTY	60	
Qy	61	YNPSLSKRYTISVDTSKNQFSLKLSVTAADTAVYVCAREGDFYWGQGLTVVSS	117	
Db	61	YNPSLSKRYTISVDTSKNQFSLKLSVTAADTAVYVCAREGDFYWGQGLTVVSS	117	
RESULT 2				

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US-10-330-530-13
; Sequence 13, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-13

Query Match      100.0%; Score 624; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVYWTIRQHPGKGLEWIGFIYYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVYWTIRQHPGKGLEWIGFIYYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVVYCAREGDGFYWGQGLTVTVSS 117
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVVYCAREGDGFYWGQGLTVTVSS 117

RESULT 3
US-10-660-357-13
; Sequence 13, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-13

Query Match      100.0%; Score 624; DB 16; Length 117;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVYWTIRQHPGKGLEWIGFIYYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVYWTIRQHPGKGLEWIGFIYYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVVYCAREGDGFYWGQGLTVTVSS 117
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVVYCAREGDGFYWGQGLTVTVSS 117

RESULT 4
US-10-984-960A-20
; Sequence 20, Application US/10984960A
; Publication No. US20050142137A1
; GENERAL INFORMATION:
; APPLICANT: Gallo, Michael
; APPLICANT: Chui, Daniel
; APPLICANT: Zhong, Haihong
; APPLICANT: Ara, Gulshan
; APPLICANT: LaRoche, William J.
; TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
; FILE REFERENCE: Cura 970
; CURRENT APPLICATION NUMBER: US/10/984,960A
; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: 60/518,275
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 20
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-984-960A-20

Query Match      94.2%; Score 587.5; DB 18; Length 122;
Best Local Similarity 91.8%; Pred. No. 1.9e-44;
Matches 112; Conservative 4; Mismatches 1; Indels 5; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVYWTIRQHPGKGLEWIGFIYYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGVSISSGGYVYWTIRQHPGKGLEWIGFIYYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVVYCAREGD-----GFDYWGQGLTVTV 115
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVFYCAREGSYVDEGGFDYWGQGLTVTV 120

QY 116 SS 117
Db 121 SS 122

RESULT 5
US-10-330-613-5
; Sequence 5, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-5

Query Match      94.1%; Score 587; DB 14; Length 117;
Best Local Similarity 94.0%; Pred. No. 2e-44;
Matches 110; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVYWTIRQHPGKGLEWIGFIYYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVYWTIRQHPGKGLEWIGFIYYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVVYCAREGDGFYWGQGLTVTVSS 117
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVVYCAARGDGYKYGQGLTVTVSS 117

RESULT 6
US-10-330-530-5
; Sequence 5, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
```



```
RESULT 10
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-309-762-10

Query Match          92.8%; Score 579; DB 15; Length 123;
Best Local Similarity 90.2%; Pred. No. 1.1e-43;
Matches 111; Conservative 3; Mismatches 3; Indels 6; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYSGSY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWWSWIRQHPGKGLEWIGFIYSGSY 60

QY 61 YNPGLKSRVTISVDTSKNQFSLKLSVTAADTAVVYICAREGDG-----DYWGQGLTVT 114
Db 61 YNPGLKSRVTISVDTSKNQFSLKLSVTAADTAVVYICAREGDG-----DYWGQGLTVT 120

QY 115 VSS 117
Db 121 VSS 123

RESULT 11
US-10-309-762-13
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 120
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-309-762-13

Query Match          92.2%; Score 575.5; DB 15; Length 120;
Best Local Similarity 91.7%; Pred. No. 2.1e-43;
Matches 110; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYSGSY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWWSWIRQHPGKGLEWIGFIYSGSY 60

QY 61 YNPGLKSRVTISVDTSKNQFSLKLSVTAADTAVVYICAREGDG-----FDYWGQGLTVTSS 117
Db 61 YNPGLKSRVTISVDTSKNQFSLKLSVTAADTAVVYICAREGDG-----FDYWGQGLTVTSS 120

RESULT 12
US-10-309-762-144
; Sequence 144, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 120
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-309-762-144

Query Match          92.2%; Score 575.5; DB 15; Length 120;
Best Local Similarity 91.7%; Pred. No. 2.1e-43;
Matches 110; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYSGSY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWWSWIRQHPGKGLEWIGFIYSGSY 60

QY 61 YNPGLKSRVTISVDTSKNQFSLKLSVTAADTAVVYICAREGDG-----FDYWGQGLTVTSS 117
Db 61 YNPGLKSRVTISVDTSKNQFSLKLSVTAADTAVVYICAREGDG-----FDYWGQGLTVTSS 120

RESULT 13
US-10-984-960A-56
; Sequence 56, Application US/10984960A
; Publication No. US20050142137A1
; GENERAL INFORMATION:
; APPLICANT: Gallo, Michael
; APPLICANT: Chui, Daniel
; APPLICANT: Zhong, Hailong
; APPLICANT: Ara, Gulshan
; APPLICANT: LaRoche, William J.
; TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
; FILE REFERENCE: Cura 970
; CURRENT APPLICATION NUMBER: US/10/984,960A
; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: 60/518,275
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 56
; LENGTH: 122
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-984-960A-56

Query Match          92.1%; Score 574.5; DB 18; Length 122;
Best Local Similarity 89.3%; Pred. No. 2.6e-43;
Matches 109; Conservative 4; Mismatches 4; Indels 5; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYSGSY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWWSWIRQHPGKGLEWIGFIYSGSY 60
```

Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSIKSGDYYSWVRQLPGKGLWIGIYIYSGSTY 60  
QY 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCAREGD-----GFDYWGQGTLLTV 115  
Db 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCAREGSYYDSGGFDYWGQGTLLTV 120  
QY 116 SS 117  
Db 121 SS 122

RESULT 14  
US-10-309-762-75  
; Sequence 75, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
; FILE REFERENCE: AGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309,762  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/337275  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 75  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-75

Query Match 92.1%; Score 574.5; DB 15; Length 124;  
Best Local Similarity 89.5%; Pred. No. 2.7e-43;  
Matches 111; Conservative 3; Mismatches 3; Indels 7; Gaps 1;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYVYTWIRQHPKGLWIGIYIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYVYTWIRQHPKGLWIGIYIYSGSTY 60  
QY 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCAREG-----DGFYWGQGTLLV 113  
Db 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARENYDILITGFNWFDPWGQGTLLV 120  
QY 114 TVSS 117  
Db 121 TVSS 124

RESULT 15  
US-10-309-762-96  
; Sequence 96, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
; FILE REFERENCE: AGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309,762  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/337275  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 96  
; LENGTH: 143  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-10-309-762-96  
Query Match 92.1%; Score 574.5; DB 15; Length 143;  
Best Local Similarity 89.5%; Pred. No. 3.1e-43;  
Matches 111; Conservative 3; Mismatches 3; Indels 7; Gaps 1;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYVYTWIRQHPKGLWIGIYIYSGSTY 60  
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYVYTWIRQHPKGLWIGIYIYSGSTY 79  
QY 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCAREG-----DGFYWGQGTLLV 113  
Db 80 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARENYDILITGFNWFDPWGQGTLLV 139  
QY 114 TVSS 117  
Db 140 TVSS 143  
Search completed: November 9, 2005, 12:42:59  
Job time : 66 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2005, 12:25:58 ; Search time 12.609 Seconds  
(without alignments)  
892.802 Million cell updates/sec

Title: US-10-660-357A-13

Perfect score: 624

Sequence: 1 QVQLQESGPGLVKPSQTLTL.....AREGDFYWGQGLTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	549	88.0	147	2 S13519	Ig heavy chain V r
2	537	86.1	140	2 I37782	Ig variable region
3	530	84.9	135	2 S78051	Ig heavy chain pre
4	525	84.1	121	2 S44113	Ig heavy chain V r
5	524.5	84.1	130	2 S30534	Ig heavy chain V r
6	523	83.8	130	2 S31690	Ig heavy chain V r
7	518	83.0	128	2 S31514	Ig heavy chain - h
8	517	82.9	99	2 S26801	Ig heavy chain V r
9	517	82.9	116	2 S37456	Ig mu chain - huma
10	509	81.6	155	2 S31511	Ig heavy chain - h
11	507	81.2	146	2 S09710	Ig heavy chain V r
12	507	81.2	155	2 S31512	Ig heavy chain - h
13	506.5	81.2	139	2 S31586	Ig heavy chain V r
14	503.5	80.7	122	2 S69912	Ig V-D-J region (N
15	500	80.1	99	2 S26803	Ig heavy chain V r
16	499.5	80.0	137	2 S31676	Ig heavy chain V r
17	496.5	79.6	129	2 S44114	Ig heavy chain V r
18	495	79.3	99	2 S26802	Ig heavy chain V r
19	495	79.3	123	2 S30530	Ig heavy chain V r
20	494	79.2	146	2 S09711	Ig heavy chain V r
21	493.5	79.1	118	2 S20780	Ig heavy chain V r
22	488.5	78.3	145	2 S78055	Ig heavy chain pre
23	488	78.2	118	2 A26340	Ig heavy chain pre
24	488	78.2	140	2 A49045	Ig heavy chain V r
25	487	78.0	127	2 S19668	Ig heavy chain V r
26	486	77.9	99	2 S26807	Ig heavy chain V r
27	485.5	77.8	110	2 S44110	Ig heavy chain V-D
28	483.5	77.5	140	2 S78052	Ig heavy chain pre
29	483	77.4	139	2 S31696	Ig heavy chain V r

30	481	77.1	99	2 S12418	Ig heavy chain V r
31	480	76.9	109	2 PH1673	Ig heavy chain V r
32	478	76.6	135	2 S31604	Ig heavy chain V r
33	476.5	76.4	137	2 S31585	Ig heavy chain V r
34	472.5	75.7	126	2 S47010	Ig heavy chain V4.
35	472	75.6	97	2 S26906	Ig heavy chain V r
36	472	75.6	99	2 S26800	Ig heavy chain V r
37	472	75.6	105	2 S44125	Ig lambda chain V
38	472	75.6	124	2 S31684	Ig heavy chain V r
39	471.5	75.6	139	2 A41287	Ig heavy chain pre
40	471	75.5	99	2 S12412	Ig heavy chain V r
41	471	75.5	99	2 S26899	Ig heavy chain V r
42	471	75.5	116	2 B26340	Ig heavy chain pre
43	470	75.3	97	2 S12416	Ig heavy chain V r
44	470	75.3	120	2 PT0370	Ig mu chain precu
45	468.5	75.1	118	2 S24443	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S13519

Ig heavy chain V region precursor - human

C;Species: Homo sapiens (man)

C;Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C;Accession: S13519

R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.

Nucleic Acids Res. 19, 673, 1991

A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked A;Reference number: S13519; MUID:91187691; PMID:2011536

A;Accession: S13519

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-147 <MOR>

A;Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;41-125/Domain: immunoglobulin homology <IMM>

Query Match 88.0%; Score 549; DB 2; Length 147;  
Best Local Similarity 88.4%; Pred. No. 7.3e-42;  
Matches 107; Conservative 3; Mismatches 7; Indels 4; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLTLCTVSGSISGGYVWTWIRQHPGKLEWIGFYYSGSTY 60

Db 27 QLQLQESGPGLVKPSQTLTLCTVSGSISGGYVWTWIRQHPGKLEWIGFYYSGSTY 86

QY 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYICARE---GDGFDYWGQGLTVTVS 116

Db 87 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYICAREPDLWFGELFDYWGQGLTVTVS 146

QY 117 S 117

Db 147 S 147

RESULT 2

I37782

Ig variable region (VDJ) (clone T23-9) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999

C;Accession: I37782; S25476

R;Demaision, C.; Chaetagner, P.; Theze, J.; Zouali, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A;Title: Somatic diversification in the heavy chain variable region genes expressed by A;Reference number: A36876; MUID:94119917; PMID:8290556

A;Accession: I37782

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140 <RES>

A;Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583

C;Superfamily: immunoglobulin V region; immunoglobulin homology



A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-130 <CUI>  
A;Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;20-102/Domain: immunoglobulin homology <IMM>

Query Match 83.8%; Score 523; DB 2; Length 130;  
Best Local Similarity 82.7%; Pred. No. 1.3e-39;  
Matches 105; Conservative 3; Mismatches 7; Indels 12; Gaps 2;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPKGLGIEWGFIYSGSTY 60  
Db 6 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPKGLGIEWGFIYSGSTN 63

Qy 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAREGQD-----GFDYWGQG 110  
Db 64 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGSSVLLMFGELLYYFDYWGQG 123

Qy 111 TLVTVSS 117  
Db 124 TLVTVSS 130

RESULT 7  
S31514  
Ig heavy chain - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S31514  
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autoantibodies from

A;Reference number: S31509  
A;Accession: S31514  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-128 <CHA>  
A;Cross-references: EMBL:X69862; NID:g33086; PIDN:CAA49496.1; PID:g33087  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;22-106/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 518; DB 2; Length 128;  
Best Local Similarity 82.6%; Pred. No. 3.5e-39;  
Matches 100; Conservative 7; Mismatches 10; Indels 4; Gaps 1;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPKGLGIEWGFIYSGSTY 60  
Db 8 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPKGLGIEWGFIYSGSTY 67

Qy 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAR-----EGDGFYWGQGLTVTVSS 116  
Db 68 YNPFLKSRVTISVDTSKNQFSLRSTVTPADTAVYYCARINFGYGFDPWGQGLTVTVSS 127

Qy 117 S 117  
Db 128 S 128

RESULT 8  
S26801  
Ig heavy chain V region (DP-65) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 25-Oct-1996 #text\_change 20-Jun-2000  
C;Accession: S26801; S26900  
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.  
Eur. J. Immunol. 22, 1075-1082, 1992  
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.  
A;Reference number: S26800; MUID:92201299; PMID:1348029  
A;Accession: S26801  
A;Status: preliminary

A;Molecule type: DNA  
A;Residues: 1-99 <WEN>  
A;Cross-references: EMBL:Z14237; NID:g37706; PIDN:CAA78606.1; PID:g1335372  
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 517; DB 2; Length 99;  
Best Local Similarity 98.0%; Pred. No. 3.3e-39;  
Matches 97; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPKGLGIEWGFIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPKGLGIEWGFIYSGSTY 60

Qy 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAR 99  
Db 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAR 99

RESULT 9  
S37456  
Ig mu chain - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S37456  
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.  
submitted to the EMBL Data Library, September 1993  
A;Description: Cloning and analysis of human IGM anti-Thyroglobulin autoantibodies from

A;Reference number: S37453  
A;Accession: S37456  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-116 <NCI>  
A;Cross-references: EMBL:X75024; NID:g404313; PIDN:CAA52932.1; PID:g758095  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;6-90/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 517; DB 2; Length 116;  
Best Local Similarity 85.3%; Pred. No. 3.9e-39;  
Matches 99; Conservative 4; Mismatches 5; Indels 8; Gaps 1;

Qy 10 GLVKPSQTLSTCTVSGSISGGYYWTWIRQHPKGLGIEWGFIYSGSTYYPNPSLSRV 69  
Db 1 GLVKPSQTLSTCTVSGSISGGYYWTWIRQHPKGLGIEWGFIYSGSTYYPNPSLSRV 60

Qy 70 TISVDTSKNQFSLKSSVTAADTAVYYCAREGDFY-----KQGLTVTVSS 117  
Db 61 TISVDTSKNQFSLKSSVTAADTAVYYCARGGYSYGYYYMDVWGKGLTVTVSS 116

RESULT 10  
S31511  
Ig heavy chain - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S31511  
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autoantibodies from

A;Reference number: S31509  
A;Accession: S31511  
A;Status: preliminary

```
A:Molecule type: mRNA
A:Residues: 1-155 <CHA>
A:Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:47-129/Domain: immunoglobulin homology <IMM>

Query Match      81.6%; Score 509; DB 2; Length 155;
Best Local Similarity 80.8%; Pred. No. 2.7e-38;
Matches 101; Conservative 5; Mismatches 9; Indels 10; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKLEWIGFIYSGSTY 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 33 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYWSWIRQPPGKLEWIGFIYSGSAT 90
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 YNPPLKSRVTISVDTSKQFSLKSLSVTAADTAVYYCAREGD-----GFDYWGQGT 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 91 YNPPLKSRVTISVDTSKQFSLKSVTAADTAVYYCARGGGISSWYVYGMVDVWGQGT 150
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 113 VTVSS 117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 151 VTVSS 155

RESULT 11
S09710
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S09710
R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains
A:Reference number: S09710; MUID:90262535; PMID:2111699
A:Accession: S09710
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-146 <HUG>
A:Cross-references: GB:X52110; NID:g31447; PIDN:CAA36344.1; PID:g31448
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-118/Domain: immunoglobulin homology <IMM>

Query Match      81.2%; Score 507; DB 2; Length 146;
Best Local Similarity 77.2%; Pred. No. 3.9e-38;
Matches 98; Conservative 7; Mismatches 12; Indels 10; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKLEWIGFIYSGSTY 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20 QLRLQESGPGLVKPSQTLSTCTVSGGSISSGGLYWGWVROPFGKLEWIGSIFYSGSTY 79
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 YNPPLKSRVTISVDTSKQFSLKSLSVTAADTAVYYCAREGD-----FDYWGQ 110
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 YNPPLKSRVTISVDTLKNNFSLKSLSVTAADTAVYYCTRPGYGDTSVRKRVMNDLWGQ 139
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 111 TLTVSS 117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 140 TLTVSS 146

RESULT 12
S31512
Ig heavy chain - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31512
R:Chastagner, P.; Demaison, C.; There, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A:Reference number: S31509
A:Accession: S31512
A>Status: preliminary
A:Molecule type: mRNA
```

```
A:Residues: 1-155 <CHA>
A:Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:47-129/Domain: immunoglobulin homology <IMM>

Query Match      81.2%; Score 507; DB 2; Length 155;
Best Local Similarity 80.0%; Pred. No. 4.1e-38;
Matches 100; Conservative 6; Mismatches 9; Indels 10; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKLEWIGFIYSGSTY 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 33 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYWSWIRQPPGKLEWIGFIYSGSAT 90
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 YNPPLKSRVTISVDTSKQFSLKSLSVTAADTAVYYCAREGD-----GFDYWGQGT 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 91 YNPPLKSRVTISVDTSKQFSLKSVTAADTAVYYCARGGGISSWYVYGMVDVWGQGT 150
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 113 VTVSS 117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 151 VTVSS 155

RESULT 13
S31586
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31586
R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31586
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-139 <CU1>
A:Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match      81.2%; Score 506.5; DB 2; Length 139;
Best Local Similarity 84.4%; Pred. No. 4.1e-38;
Matches 103; Conservative 4; Mismatches 8; Indels 7; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKLEWIGFIYSGSTY 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYWSWIRQPPGKLEWIGFIYSGSTN 77
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 YNPPLKSRVTISVDTSKQFSLKSLSVTAADTAVYYCAREGD-----PDYWGQGT 115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 78 YNPPLKSRVTISVDTSKQFSLKSLSVTAADTAVYYCARGGLGIRRGAFDIWGQGTMTVT 137
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 116 SS 117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 138 SS 139

RESULT 14
S69912
Ig V-D-J region (ND) - human
C:Species: Homo sapiens (man)
C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69912
R:Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
Leukemia 8, 1285-1289, 1994
A:Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multi
A:Reference number: S69909; MUID:94335315; PMID:8057663
A:Accession: S69912
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-122 <SAH>
```

A; Cross-references: EMBL:Z33398; NID:g87l347; PIDN:CAA83849.1; PID:g9887460  
 A; Note: the sequence of residues 108-122 and the corresponding nucleic acid sequence are  
 C; Superfamily: immunoglobulin V region; immunoglobulin homology  
 F; 15-99/Domain: immunoglobulin homology <IMM>

Query Match	80.7%;	Score	503.5;	DB	2;	Length	122;
Best Local Similarity	79.5%;	Pred. No.	6.5e-38;				
Matches	97;	Conservative	11;	Mismatches	9;	Indels	5; Gaps 2;

  

QY	1	QVQLQSGGPGLVKPSQTLSLTCTVSGGSISGGYYWTWIRHCPKGLEWIGFIYVGSSGY	60	
	:	: :		
Dd	1	RVLQSQSGGLVPSPQSLTSCVSIGSISDGHFWNWIQHCPKGLEWIGNIYFGSSY	60	
	:	: :~		
QY	61	YNPFLSKSRVTISVDTSKNQFSLKLSSVTAADTAIVYCAR---	EGD-GFDYWGQGTILVTV	115
	:	: :~		
Dd	61	YNPFLSKRSISVDTSKNQFSLRLKSVTAADTAIVYFCARGFFPRGT	VGLDTWGQGTILVRL	120
	:	: :~		
QY	116	SS	117	
Dd	121	SS	122	

**RESULT 15**

S26803  
IG heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13  
C:Accession: S26803  
R:Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.  
Eur. J. Immunol. 22, 1075-1082, 1992  
A:Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.  
A:Reference number: S26800; MUID:92201299; PMID:1348029  
A:Accession: S26803  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-99 <WEN>  
A:Cross-references: EMBL:Z14238; NID:g37710; PIDN:CAA78607.1; PID:g1335374  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F15-99/Domain: immunoglobulin homology <IMM>

	Query Match Best Local Matches	Similarity 96.0%; 95;	Conservative 2;	Mismatches 2;	Indels 0;	Gaps 0;	Score 500;	DB 2;	Length 99;
QY	1	QVQLQESGPGLVKPSQTL	SLTCTCTVSGGSI	SSGGYYT	WI	RQHPGKGL	EWIGFI	YSGSTY	60
Db	1	QVQLQESGPGLVKPSQTL	SLTCTCTVSGGSI	SSGGYYW	SWIRQ	HPGKGL	EWIGFI	YSGSTY	60
QY	61	YNPSLKS	RVTISVD	TSKNQFSL	KSSV	TAADTAV	YVCAR		99
Db	61	YNPSLKS	RVTISVD	TSKNQFSL	KSSV	TAADTAV	YVCAR		99

Search completed: November 9, 2005, 13:08:02  
Job time : 12.609 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:46:52 ; Search time 60.406 Seconds  
(without alignments)  
991.843 Million cell updates/sec

Title: US-10-660-357A-13  
Perfect score: 624  
Sequence: 1 QVQLQSGPGLVKPQSTLSL.....AREGDGFDYWGQTLTVTSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	552	88.5	476	2	Q6GMX1
2	518.5	83.1	478	2	Q7Z379
3	507.5	81.3	465	2	Q6GMX6
4	506	81.1	119	2	Q9UL73
5	503.5	80.7	150	2	Q95973
6	499.5	80.0	436	2	Q96KX8
7	497.5	79.7	477	2	Q6GMX7
8	492.5	78.9	620	2	Q96EY0
9	492	78.8	492	2	Q7Z374
10	488.5	78.3	576	2	Q6P418
11	481.5	77.2	130	2	Q81ZD7
12	474.5	76.0	139	2	Q86SX2
13	465	74.5	129	1	HV2F_HUMAN
14	445	71.3	478	2	Q6NYH3
15	444	71.2	595	2	Q8WUX4
16	444	71.2	597	2	Q6GMX5
17	444	71.2	597	2	Q9BU10
18	444	71.2	625	2	Q96AA6
19	438	70.2	597	2	Q9BQB8
20	437.5	70.1	146	1	HV2I_HUMAN
21	432	69.2	137	1	HV46_MOUSE
22	428.5	68.7	136	2	Q6L8Q5
23	425	68.1	479	2	Q99M22
24	423.5	67.9	122	2	Q9UL75
25	419.5	67.2	473	2	Q8TC63
26	415	66.5	117	1	HV2G_HUMAN
27	410	65.2	262	2	Q65ZT1
28	407	65.2	116	2	Q7Z3Y6
29	405	64.9	113	1	HV47_MOUSE
30	404	64.7	476	2	Q6MZX7
31	379.5	60.8	116	1	HV60_MOUSE

32	378	60.6	117	1	HV62_MOUSE
33	374.5	60.0	116	1	HV61_MOUSE
34	367	58.8	121	2	Q9UL96
35	359.5	57.6	482	2	Q91X92
36	359	57.5	144	1	HV43_MOUSE
37	357.5	57.3	118	2	Q811U5
38	353.5	56.7	121	2	Q99NG4
39	353.5	56.7	135	1	HV02_XENLA
40	340	54.5	118	2	Q9UL74
41	330	52.9	470	2	Q6PJA4
42	329.5	52.8	118	2	Q9UL72
43	329	52.7	240	2	Q65ZC9
44	328.5	52.6	147	2	Q9Y509
45	328	52.6	125	1	HV2D_HUMAN

#### ALIGNMENTS

RESULT 1  
Q6GMX1 PRELIMINARY; PRT; 476 AA.  
AC Q6GMX1  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan K.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalón D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
EMBL; BC073773; AAH73773.1; -  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; C1-set; 3.  
DR Pfam; PF00047; IG; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00230; IG\_MHC; UNKNOWN\_2.

```
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DD59D CRC64;

Query Match      88.5%; Score 552; DB 2; Length 476;
Best Local Similarity 82.7%; Pred. No. 8.3e-48;
Matches 105; Conservative 8; Mismatches 4; Indels 10; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSGGYVYTWIRQHPGKGLEWIGFIYYSGSTY 60
   |||||
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGSISSGGYVYTWIRQHPGKGLEWIGFIYYSGSTY 79
   |||||

QY 61 YNPSLSKSRVTISVDTSKNQFSLKSSVTAADTAATVAVYCAR-EGDGFYWGQGLTVTVSS 110
   |||||
Db 80 YNPSLSKSRVTISLDTSKNQFSLKNSVTAADTAATVAVYCARAGVWGSFRSAIDGFIWQGG 139
   |||||

QY 111 TLTVTVSS 117
   |||||
Db 140 TMVTVSS 146
   |||||

RESULT 2
Q72379 PRELIMINARY; PRT; 478 AA.
AC Q72379;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686K04218 (Fragment).
GN Names=DKFZp686K04218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Human rectum tumor;
RC Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538066; CAD97996.1; -.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match      83.1%; Score 518.5; DB 2; Length 478;
Best Local Similarity 80.0%; Pred. No. 2.2e-44;
Matches 96; Conservative 14; Mismatches 7; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSGGYVYTWIRQHPGKGLEWIGFIYYSGSTY 60
   |||||
Db 19 QVQLQESGPGLVKPSQTLSTCTVSGSISSGGYVYTWIRQHPGKGLEWIGFIYYSGSTY 78
   |||||

QY 61 YNPSLSKSRVTISVDTSKNQFSLKSSVTAADTAATVAVYCAR-EGDGFYWGQGLTVTVSS 117
   |||||
Db 79 YNPSLSKSRVTISLDTSKNQFSLKNSVTAADTAATVAVYCARAGVWGLGTAFDIWMGQGVTVTVSS 138
   |||||

RESULT 3
Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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```
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Primary B-Cells;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP TISSUE=Primary B-Cells;
RC Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match      81.3%; Score 507.5; DB 2; Length 465;
Best Local Similarity 87.3%; Pred. No. 2.8e-43;
Matches 103; Conservative 3; Mismatches 9; Indels 3; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSGGYVYTWIRQHPGKGLEWIGFIYYSGSTY 60
   |||||
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGSIS--GYVSWIRQHPGKLEWIGFIYYSGSTN 77
   |||||

QY 61 YNPSLSKSRVTISVDTSKNQFSLKSSVTAADTAATVAVYCAR-EGDGFYWGQGLTVTVSS 117
   |||||
Db 78 YNPSLSKSRVTMSVDTSKNQFSLKSSVTAADTAATVAVYCARGRFTYFDYWGQGLTVTVSS 135
   |||||

RESULT 4
Q9UL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1] NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035041; AAD56277.1; -.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM003596; Ig_v.
DR PROSITE; PS00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER 1
FT NON TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;

Query Match 81.1%; Score 506; DB 2; Length 119;
Best Local Similarity 82.6%; Pred. No. 9.1e-44;
Matches 100; Conservative 7; Mismatches 8; Indels 6; Gaps 2;

Qy 1 QVLOESGPGGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPKGLGWIGFIYSGSTY 60
Db 1 QVLOESGPGGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPKGLGWIGFIYSGSTN 58
Qy 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVVYCAREGDG---FDYWGQGTLTVTS 116
Db 59 YTPSLKSRVTISVDRSKNQPSLKLSTLTADTAVYFCARLSNWCYFYFDYWGQGTLTVTS 118
Qy 117 S 117
Db 119 S 119

RESULT 5
ID O95973 PRELIMINARY; PRT; 150 AA.
AC O95973;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Vh4 heavy chain variable region precursor (fragment).
GN Name=IGM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1] SEQUENCE FROM N.A.
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103795; AAC79084.1; -.
DR PIR; S31673; S31673.
DR HSSP; P01820; 1G7J.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 >150 Vh4 heavy chain variable region.
FT NON TER 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 80.7%; Score 503.5; DB 2; Length 150;
Best Local Similarity 83.1%; Pred. No. 2.1e-43;

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Matches 98; Conservative 8; Mismatches 11; Indels 1; Gaps 1;

Qy 1 QVLOESGPGGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPKGLGWIGFIYSGSTY 60
Db 20 QLOLQESGPGGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPKGLGWIGFIYSGSDY 79
Qy 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVVYCAREGDG---FDYWGQGTLTVTS 117
Db 80 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVVYCARLGMGAFFDWGHTMTVTS 137

RESULT 6
Q96KX8
ID O96KX8 PRELIMINARY; PRT; 496 AA.
AC O96KX8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC27165 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1] SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Ziegler B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.M., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2] SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016369; AAH16369.1; -.
DR HSSP; P01876; 1OW0.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 80.0%; Score 499.5; DB 2; Length 496;
Best Local Similarity 79.0%; Pred. No. 2e-42;
Matches 98; Conservative 4; Mismatches 15; Indels 7; Gaps 1;

Qy 1 QVLOESGPGGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPKGLGWIGFIYSGSTY 60
Db 20 QLOLQESGPGGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPKGLGWIGFIYSGIT 79
Qy 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVVYCAREGD-----DGFYWGQGT 113

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Qy 116 SS 117
Db 145 SS 146

RESULT 9
Q72374 PRELIMINARY; PRT; 492 AA.
AC Q72374;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZ5686C02218 (Fragment).
GN Name=DKFZ5686C02218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Bocher M., Newes H.W., Weil B., Amid C., Osanger A.,
RA Robo G., Han M., Wleemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538077; CAD98001.1; -.
DR HSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 78.8%; Score 492; DB 2; Length 492;
Best Local Similarity 77.7%; Pred.No. 1.1e-41;
Matches 94; Conservative 11; Mismatches 12; Indels 4; Gaps 1;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVWIRQHPGKGLWIGFIYSGSTY 60
Db 32 QLQLQESGPGLVKPSQTLSTCTVSGSISGGYVWIRQHPGKGLWIGFIYSGSTY 91
Qy 61 YNPSLKSRLTIFVDTSKNHFSLRLTSVTAADTAVYVCAREGDG----FDYWGQGLTVTS 116
Db 92 YSPSLKSLRTIFVDTSKNHFSLRLTSVTAADTAVYVCAREGDG----FDYWGQGLTVTS 151
Qy 117 S 117
Db 152 S 152

RESULT 10
Q6P418 PRELIMINARY; PRT; 576 AA.
AC Q6P418;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG protein.
GN Name=IGHB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -.
DR HSP; P01820; 1A7N.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 576 AA; 63363 MW; FB897C949D720F1E CRC64;

Query Match 78.3%; Score 488.5; DB 2; Length 576;
Best Local Similarity 81.8%; Pred.No. 3.1e-41;
Matches 99; Conservative 4; Mismatches 13; Indels 5; Gaps 2;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVWIRQHPGKGLWIGFIYSGSTY 60
Db 27 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVWIRQHPGKGLWIGFIYSGSTN 85
Qy 61 YNPSLKSRLTISVDTSKNQFSLKSLSSVTAADTAVYVCAREGD---GFDYWGQGLTVTS 116
Db 86 YNPSLKSRLTISVDTSKNQFSLKSLSSVTAADTAVYVCAREGD---GFDYWGQGLTVTS 145
Qy 117 S 117
Db 146 S 146

RESULT 11
Q81ZD7 PRELIMINARY; PRT; 130 AA.
AC Q81ZD7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-thyroglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jang Y.-J., Chung J., Park J.-Y.;

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RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV145445; AAN64329.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 130
FT SEQUENCE 130 AA; 13901 MW; 036131FC6EC1551E CRC64;

Query Match 77.2%; Score 481.5; DB 2; Length 130;
Best Local Similarity 75.4%; Pred. No. 3.2e-41;
Matches 98; Conservative 6; Mismatches 13; Indels 13; Gaps 3;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKLEWIGFIYSGST- 59
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKLEWIGFIYSGSTV 60

QY 60 ----YNPISLKSRTVISVDTSKNQFSLKLSSTVTAADTAVYYCAR----EGDG----FDYW 107
Db 61 SGSPYAPSLRSRVIIISVDTSKNQLSLRSSVTAADTAVYYCASPTHCSGGGCGYAFFQHW 120

QY 108 GQGLTVTVSS 117
Db 121 GQGLTVTVSS 130

RESULT 12
Q86SX2 PRELIMINARY; PRT; 139 AA.
AC Q86SX2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line) of
DE Homo sapiens (human) (Fragment).
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=B cells;
RC SEQUENCE FROM N.A.
RA Li W.B., Gruber C., Jesse J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP TISSUE=B cells;
RC SEQUENCE FROM N.A.
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248300; CAD62627.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 139
FT SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 76.0%; Score 474.5; DB 2; Length 139;
Best Local Similarity 89.5%; Pred. No. 1.8e-40;
Matches 94; Conservative 4; Mismatches 2; Indels 5; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKLEWIGFIYSGSTY 60
Db 33 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYWSWIRQHPGKLEWIGFIYSGSTN 90

QY 61 YNPISLKSRTVISVDTSKNQFSLKLSSTVTAADTAVYYCARE---GD 102
Db 91 YNPISLKSRTVISVDTSKNQFSLKLSSTVTAADTAVYYCARDTVRGD 135
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RESULT 13
HV2F_HUMAN STANDARD; PRT; 129 AA.
ID HV2F_HUMAN
AC P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-II region WAH.
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82222235; PubMed=6806818;
RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
RT immunoglobulin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
CC -!- MISCELLANEOUS: This chain was isolated from an IgD myeloma
CC protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02099; D2HUWA.
DR HSSP; P01820; IG7J.
DR GlycoSuiteDB; P01824; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 113
FT NON_TER 129 129
FT SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 74.5%; Score 465; DB 1; Length 129;
Best Local Similarity 69.0%; Pred. No. 1.5e-39;
Matches 89; Conservative 10; Mismatches 18; Indels 12; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKLEWIGFIYSGSTY 60
Db 1 RLQLQESGPGLVKPSQTLSTCTVSGGPIRRRTGIYWGWIQPPGKLEWIGGIYSGSIY 60

QY 61 YNPISLKSRTVISVDTSKNQFSLKLSSTVTAADTAVYYCAR-----EGDGFYWG 108
Db 61 YNPISLGRVTISVDTSRNQFSLNLSMSAADTAMYYCARGNPPYYDICTGSDGIDVNG 120

QY 109 GQGLTVTVSS 117
Db 121 GQGLTVTVSS 129

RESULT 14
Q6NYH3 PRELIMINARY; PRT; 478 AA.
ID Q6NYH3
AC Q6NYH3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
```

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RA Strausberg R.;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC066594; AAH66594.1; -  
 DR HSSP; P01820; 1A7N.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 2.  
 DR SMART; SM00409; IG; 4.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 478 AA; 51856 MW; 5F8B98F60F077256 CRC64;

Query Match 71.3%; Score 445; DB 2; Length 478;  
 Best Local Similarity 71.3%; Pred. No. 7e-37;  
 Matches 86; Conservative 17; Mismatches 12; Indels 6; Gaps 2;

QY 1 QVQLQSGPGLVPSQTLSTCTVSGGSISSGGYYVTWIRQHPGKGLWIGFIYSGSTY 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 DB 20 QVQLQSGPGLVPSQTLSTCTVSGGSISSGGYYVTWIRQHPGKGLWIGFIYSGSTL 77  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 QY 61 YNPGLSRVTISVDTSKNQPSLKLSSVTAADTAVYYCAR---FDYWGQGLTVTS 116  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 DB 78 YNPGLSRVTISVDTSKNQPSLKLSSVTAADTAVYYCAR---FDYWGQGLTVTS 137  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 QY 117 S 117  
 DB 138 S 138

RESULT 15

Q8WUX4 PRELIMINARY; PRT; 595 AA.  
 AC Q8WUX4;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC019235; AAH19235.2; -  
 DR PIR; G34964; G34964.  
 DR HSSP; P01861; 1ADQ.  
 DR Pfam; PF07654; Cl-set; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 4.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS00835; IG LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;

Query Match 71.2%; Score 444; DB 2; Length 595;  
 Best Local Similarity 73.2%; Pred. No. 1.1e-36;  
 Matches 93; Conservative 6; Mismatches 16; Indels 12; Gaps 3;

QY 1 QVQLQSGPGLVPSQTLSTCTVSGGSISSGGYYVTWIRQHPGKGLWIGFIYSGSTY 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 DB 27 QVQLQSGPGLVPSQTLSTCTVSGGSISSGGYYVTWIRQHPGKGLWIGFIYSGSTN 84  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 QY 61 YNPGLSRVTISVDTSKNQPSLKLSSVTAADTAVYYCAR-----EGD-CFDYWGQ 110  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 DB 85 YNPGLSRVTISVDTSKNQPSLKLSSVTAADTAVYYCAR-----EGD-CFDYWGQ 144  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 QY 111 TLTVSS 117  
 DB 145 TLTVSS 151

Search completed: November 9, 2005, 13:05:48  
 Job time : 61.406 secs

CHINA XIN KONG CHINA

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:43:32 ; Search time 74.6015 Seconds  
(without alignments)  
627.306 Million cell updates/sec

Title: US-10-660-357A-17

Perfect score: 649

Sequence: 1 QVQLQESGGLVLRPSETLSL.....WLLPDAFDINGQGTMTVTSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	649	100.0	121	7	ADC99772 Anti-huma
2	649	100.0	121	7	ADC99788 Anti-huma
3	649	100.0	121	7	Ado05376 Anti-MUC1
4	649	100.0	121	7	Ado05392 Anti-MUC1
5	649	100.0	121	7	Adf09814 Human ant
6	649	100.0	121	7	Adf09830 Human ant
7	643	99.1	121	7	Adc99780 Anti-huma
8	643	99.1	121	7	Ado05384 Anti-MUC1
9	643	99.1	121	7	Adf09822 Human ant
10	597	92.0	121	7	Adc99808 Anti-huma
11	597	92.0	121	7	Ado05412 Anti-MUC1
12	597	92.0	121	7	Adf09850 Human ant
13	565	87.1	243	8	Ado058076 S9 cell d
14	547	84.3	121	5	Abg92884 Human imm
15	545	84.1	121	5	Abb07171 ebvHigM M
16	545	84.1	121	8	Adi26658 Human ant
17	545	84.1	122	7	Adp03887 Murine-ex
18	545	84.1	122	7	Adp03884 Murine-ex
19	544	83.9	122	7	Adp03885 Murine-ex
20	544	83.9	122	7	Adp03889 Murine-ex
21	540	83.2	119	2	Aaw27554 Human Ab
22	540	83.2	119	6	Abj18676 Antibody
23	539	83.1	118	8	Adp22272 Human ant
24	539	83.1	123	6	Ada89258 Human ant
25	538	83.0	122	7	Adp03931 Murine-ex

26	536.5	82.7	120	7	ADP03864	Adp03864 Murine-ex
27	536.5	82.7	120	7	ADP03862	Adp03862 Murine-ex
28	536.5	82.7	121	7	ADP03984	Adp03984 Murine-ex
29	536	82.6	119	7	ADP03973	Adp03973 Murine-ex
30	536	82.6	125	7	ADP03871	Adp03871 Murine-ex
31	535.5	82.5	246	3	AAy15126	AAy15126 Anti-muri
32	534.5	82.4	122	7	ADP03933	Adp03933 Murine-ex
33	533.5	82.2	124	7	ADP03886	Adp03886 Murine-ex
34	533.5	82.2	193	5	ABP43199	ABp43199 Human ova
35	532.5	82.0	128	8	ADP19313	Adp19313 Heavy cha
36	531.5	81.9	120	2	AAW90287	AAw90287 Human ant
37	531.5	81.9	126	5	ABG92888	ABg92888 Human imm
38	531	81.8	125	7	ADP03868	Adp03868 Murine-ex
39	531	81.8	125	7	ADP03876	Adp03876 Murine-ex
40	529.5	81.6	114	5	ABG97827	ABg97827 Human MPL
41	529.5	81.6	114	5	ABG53504	ABg53504 Thrombopo
42	529.5	81.6	133	5	ABG97829	ABg97829 Mouse 12E
43	529.5	81.6	133	5	ABG53531	ABg53531 Thrombopo
44	529.5	81.6	244	2	AAy06718	AAy06718 Antibody
45	529.5	81.6	244	8	ADO39737	Ado39737 Human C-m

## ALIGNMENTS

## RESULT 1

ADC99772  
ID ADC99772 standard; protein; 121 AA.

XX AC ADC99772;

XX AC (first entry)

DT 01-JAN-2004 (first entry)

DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 1.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
cystostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
lung cancer; human.

XX Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

XX N-PSDB; ADCS9774.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
or condition associated with expression of MUC18 in a patient, e.g.  
tumors, cancers, and other malignancies.

XX Claim 1; SEQ ID NO 1; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising  
a heavy or light chain amino acid or a heavy or light chain variable  
domain where the antibody binds to MUC18. The monoclonal antibody of the  
invention demonstrates cytostatic activity and may be useful for treating  
a disease or condition associated with the expression of MUC18 on the  
cell surface such as tumours, specifically melanoma, oesophageal,  
pancreatic or colorectal tumours, carcinomas, particularly cervical  
carcinomas and cervical intraepithelial neoplasia and cancers including  
colorectal, breast or lung cancer, as well as other malignancies. The  
current sequence is that of the anti-human MUC18 monoclonal antibody

CC heavy chain protein of the invention.  
XX  
SQ Sequence 121 AA;

Query Match 100.0%; Score 649; DB 7; Length 121;  
Best Local Similarity 100.0%; Pred. No. 6.4e-46;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSYYWSWIROPKGLWIGYIYYTWSN 60  
Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSYYWSWIROPKGLWIGYIYYTWSN 60  
  
QY 61 PSLKSRVTISVDTSKNQPSLRSLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
Db 61 PSLKSRVTISVDTSKNQPSLRSLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
  
QY 121 S 121  
Db 121 S 121

RESULT 2  
ADC99788  
ID ADC99788 standard; protein; 121 AA.  
XX  
AC ADC99788;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 17.  
XX  
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003057838-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 26-DEC-2002; 2002WO-US041581.  
XX  
PR 28-DEC-2001; 2001US-0346299P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J;  
XX  
XX WPI; 2003-587113/55.  
DR N-PSDB; ADC99790.  
XX  
XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
PT or condition associated with expression of MUC18 in a patient, e.g.  
PT tumors, cancers, and other malignancies.  
XX  
XX Claim 1; SEQ ID NO 17; 78pp; English.  
PS  
XX The invention relates to a novel isolated monoclonal antibody comprising  
CC a heavy or light chain amino acid or a heavy or light chain variable  
CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
CC invention demonstrates cytostatic activity and may be useful for treating  
CC a disease or condition associated with the expression of MUC18 on the  
CC cell surface such as tumours, specifically melanoma, oesophageal,  
CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
CC carcinomas and cervical intraepithelial neoplasia and cancers including  
CC colorectal, breast or lung cancer, as well as other malignancies. The  
CC current sequence is that of the anti-human MUC18 monoclonal antibody  
CC heavy chain protein of the invention.  
XX  
SQ Sequence 121 AA;

Query Match 100.0%; Score 649; DB 7; Length 121;  
Best Local Similarity 100.0%; Pred. No. 6.4e-46;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSYYWSWIROPKGLWIGYIYYTWSN 60  
Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSYYWSWIROPKGLWIGYIYYTWSN 60  
  
QY 61 PSLKSRVTISVDTSKNQPSLRSLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
Db 61 PSLKSRVTISVDTSKNQPSLRSLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
  
QY 121 S 121  
Db 121 S 121

RESULT 3  
ADD05376  
ID ADD05376 standard; protein; 121 AA.  
XX  
AC ADD05376;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 1.  
XX  
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
XX  
OS Homo sapiens.  
XX  
PN WO2003057006-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 26-DEC-2002; 2002WO-US041582.  
XX  
PR 28-DEC-2001; 2001US-0346460P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J, Bar-Eli M;  
XX  
XX WPI; 2003-577496/54.  
DR N-PSDB; ADD05378.  
XX  
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
PT associated with melanoma, or increasing survival of an animal having a  
PT metastatic tumor.  
XX  
XX Claim 1; SEQ ID NO 1; 87pp; English.  
PS  
XX The invention relates to a novel monoclonal antibody used for inhibiting  
CC tumour growth in an animal. The tumour inhibition process comprises  
CC selecting an animal in need of treatment for a tumour, providing a  
CC monoclonal antibody comprising a heavy chain amino acid, where the  
CC antibody consists of any one of 10 fully defined sequences of 117-123  
CC amino acids given in the specification, and where the monoclonal antibody  
CC binds MUC18, and contacting the tumour with the antibody resulting in  
CC inhibited proliferation of the cells. The monoclonal antibody has  
CC cytostatic and can be used in the production of a vaccine. The monoclonal  
CC antibodies against the MUC18 antigen are useful for diagnosing and  
CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or  
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
CC increasing survival of an animal having a metastatic tumour. This  
CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
CC protein of the invention.  
XX  
SQ Sequence 121 AA;

Query Match 100.0%; Score 649; DB 7; Length 121;



Best Local Similarity 100.0%; Pred. No. 6.4e-46;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPESETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGIYYTWTSNYN 60  
Db 1 QVQLQESGPGLVKPESETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGIYYTWTSNYN 60

Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAIVYCARDQGWLLPDAFDIWGQGTMTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAIVYCARDQGWLLPDAFDIWGQGTMTVTS 120

Qy 121 S 121  
Db 121 S 121

RESULT 4  
ADD05392  
ID ADD05392 standard; protein; 121 AA.

XX AC ADD05392;  
XX  
DT 01-JAN-2004 (first entry)  
XX DE  
XX DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 17.  
XX KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
XX KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
XX OS Homo sapiens.  
XX PN WO2003057006-A2.  
XX PD 17-JUL-2003.  
XX PF 26-DEC-2002; 2002WO-US041582.  
XX PR 28-DEC-2001; 2001US-0346460P.  
XX PA (ABGE-) ABGENIX INC.  
XX PI Gudas J, Bar-Eli M;  
XX PI WPI; 2003-577496/54.  
XX DR N-PSDB; ADD05394.  
XX

PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
PT associated with melanoma, or increasing survival of an animal having a  
PT metastatic tumor.  
XX  
PS Claim 1; SEQ ID NO 17; 87pp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting  
XX tumour growth in an animal. The tumour inhibition process comprises  
XX selecting an animal in need of treatment for a tumour, providing a  
XX monoclonal antibody comprising a heavy chain amino acid, where the  
XX antibody consists of any one of 10 fully defined sequences of 117-123  
XX amino acids given in the specification, and where the monoclonal antibody  
XX binds MUC18, and contacting the tumour with the antibody resulting in  
XX inhibited proliferation of the cells. The monoclonal antibody has  
XX cytostatic and can be used in the production of a vaccine. The monoclonal  
XX antibodies against the MUC18 antigen are useful for diagnosing and  
XX treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or  
XX tumour metastasis), inhibiting cell invasion associated with melanoma, or  
XX increasing survival of an animal having a metastatic tumour. This  
XX sequence represents an anti-MUC18 antibody heavy chain, variable region,  
XX protein of the invention.

XX SQ Sequence 121 AA;  
Query Match 100.0%; Score 649; DB 7; Length 121;  
Best Local Similarity 100.0%; Pred. No. 6.4e-46;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPESETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGIYYTWTSNYN 60  
Db 1 QVQLQESGPGLVKPESETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGIYYTWTSNYN 60

Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAIVYCARDQGWLLPDAFDIWGQGTMTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAIVYCARDQGWLLPDAFDIWGQGTMTVTS 120

Qy 121 S 121  
Db 121 S 121

RESULT 5  
ADF09814  
ID ADF09814 standard; protein; 121 AA.

XX AC ADF09814;  
XX  
DT 12-FEB-2004 (first entry)  
XX DE  
XX DE Human anti-MUC18 monoclonal antibody heavy chain #1.  
XX KW cell proliferation inhibition; MUC18 tumour antigen;  
XX KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
XX KW carcinoma; cancer; malignancy; heavy chain; human.  
XX OS Homo sapiens.  
XX PN WO2003057837-A2.  
XX PD 17-JUL-2003.  
XX PF 26-DEC-2002; 2002WO-US041580.  
XX PR 28-DEC-2001; 2001US-0346414P.  
XX PA (ABGE-) ABGENIX INC.  
XX PI Gudas J;  
XX PI WPI; 2003-598367/56.  
XX DR N-PSDB; ADF09816.  
XX

PT Inhibiting cell proliferation associated with expression of MUC18 tumour  
PT antigen, involves incubating and inhibiting cell by administering anti-  
PT MUC18 monoclonal antibody.  
XX  
PS Claim 1; SEQ ID NO 1; 83pp; English.

XX The invention comprises a method for inhibiting cell proliferation  
XX associated with expression of MUC18 tumour antigen. The method involves  
XX administering anti-MUC18 monoclonal antibody. The method of the invention  
XX is useful for inhibiting cell (e.g. melanoma or tumour cell)  
XX proliferation associated with the expression of MUC18 tumour antigen, the  
XX method is preferably useful for inhibiting tumour metastasis. The method  
XX is useful for inhibiting cell proliferation in patients with tumours,  
XX carcinomas, cancer and other malignancies. The present amino acid  
XX sequence represents a heavy chain from an MUC18 tumour antigen-specific  
XX monoclonal antibody.

XX SQ Sequence 121 AA;  
Query Match 100.0%; Score 649; DB 7; Length 121;  
Best Local Similarity 100.0%; Pred. No. 6.4e-46;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPESETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGIYYTWTSNYN 60  
Db 1 QVQLQESGPGLVKPESETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGIYYTWTSNYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTS 120  
 Db |||||  
 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTS 120

QY 121 S 121  
 Db |  
 121 S 121

RESULT 6  
 ADF09830  
 ID ADF09830 standard; protein; 121 AA.  
 XX  
 AC ADF09830;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human anti-MUC18 monoclonal antibody heavy chain #5.  
 XX  
 KW cell proliferation inhibition; MUC18 tumour antigen;  
 KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
 KW carcinoma; cancer; malignancy; heavy chain; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003057837-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 26-DEC-2002; 2002WO-US041580.  
 XX  
 PR 28-DEC-2001; 2001US-0346414P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas J;  
 XX  
 DR WPI; 2003-598367/56.  
 DR N-PSDB; ADF09832.  
 XX

Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.

Claim 1; SEQ ID NO 17; 83pp; English.

The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUC18 tumour antigen-specific monoclonal antibody.

Sequence 121 AA;

Query Match 100.0%; Score 649; DB 7; Length 121;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-46;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIROPKGLGWIGYIYTTSTNYN 60  
 Db |||||  
 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIROPKGLGWIGYIYTTSTNYN 60  
 QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTS 120  
 Db |||||  
 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTS 120  
 QY 121 S 121  
 Db |  
 121 S 121

Db 121 S 121

RESULT 7

ADC99780  
 ID ADC99780 standard; protein; 121 AA.  
 XX

AC ADC99780;

XX  
 DT 01-JAN-2004 (first entry)

XX  
 DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 9.

XX  
 KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
 KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
 KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
 KW lung cancer; human.

XX Homo sapiens.

XX WO2003057838-A2.

XX  
 PD 17-JUL-2003.

XX  
 PF 26-DEC-2002; 2002WO-US041581.

XX  
 PR 28-DEC-2001; 2001US-0346299P.

XX  
 PA (ABGE-) ABGENIX INC.

XX  
 PI Gudas J;

XX  
 DR WPI; 2003-587113/55.

XX  
 DR N-PSDB; ADC99782.

XX  
 PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
 PT or condition associated with expression of MUC18 in a patient, e.g.  
 PT tumors, cancers, and other malignancies.

XX  
 PS Claim 1; SEQ ID NO 9; 78pp; English.

XX  
 CC The invention relates to a novel isolated monoclonal antibody comprising  
 CC a heavy or light chain amino acid or a heavy or light chain variable  
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
 CC invention demonstrates cytostatic activity and may be useful for treating  
 CC a disease or condition associated with the expression of MUC18 on the  
 CC cell surface such as tumours, specifically melanoma, oesophageal,  
 CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
 CC carcinomas and cervical intraepithelial neoplasia and cancers including  
 CC colorectal, breast or lung cancer, as well as other malignancies. The  
 CC current sequence is that of the anti-human MUC18 monoclonal antibody  
 CC heavy chain protein of the invention.

XX  
 SQ Sequence 121 AA;

Query Match 99.1%; Score 643; DB 7; Length 121;  
 Best Local Similarity 98.3%; Pred. No. 2e-45;  
 Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIROPKGLGWIGYIYTTSTNYN 60  
 Db |||||  
 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIROPKGLGWIGYIYTTSTNYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTS 120  
 Db |||||  
 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTS 120

QY 121 S 121  
 Db |  
 121 S 121

RESULT 8

ADD05384  
 ID ADD05384 standard; protein; 121 AA.  
 AC ADD05384;  
 XX  
 XX  
 DT 01-JAN-2004 (first entry)  
 DE  
 DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID NO 9.  
 KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
 KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003057006-A2.  
 PN  
 XX  
 PD 17-JUL-2003.  
 XX  
 XX 26-DEC-2002; 2002WO-US041582.  
 PF  
 XX 28-DEC-2001; 2001US-0346460P.  
 PR  
 XX (ABGE-) ABGENIX INC.  
 PA  
 XX Gudas J, Bar-Eli M;  
 PI  
 XX WPI; 2003-577496/54.  
 DR  
 DR N-PSDB; ADD05386.  
 XX  
 XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
 PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
 PT associated with melanoma, or increasing survival of an animal having a  
 PT metastatic tumor.  
 XX  
 XX Claim 1; SEQ ID NO 9; 87pp; English.  
 PS  
 XX The invention relates to a novel monoclonal antibody used for inhibiting  
 CC tumour growth in an animal. The tumour inhibition process comprises  
 CC selecting an animal in need of treatment for a tumour, providing a  
 CC monoclonal antibody comprising a heavy chain amino acid, where the  
 CC antibody consists of any one of 10 fully defined sequences of 117-123  
 CC amino acids given in the specification, and where the monoclonal antibody  
 CC binds MUC18, and contacting the tumour with the antibody resulting in  
 CC inhibited proliferation of the cells. The monoclonal antibody has  
 CC cytostatic and can be used in the production of a vaccine. The monoclonal  
 CC antibodies against the MUC18 antigen are useful for diagnosing and  
 CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or  
 CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
 CC increasing survival of an animal having a metastatic tumour. This  
 CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
 CC protein of the invention.  
 XX  
 SQ Sequence 121 AA;  
 Query Match 99.1%; Score 643; DB 7; Length 121;  
 Best Local Similarity 98.3%; Pred. No. 2e-45;  
 Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSISSYVSWIRQPPGKLEWIGIYYTWTN 60  
 Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSISSYVSWIRQPPGKLEWIGIYYTWTN 60  
 QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
 Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
 QY 121 S 121  
 Db 121 S 121  
 QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
 Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
 QY 121 S 121  
 Db 121 S 121  
 RESULT 9  
 ADF09822

ADF09822 standard; protein; 121 AA.  
 ID  
 XX  
 AC ADF09822;  
 XX  
 XX  
 DT 12-FEB-2004 (first entry)  
 DE  
 DE Human anti-MUC18 monoclonal antibody heavy chain #3.  
 KW cell proliferation inhibition; MUC18 tumour antigen;  
 KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
 KW carcinoma; cancer; malignancy; heavy chain; human.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003057837-A2.  
 PN  
 XX  
 PD 17-JUL-2003.  
 XX  
 XX 26-DEC-2002; 2002WO-US041580.  
 PF  
 XX 28-DEC-2001; 2001US-0346414P.  
 PR  
 XX (ABGE-) ABGENIX INC.  
 PA  
 XX Gudas J;  
 PI  
 XX WPI; 2003-598367/56.  
 DR  
 DR N-PSDB; ADF09824.  
 XX  
 XX Inhibiting cell proliferation associated with expression of MUC18 tumour  
 PT antigen, involves incubating and inhibiting cell by administering anti-  
 PT MUC18 monoclonal antibody.  
 XX  
 XX Claim 1; SEQ ID NO 9; 83pp; English.  
 PS  
 XX The invention comprises a method for inhibiting cell proliferation  
 CC associated with expression of MUC18 tumour antigen. The method involves  
 CC administering anti-MUC18 monoclonal antibody. The method of the invention  
 CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
 CC proliferation associated with the expression of MUC18 tumour antigen, the  
 CC method is preferably useful for inhibiting tumour metastasis. The method  
 CC is useful for inhibiting cell proliferation in patients with tumours,  
 CC carcinomas, cancer and other malignancies. The present amino acid  
 CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
 CC monoclonal antibody.  
 XX  
 SQ Sequence 121 AA;  
 Query Match 99.1%; Score 643; DB 7; Length 121;  
 Best Local Similarity 98.3%; Pred. No. 2e-45;  
 Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSISSYVSWIRQPPGKLEWIGIYYTWTN 60  
 Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSISSYVSWIRQPPGKLEWIGIYYTWTN 60  
 QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
 Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
 QY 121 S 121  
 Db 121 S 121  
 QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
 Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
 QY 121 S 121  
 Db 121 S 121  
 RESULT 10  
 ADF09808  
 ID ADF09808 standard; protein; 121 AA.  
 XX  
 XX ADF09808;  
 AC  
 XX  
 XX 01-JAN-2004 (first entry)  
 DT  
 XX

DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 37.  
XX  
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytotatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.  
XX  
OS Homo sapiens.  
XX WO2003057838-A2.  
XX PN 17-JUL-2003.  
XX PD 26-DEC-2002; 2002WO-US041581.  
XX PF 28-DEC-2001; 2001US-0346299P.  
XX PR (ABGE-) ABGENIX INC.  
XX PA Gudas J;  
XX PI WPI; 2003-587113/55.  
XX DR N-PSDB; ADC99810.  
XX DR  
XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
PT or condition associated with expression of MUC18 in a patient, e.g.  
PT tumors, cancers, and other malignancies.  
PT  
XX  
XX Claim 1; SEQ ID NO 37; 78pp; English.  
XX  
XX The invention relates to a novel isolated monoclonal antibody comprising  
CC a heavy or light chain amino acid or a heavy or light chain variable  
CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
CC invention demonstrates cytostatic activity and may be useful for treating  
CC a disease or condition associated with the expression of MUC18 on the  
CC cell surface such as tumors, specifically melanoma, oesophageal,  
CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
CC carcinomas and cervical intraepithelial neoplasia and cancers including  
CC colorectal, breast or lung cancer, as well as other malignancies. The  
CC current sequence is that of the anti-human MUC18 monoclonal antibody  
CC heavy chain protein of the invention.  
XX  
XX  
SQ Sequence 121 AA;

Query Match 92.0%; Score 597; DB 7; Length 121;  
Best Local Similarity 90.9%; Pred. No. 1.2e-41;  
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSTVYWSWIRQPPGKLEWIGYIYYTWSNYN 60  
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSTVYWSWIRQPPGKLEWIGYIYYTWSNYN 60  
QY 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTS 120  
DB 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTS 120  
QY 121 S 121  
DB 121 S 121

RESULT 11  
ADD05412  
ID ADD05412 standard; protein; 121 AA.  
XX  
XX ADD05412;  
XX  
DT 01-JAN-2004 (first entry)

XX Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 37.  
DE monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
KW

XX Homo sapiens.  
XX WO2003057006-A2.  
XX PN 17-JUL-2003.  
XX PD 26-DEC-2002; 2002WO-US041582.  
XX PF 28-DEC-2001; 2001US-0346460P.  
XX PR (ABGE-) ABGENIX INC.  
XX PA Gudas J, Bar-Eli M;  
XX PI WPI; 2003-577496/54.  
XX DR N-PSDB; ADD05414.  
XX DR  
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
PT associated with melanoma, or increasing survival of an animal having a  
PT metastatic tumor.  
PT  
XX  
XX Claim 1; SEQ ID NO 37; 87pp; English.  
XX  
XX The invention relates to a novel monoclonal antibody used for inhibiting  
CC tumour growth in an animal. The tumour inhibition process comprises  
CC selecting an animal in need of treatment for a tumour, providing a  
CC monoclonal antibody comprising a heavy chain amino acid, where the  
CC antibody consists of any one of 10 fully defined sequences of 117-123  
CC amino acids given in the specification, and where the monoclonal antibody  
CC binds MUC18, and contacting the tumour with the antibody resulting in  
CC inhibited proliferation of the cells. The monoclonal antibody has  
CC cytostatic and can be used in the production of a vaccine. The monoclonal  
CC antibodies against the MUC18 antigen are useful for diagnosing and  
CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or  
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
CC increasing survival of an animal having a metastatic tumour. This  
CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
CC protein of the invention.  
XX  
XX  
SQ Sequence 121 AA;

Query Match 92.0%; Score 597; DB 7; Length 121;  
Best Local Similarity 90.9%; Pred. No. 1.2e-41;  
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSTVYWSWIRQPPGKLEWIGYIYYTWSNYN 60  
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSTVYWSWIRQPPGKLEWIGYIYYTWSNYN 60  
QY 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTS 120  
DB 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTS 120  
QY 121 S 121  
DB 121 S 121

RESULT 12  
ADF09850  
ID ADF09850 standard; protein; 121 AA.  
XX  
XX ADF09850;  
XX  
DT 12-FEB-2004 (first entry)

XX Human anti-MUC18 monoclonal antibody heavy chain #10.  
DE cell proliferation inhibition; MUC18 tumour antigen;  
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
KW carcinoma; cancer; malignancy; heavy chain; human.

XX OS Homo sapiens.  
XX PN WO2003057837-A2.  
XX PD 17-JUL-2003.  
XX PF 26-DEC-2002; 2002WO-US041580.  
XX PR 28-DEC-2001; 2001US-0346414P.  
XX PA (ABGE-) ARGENIX INC.  
XX PI Gudas J;  
XX DR WPI; 2003-598367/56.  
XX DR N-PSDB; ADF09852.  
XX PT Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.  
XX PS Claim 1; SEQ ID NO 37; 83pp; English.  
XX CC The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUC18 tumour antigen-specific monoclonal antibody.  
XX SQ Sequence 121 AA;  
Query Match 92.0%; Score 597; DB 7; Length 121;  
Best Local Similarity 90.9%; Pred. No. 1.2e-41;  
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIRQPPGKLEWIGYIYYTWSNYN 60  
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIRQPPGKLEWIGYIYYTWSNYN 60  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDADFIDWGQGTMTVTS 120  
DB 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDADFIDWGQGTMTVTS 120  
QY 121 S 121  
DB 121 S 121  
RESULT 13  
AD058076 ID AD058076 standard; protein; 243 AA.  
XX AC AD058076;  
XX DT 12-AUG-2004 (first entry)  
XX DE S9 cell derived human scFvVL-VH protein.  
XX KW B cell; surface immunoglobulin; Ig; binding site; antigen; human CD28;  
XX KW closed system; detection laser-beam; catcher tube;  
XX KW electrochemical device; fluorescence activated cell sorter; FACS;  
XX KW antibody variable region; human.  
XX OS Homo sapiens.  
XX PN WO2004044584-A1.

PD 27-MAY-2004.  
XX XX  
PF 12-NOV-2003; 2003WO-EP012664.  
XX XX  
PR 13-NOV-2002; 2002EP-00025335.  
XX XX  
PA (MICR-) MICROMET AG.  
XX XX  
PI Baeuerle P, Hoffmann P, Weinberger S, Kischel R;  
XX DR WPI; 2004-449579/42.  
XX DR N-PSDB; ADO58077.  
XX PT Identifying a B cell carrying a surface immunoglobulin molecule having a binding site for an antigen of interest, useful for constructing therapeutic antibodies, comprises contacting a sample with the antigen and a receptor.  
XX PS Claim 22; SEQ ID NO 76; 156pp; English.  
XX CC The invention relates to a novel method for identifying a B cell carrying a surface immunoglobulin (Ig) molecule having a binding site for an antigen of interest. The method comprises contacting a sample putatively containing the B cell with the antigen of interest and with a receptor specifically binding to the Ig molecule, and assessing the presence of the detectable signal. The invention further comprises: an antibody generated by the method above which is specific for human CD28 or comprising an amino acid(s) sequence(s) given in the specification, and/or are encoded by a nucleic acid sequence(s) also given in the specification; and a device for assessing the presence of a detectable signal defined above, where the device comprises a closed system for the detection laser-beam and a catcher tube, and where the B cell of interest can be collected as a single cell by means of an electrochemical device, which is triggered by an electric signal generated by the fluorescence activated cell sorter (FACS) device, where the electrochemical device moves the nozzle of the steady catcher tube liquid stream for a programmed time over a collecting tube, microtiter plate or other container after a B cell is sorted. The method is useful for identifying a B cell carrying a surface Ig molecule having a binding site for an antigen of interest. The method is also useful for cloning of antibody variable regions from the identified B cells, which may subsequently be employed in the construction of proteins such as antibodies or its fragments or derivatives useful in therapeutic approaches. The method is useful as an alternative to phage display for the gain of antibodies or its fragments. This sequence represents an S2 cell derived human polypeptide of the invention.  
XX SQ Sequence 243 AA;  
Query Match 87.1%; Score 565.5; DB 8; Length 243;  
Best Local Similarity 90.1%; Pred. No. 9.5e-39;  
Matches 109; Conservative 6; Mismatches 5; Indels 1; Gaps 1;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIRQPPGKLEWIGYIYYTWSNYN 60  
DB 124 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIRQPPGKLEWIGYIYYTWSNYN 183  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDADFIDWGQGTMTVTS 120  
DB 184 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDADFIDWGQGTMTVTS 242  
QY 121 S 121  
DB 243 S 243  
RESULT 14  
ABG92884 ID ABG92884 standard; protein; 121 AA.  
XX AC ABG92884;  
XX DT 19-NOV-2002 (first entry)

XX DE Human immunoglobulin variable light domain #1.

XX KW Immunoglobulin; variable heavy chain; variable light chain; human;

XX KW G-protein chemokine receptor; CCR5; HDGMR10; cancer; inflammation;

XX KW immunologic deficiency syndrome; blood protein disorder; nephritis;

XX KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;

XX KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;

XX KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;

XX KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;

XX KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;

XX KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;

XX KW lymphocytopenia.

XX KW Homo sapiens.

XX KW WO200264612-A2.

XX PD 22-AUG-2002.

XX PF 08-FEB-2002; 2002WO-US003634.

XX PR 09-FEB-2001; 2001US-00779880.

XX PR 09-FEB-2001; 2001WO-US004153.

XX PR 12-JUN-2001; 2001US-0297257P.

XX PR 08-AUG-2001; 2001US-0310458P.

XX PR 12-OCT-2001; 2001US-0328447P.

XX PR 21-DEC-2001; 2001US-0341725P.

XX KW (HUMA-) HUMAN GENOME SCI INC.

XX KW Roschke V, Rosen CA, Ruben SM;

XX KW WPI; 2002-643455/69.

XX KW N-PSDB; ABS68607.

XX KW New human G-protein Chemokine Receptor gene (HDGMR10) useful for

XX KW treating, preventing, ameliorating or monitoring diseases or disorders

XX KW associated with aberrant expression of HDGMR10 e.g. cancer.

XX KW Example 55; Fig 4; 562pp; English.

XX KW The invention describes an isolated polynucleotide encoding a first

XX KW antibody at least 95-100% identical to a second antibody consisting of an

XX KW amino acid sequence comprising at least one, two or three CDR regions of

XX KW a variable heavy (VH) or variable light (VL) domain of the antibody

XX KW expressed by a hybridoma cell line consisting of XF3.5P1, XF11.1P8,

XX KW XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9B6, XF27/28.7D5, XF27/28.1B85,

XX KW XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody

XX KW is useful treating, preventing, ameliorating, prognosing or monitoring

XX KW cancers or other diseases or disorders e.g. immunologic deficiency

XX KW syndromes such as blood protein disorders and ataxia telangiectasia,

XX KW inflammation associated disorders such as endotoxin lethality, nephritis

XX KW and inflammatory bowel disease, conditions associated with an increase in

XX KW certain haematopoietic cells such as histiocytosis, defective or aberrant

XX KW chemotaxis of immune cells or T-cell antigen presenting cell interaction,

XX KW an infectious disease, an autoimmune disease such as Addison's disease,

XX KW dermatitis and rheumatoid arthritis, allergies, a neurodegenerative

XX KW disorder, a viral infection e.g. HIV infection, cytomegalovirus or

XX KW poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,

XX KW cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a

XX KW disease or disorder associated with aberrant expression of novel human G-

XX KW protein chemokine receptor (CCR5) HDGMR10. This is the amino acid

XX KW sequence of human immunoglobulin sequence associated with the antibodies

XX KW against HDGMR10

XX KW Sequence 121 AA;

SQ Query Match 84.3%; Score 547; DB 5; Length 121;

Best Local Similarity 86.0%; Pred. No. 1.6e-37;

Matches 104; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVQLQESGFLVKPSETLSLTCTVSGGSISSYFWSWIRQPGKGLDWIGRIYTSNNTYN 60

Db 1 QVQLQESGFLVKPSETLSLTCTVSGGSISSYFWSWIRQPGKGLDWIGRIYTSNNTYN 60

QY 61 PSLKSRVITSVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

Db 61 PSLKSRVITSVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

QY 121 S 121

Db 121 S 121

RESULT 15

ABB07171

ID ABB07171 standard; protein; 121 AA.

XX AC ABB07171;

XX DT 13-MAR-2002 (first entry)

XX DE ebvHigM MS19D10 heavy chain variable region sequence.

XX KW Neuromodulatory; central nervous system; CNS; SHIGM22; LYM 22; AKJR4;

XX KW ebvHigM MS19D10; ebv HIGM CB2bG8; CB2iE12; CB2iE7; MS19E5; virucide;

XX KW antiparkinsonian; neuroprotective; nootropic; vulnerary.

XX OS Homo sapiens.

XX KW WO200185797-A1.

XX PD 15-NOV-2001.

XX PF 30-MAY-2000; 2000WO-US014902.

XX PR 10-MAY-2000; 2000US-00568351.

XX KW (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.

XX KW Rodriguez M, Miller DJ, Pease LR;

XX KW WPI; 2002-066596/09.

XX KW N-PSDB; ABA94218.

XX KW Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting

XX KW neurite outgrowth, regeneration, remyelination and neuroprotection in

XX KW central nervous system, useful to treat post-infectious

XX KW encephalomyelitis.

XX KW Claim 23; Fig 19; 219pp; English.

XX KW The invention provides a neuromodulatory agent (I) capable of promoting

XX KW neurite outgrowth, regeneration, remyelination and neuroprotection in

XX KW central nervous system (CNS). (I) is capable of inducing remyelination,

XX KW promoting cellular proliferation of glial cells, and promoting Ca2+

XX KW signaling with oligodendrocytes. An humanised antibody to (I) can be

XX KW selected from antibody SHIGM22 (LYM 22), ebvHigM MS19D10, ebv HIGM

XX KW CB2bG8, AKJR4, CB2iE12, CB2iE7 or MS19E5. (I) is useful for stimulating

XX KW remyelination of CNS axons, stimulating proliferation of glial cells in

XX KW CNS axons, or treating demyelinating disease of CNS in a mammal in need

XX KW of such therapy. (I) is capable of binding to structures and cells within

XX KW CNS. (I) is preferably useful for treating a demyelinating disease of CNS

XX KW of a mouse infected with Strain DA of Theiler's murine encephalomyelitis

XX KW (TMEMV) or for treating a human being having multiple sclerosis, or a

XX KW human or domestic animal with a viral demyelinating disease, or a post-

XX KW neural disease of CNS. (I) is also useful for an in vitro method of

XX KW stimulating the proliferation of glial cells from mixed cell culture. (I)

XX KW is also useful for stimulating remyelination of CNS axons. The antibodies

XX KW are useful for preventing infection by a bacterium, virus or like

XX KW pathogen that causes demyelination or other neurodegenerative condition

XX KW in a subject. Methods where (I) is administered to a patient are useful

XX KW for treating multiple sclerosis, Parkinson's disease, Alzheimer's

XX KW disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating

XX KW disease, CNS diseases, and other conditions in the CNS where nerves are

CC damaged as by trauma. The present sequence represents the ebvHgm  
CC MS119D10 heavy chain variable region amino acid sequence

XX  
SQ Sequence 121 AA;

Query Match 84.1%; Score 545.5; DB 5; Length 121;  
Best Local Similarity 87.6%; Pred. No. 2.1e-37;  
Matches 106; Conservative 6; Mismatches 8; Indels 1; Gaps 1;  
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QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGQGTMTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGQGTMTVTS 120  
QY 121 S 121  
Db 120 S 120

Search completed: November 9, 2005, 12:55:26  
Job time : 75.6015 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55 ; Search time 18.802 Seconds  
(without alignments)  
480.403 Million cell updates/sec

Title: US-10-660-357A-17

Perfect score: 649

Sequence: 1 QVQLQSGGLVPESETLSL.....WLLPDAFDIWGQGTWTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/6C\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	540	83.2	119	3	US-09-025-769B-39
2	540	83.2	119	3	US-09-025-769B-65
3	540	83.2	119	4	US-09-490-070A-39
4	540	83.2	119	4	US-09-490-070A-65
5	540	83.2	119	4	US-09-490-153-39
6	540	83.2	119	4	US-09-490-153-65
7	540	83.2	119	4	US-09-490-324-39
8	540	83.2	119	4	US-09-490-324-65
9	531.5	81.9	118	3	US-09-025-769B-25
10	531.5	81.9	118	4	US-09-490-070A-25
11	531.5	81.9	118	4	US-09-490-153-25
12	531.5	81.9	118	4	US-09-490-324-25
13	531.5	81.9	120	4	US-09-424-840B-20
14	529.5	81.6	244	3	US-08-918-148-79
15	529.5	81.6	244	4	US-09-138-091A-77
16	515.5	79.4	473	3	US-09-049-672A-4
17	502	77.3	142	2	US-08-480-774A-2
18	500	77.0	117	4	US-09-720-493-2
19	499.5	77.0	139	4	US-09-471-276-837
20	498.5	76.8	122	1	US-08-360-125-11
21	498.5	76.8	122	2	US-08-450-578-11
22	498.5	76.8	122	2	US-09-017-628-11
23	498.5	76.8	122	2	US-09-014-880-11
24	498.5	76.8	122	4	US-08-450-363-11
25	498.5	76.8	122	4	US-09-467-903-11
26	494.5	76.2	487	4	US-09-800-729-145
27	488	75.2	116	3	US-08-545-809A-140

28	485	74.7	119	1	US-08-360-125-5	Sequence 5, Appli
29	485	74.7	119	2	US-08-450-578-5	Sequence 5, Appli
30	485	74.7	119	2	US-09-017-628-5	Sequence 5, Appli
31	485	74.7	119	2	US-09-014-880-5	Sequence 5, Appli
32	485	74.7	119	4	US-08-450-363-5	Sequence 5, Appli
33	485	74.7	119	4	US-09-467-903-5	Sequence 5, Appli
34	484	74.6	119	2	US-08-652-816A-10	Sequence 10, Appli
35	479.5	73.9	172	4	US-09-472-087-7	Sequence 7, Appli
36	479.5	73.9	172	4	US-09-472-087-86	Sequence 86, Appli
37	479	73.8	123	3	US-08-793-450-4	Sequence 4, Appli
38	477	73.5	118	3	US-08-545-809A-142	Sequence 142, App
39	476	73.3	472	3	US-08-793-450-8	Sequence 8, Appli
40	472.5	72.8	139	4	US-09-203-768A-2	Sequence 2, Appli
41	471	72.6	155	4	US-09-471-276-888	Sequence 888, App
42	470.5	72.5	118	4	US-09-343-698-6	Sequence 6, Appli
43	470.5	72.5	118	4	US-08-325-955-6	Sequence 6, Appli
44	469.5	72.3	832	3	US-08-630-820-7	Sequence 7, Appli
45	469.5	72.3	832	4	US-09-273-453-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1  
US-09-025-769B-39  
; Sequence 39 Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-39  
  
Query Match 83.2%; Score 540; DB 3; Length 119;  
Best Local Similarity 86.8%; Pred. No. 7.3e-45;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;



Patent No. 6696248  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-070A-65  
Query Match 83.2%; Score 540; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 7.3e-45;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;  
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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGIYYTWTSNYN 60  
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Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTWTVTVS 120  
Qy 121 S 121  
Db 119 S 119  
RESULT 5  
US-09-490-153-39  
Sequence 39, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York

TITLE OF INVENTION: Protein/(poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-153-39  
Query Match 83.2%; Score 540; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 7.3e-45;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;  
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Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTWTVTVS 120  
Qy 121 S 121  
Db 119 S 119  
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US-09-490-153-65  
Sequence 65, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York

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; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-153-65

Query Match      83.2%; Score 540; DB 4; Length 119;
Best Local Similarity 86.8%; Pred. No. 7.3e-45;
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

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QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
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QY 121 S 121
Db 119 S 119

RESULT 7
US-09-490-324-39
; Sequence 39, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-324-39

Query Match      83.2%; Score 540; DB 4; Length 119;
Best Local Similarity 86.8%; Pred. No. 7.3e-45;
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWVSWIROPPGKGLWIGYIYWTSTNYN 60
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QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARDWGGDGFY--AMDYWGQGLITVTS 118

QY 121 S 121
Db 119 S 119

RESULT 8
US-09-490-324-65
; Sequence 65, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
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; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-324-65

Query Match      83.2%; Score 540; DB 4; Length 119;
Best Local Similarity 86.8%; Pred. No. 7.3e-45;
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMTIRQPPGKLEWIGIYYTWTSTN 60
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Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTVS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTVS 118

Qy 121 S 121
Db 119 S 119

RESULT 9
US-09-025-769B-25
; Sequence 25, Application US/09025769B
; Patent No. 630064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
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; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-25

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Best Local Similarity 85.1%; Pred. No. 4.9e-44;
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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMTIRQPPGKLEWIGIYYTWTSTN 60

Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTVS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTVS 117

Qy 121 S 121
Db 118 S 118

RESULT 10
US-09-490-070A-25
; Sequence 25, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25

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Best Local Similarity 85.1%; Pred. No. 4.8e-44;
Matches 103; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

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QY 121 S 121
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Db 118 S 118

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; Sequence 25, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-09-490-324-25

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Best Local Similarity 85.1%; Pred. No. 4.8e-44;
Matches 103; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

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QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDGQWLLPDAFDIWGQGTMTVTS 120
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Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDGQWLLPDAFDIWGQGTMTVTS 120
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QY 121 S 121
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Db 118 S 118

RESULT 11
US-09-490-153-25
; Sequence 25, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-153-25

Query Match      81.9%; Score 531.5; DB 4; Length 118;
Best Local Similarity 85.1%; Pred. No. 4.8e-44;
Matches 103; Conservative 7; Mismatches 8; Indels 3; Gaps 1;
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121 S 121  
118 S 118

RESULT 13  
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; Sequence 20, Application US/09424840B  
; Patent No. 6790938  
; GENERAL INFORMATION:  
; APPLICANT: Berchtold, Peter  
; APPLICANT: Escher, Robert F. A.  
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES  
; FILE REFERENCE: 100564-09049  
; CURRENT APPLICATION NUMBER: US/09/424,840B  
; CURRENT FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: DE 19820663.1  
; PRIOR FILING DATE: 1998-05-08  
; PRIOR APPLICATION NUMBER: DE 19755227.7  
; PRIOR FILING DATE: 1997-12-12  
; PRIOR APPLICATION NUMBER: DE 19723904.8  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-424-840B-20

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Best Local Similarity 84.4%; Pred. No. 4.9e-44;  
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Db 1 QVKLESGLVLPKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTN 60  
Qy 61 PSLKSRVTISVDTSKNQFSLKSSVTAADTAATVYTCARDDQO-MLLPDAFDIWGGQTMVTV 119  
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Qy 120 SS 121  
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RESULT 14  
US-08-918-148-79  
; Sequence 79, Application US/08918148A  
; Patent No. 6342220  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camellia  
; APPLICANT: W.  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Fendly, Brian M.  
; APPLICANT: Gurney, Austin L.  
; TITLE OF INVENTION: Agonist Antibodies  
; FILE REFERENCE: P0979  
; CURRENT APPLICATION NUMBER: US/08/918,148A  
; CURRENT FILING DATE: 1997-08-25  
; NUMBER OF SEQ ID NOS: 79  
; SEQ ID NO 79  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: artificial  
US-08-918-148-79

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Qy 121 S 121  
Db 116 S 116

RESULT 15  
US-09-138-091A-77  
; Sequence 77, Application US/09138091A  
; Patent No. 6737249  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camellia W.  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Fendly, Brian M.  
; APPLICANT: Gurney, Austin L.  
; TITLE OF INVENTION: Agonist Antibodies  
; FILE REFERENCE: 9491-013-27  
; CURRENT APPLICATION NUMBER: US/09/138,091A  
; CURRENT FILING DATE: 1998-08-21  
; PRIOR APPLICATION NUMBER: US 60/056,736  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 77  
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; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: single chain antibody (scFv) fragments  
US-09-138-091A-77

Query Match 81.6%; Score 529.5; DB 4; Length 244;  
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Qy 121 S 121  
Db 116 S 116

Search completed: November 9, 2005, 11:46:38  
Job time : 18.802 secs

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OM protein - protein search, using sw model  
Run on: November 9, 2005, 11:40:37 ; Search time 67.2222 Seconds  
(without alignments)  
753.137 Million cell updates/sec

Title: US-10-660-357A-17  
Perfect score: 649  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues  
Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0  
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Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	649	100.0	121	14	US-10-330-530-1
4	649	100.0	121	14	US-10-330-530-17
5	649	100.0	121	16	US-10-660-357-1
6	649	100.0	121	16	US-10-660-357-17
7	643	99.1	121	14	US-10-330-613-9
8	643	99.1	121	14	US-10-330-530-9
9	643	99.1	121	16	US-10-660-357-9
10	597	92.0	121	14	US-10-330-613-37
11	597	92.0	121	14	US-10-330-530-37

12	597	92.0	121	16	US-10-660-357-37	Sequence 37, Appl
13	553.5	85.3	118	15	US-10-292-088-142	Sequence 142, App
14	549.5	84.7	118	15	US-10-292-088-109	Sequence 109, App
15	547	84.3	121	14	US-10-067-800-60	Sequence 60, Appl
16	547	84.3	121	18	US-10-994-679-60	Sequence 60, Appl
17	545.5	84.1	121	14	US-10-010-729-11	Sequence 11, Appl
18	545.5	84.1	122	15	US-10-309-762-24	Sequence 24, Appl
19	545.5	84.1	122	15	US-10-309-762-27	Sequence 27, Appl
20	545	84.0	119	17	US-10-937-596-23	Sequence 23, Appl
21	544.5	83.9	122	15	US-10-309-762-25	Sequence 25, Appl
22	544.5	83.9	122	15	US-10-309-762-29	Sequence 29, Appl
23	540	83.2	119	14	US-10-125-687-5	Sequence 5, Appl
24	540	83.2	119	18	US-10-996-191-5	Sequence 5, Appl
25	539.5	83.1	118	17	US-10-727-155-178	Sequence 178, App
26	539	83.1	123	15	US-10-371-942-102	Sequence 102, App
27	538.5	83.0	122	15	US-10-309-762-71	Sequence 71, Appl
28	538.5	83.0	141	15	US-10-309-762-90	Sequence 90, Appl
29	536.5	82.7	120	15	US-10-309-762-4	Sequence 4, Appl
30	536.5	82.7	120	15	US-10-309-762-102	Sequence 102, App
31	536.5	82.7	121	15	US-10-309-762-154	Sequence 154, App
32	536	82.6	119	15	US-10-309-762-143	Sequence 143, App
33	536	82.6	125	15	US-10-309-762-11	Sequence 11, Appl
34	534.5	82.4	142	17	US-10-893-576-37	Sequence 37, Appl
35	534.5	82.4	141	15	US-10-309-762-73	Sequence 73, Appl
36	534.5	82.4	141	15	US-10-309-762-94	Sequence 94, Appl
37	533.5	82.2	116	18	US-10-822-306A-5	Sequence 5, Appl
38	533.5	82.2	124	15	US-10-309-762-26	Sequence 26, Appl
39	533.5	82.2	193	15	US-10-264-049-4331	Sequence 4331, Ap
40	532.5	82.0	118	17	US-10-706-689-10	Sequence 10, Appl
41	532.5	82.0	118	18	US-10-988-360-10	Sequence 10, Appl
42	532.5	82.0	128	15	US-10-173-551-24	Sequence 24, Appl
43	531.5	81.9	120	16	US-10-844-424-20	Sequence 20, Appl
44	531.5	81.9	121	17	US-10-805-177-56	Sequence 56, Appl
45	531.5	81.9	126	14	US-10-067-800-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1  
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; Sequence 1, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; PRIOR FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-1

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						Gaps	0;
QY	1	QVQLQSGPGLVPESETLSLCTCTVSGGSSSYYSWIRQPPGKLEWIGYIYVTWTSNNY	60				
Db	1	QVQLQSGPGLVPESETLSLCTCTVSGGSSSYYSWIRQPPGKLEWIGYIYVTWTSNNY	60				
QY	61	PSLKSRTVTSVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGQGTWTVTS	120				
Db	61	PSLKSRTVTSVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGQGTWTVTS	120				
QY	121	\$	121				

```
Db      121 S 121

RESULT 2
US-10-330-613-17
; Sequence 17, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-17

Query Match      100.0%; Score 649; DB 14; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.8e-50;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLEWIGYIYYTTSNYN 60
      |||||
Db      1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLEWIGYIYYTTSNYN 60
      |||||

QY      61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
      |||||
Db      61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
      |||||

QY      121 S 121
      |
Db      121 S 121

RESULT 3
US-10-330-530-1
; Sequence 1, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-1

Query Match      100.0%; Score 649; DB 14; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.8e-50;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLEWIGYIYYTTSNYN 60
      |||||
Db      1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLEWIGYIYYTTSNYN 60
      |||||

QY      61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
      |||||
Db      61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
      |||||

QY      121 S 121
      |
Db      121 S 121

RESULT 4
US-10-330-530-17
; Sequence 17, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-17

Query Match      100.0%; Score 649; DB 14; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.8e-50;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLEWIGYIYYTTSNYN 60
      |||||
Db      1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLEWIGYIYYTTSNYN 60
      |||||

QY      61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
      |||||
Db      61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
      |||||

QY      121 S 121
      |
Db      121 S 121

RESULT 5
US-10-660-357-1
; Sequence 1, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-1

Query Match      100.0%; Score 649; DB 16; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.8e-50;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLEWIGYIYYTTSNYN 60
      |||||
Db      1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLEWIGYIYYTTSNYN 60
      |||||

QY      61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
      |||||
Db      61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
      |||||

QY      121 S 121
      |
Db      121 S 121
```

Db 61 PSLSKRVTTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGQGTWTVTS 120  
QY 121 S 121  
|  
Db 121 S 121

RESULT 6  
US-10-660-357-17  
; Sequence 17, Application US/10660357  
; Publication No. US20040115205A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Eli, Menashe  
; APPLICANT: Green, Larry L.  
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
; TITLE OF INVENTION: ANTIGEN  
; FILE REFERENCE: ABGENIX 030C1  
; CURRENT APPLICATION NUMBER: US/10/660,357  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 10/330,580  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-17

Query Match 100.0%; Score 649; DB 16; Length 121;  
Best Local Similarity 100.0%; Pred. No. 1.8e-50;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIRPPGKLEWIGYIYYTWTSNYN 60  
|  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIRPPGKLEWIGYIYYTWTSNYN 60  
|  
QY 61 PSLSKRVTTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGQGTWTVTS 120  
|  
Db 61 PSLSKRVTTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGQGTWTVTS 120  
|  
QY 121 S 121  
|  
Db 121 S 121

RESULT 7  
US-10-330-613-9  
; Sequence 9, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX 022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-9

Query Match 99.1%; Score 643; DB 14; Length 121;  
Best Local Similarity 98.3%; Pred. No. 6.1e-50;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIRPPGKLEWIGYIYYTWTSNYN 60  
|  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIRPPGKLEWIGYIYYTWTSNYN 60  
|

QY 61 PSLSKRVTTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGQGTWTVTS 120  
|  
Db 61 PSLSKRVTTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGQGTWTVTS 120  
|  
QY 121 S 121  
|  
Db 121 S 121

RESULT 8  
US-10-330-530-9  
; Sequence 9, Application US/10330530  
; Publication No. US20030152514A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
; FILE REFERENCE: ABGENIX 031A  
; CURRENT APPLICATION NUMBER: US/10/330,530  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: US 60/346414  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-530-9

Query Match 99.1%; Score 643; DB 14; Length 121;  
Best Local Similarity 98.3%; Pred. No. 6.1e-50;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIRPPGKLEWIGYIYYTWTSNYN 60  
|  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIRPPGKLEWIGYIYYTWTSNYN 60  
|  
QY 61 PSLSKRVTTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGQGTWTVTS 120  
|  
Db 61 PSLSKRVTTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGQGTWTVTS 120  
|  
QY 121 S 121  
|  
Db 121 S 121

RESULT 9  
US-10-660-357-9  
; Sequence 9, Application US/10660357  
; Publication No. US20040115205A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Eli, Menashe  
; APPLICANT: Green, Larry L.  
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
; TITLE OF INVENTION: ANTIGEN  
; FILE REFERENCE: ABGENIX 030C1  
; CURRENT APPLICATION NUMBER: US/10/660,357  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 10/330,580  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-9

Query Match 99.1%; Score 643; DB 16; Length 121;  
Best Local Similarity 98.3%; Pred. No. 6.1e-50;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIROPKGLGWIGYIYYTWTNTYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIROPKGLGWIGYIYYTWTNTYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTVS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTVS 120

QY 121 S 121

Db 121 S 121

## RESULT 10

US-10-330-613-37

; Sequence 37, Application US/10330613

; Publication No. US20030147809A1

; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean

; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN

; FILE REFERENCE: ABGENIX.022A

; CURRENT APPLICATION NUMBER: US/10/330,613

; PRIOR FILING DATE: 2002-12-26

; PRIOR APPLICATION NUMBER: 60/346299

; PRIOR FILING DATE: 2001-12-18

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 37

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-330-613-37

## Query Match

Best Local Similarity 92.0%; Score 597; DB 14; Length 121;

Mismatches 7; Indels 4; Gaps 0;

Matches 110; Conservative

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIROPKGLGWIGYIYYTWTNTYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIROPKGLGWIGYIYYTWTNTYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTVS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTVS 120

QY 121 S 121

Db 121 S 121

## RESULT 11

US-10-330-530-37

; Sequence 37, Application US/10330530

; Publication No. US20030152514A1

; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean

; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES

; FILE REFERENCE: ABGENIX.031A

; CURRENT APPLICATION NUMBER: US/10/330,530

; PRIOR FILING DATE: 2002-12-26

; PRIOR APPLICATION NUMBER: US 60/346414

; PRIOR FILING DATE: 2001-12-18

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 37

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-330-530-37

## Query Match

Best Local Similarity 92.0%; Score 597; DB 14; Length 121;

Mismatches 7; Indels 4; Gaps 0;

Matches 110; Conservative

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIROPKGLGWIGYIYYTWTNTYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIROPKGLGWIGYIYYTWTNTYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTVS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTVS 120

QY 121 S 121  
Db 121 S 121

## RESULT 12

US-10-660-357-37

; Sequence 37, Application US/10660357

; Publication No. US20040115205A1

; GENERAL INFORMATION:

; APPLICANT: Bar-Eli, Menashe

; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

; FILE REFERENCE: ABGENIX.030C1

; CURRENT APPLICATION NUMBER: US/10/660,357

; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 10/330,580

; PRIOR FILING DATE: 2002-12-26

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 37

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-660-357-37

## Query Match

Best Local Similarity 92.0%; Score 597; DB 16; Length 121;

Mismatches 7; Indels 4; Gaps 0;

Matches 110; Conservative

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIROPKGLGWIGYIYYTWTNTYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIROPKGLGWIGYIYYTWTNTYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTVS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTVS 120

QY 121 S 121

Db 121 S 121

## RESULT 13

US-10-292-088-142

; Sequence 142, Application US/10292088

; Publication No. US20030211100A1

; GENERAL INFORMATION:

; APPLICANT: BEDIAN, VAHE

; APPLICANT: GLADUE, RONALD P.

; APPLICANT: CORVALAN, JOSE

; APPLICANT: JIA, XIAO-CHI

; APPLICANT: FENG, XIAO

; TITLE OF INVENTION: ANTIBODIES TO CD40

; FILE REFERENCE: ABX-PF/3 US

; CURRENT APPLICATION NUMBER: US/10/292,088

; CURRENT FILING DATE: 2003-03-14

; PRIOR APPLICATION NUMBER: 60/348,980

; PRIOR FILING DATE: 2001-11-09

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 142

; LENGTH: 118

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-142

Query Match      85.3%; Score 553.5; DB 15; Length 118;
Best Local Similarity 87.6%; Pred. No. 6.2e-42;
Matches 106; Conservative 7; Mismatches 5; Indels 3; Gaps 1;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYKSWIRQPPGKLEWIGYIYYTWTSNYN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYKSWIRQPPGKLEWIGYIYYSGSTN 60
Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAIVYICARDQGWLLPDAFDIWGGQTMVT 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAIVYICARDYGDY---NWFDPNGQGLTV 117
Qy 121 S 121
Db 118 S 118
```

```
RESULT 14
US-10-292-088-109
; Sequence 109, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-109
```

```
Query Match      84.7%; Score 549.5; DB 15; Length 118;
Best Local Similarity 87.6%; Pred. No. 1.4e-41;
Matches 106; Conservative 5; Mismatches 7; Indels 3; Gaps 1;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYKSWIRQPPGKLEWIGYIYYTWTSNYN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYKSWIRQPPGKLEWIGYIYYSGSTN 60
Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAIVYICARDQGWLLPDAFDIWGGQTMVT 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAIVYICARDYGG---NSYFDYWGQGLTV 117
Qy 121 S 121
Db 118 S 118
```

```
RESULT 15
US-10-067-800-60
; Sequence 60, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRs) HDGNR10
; FILE REFERENCE: 1488.1150001
; CURRENT APPLICATION NUMBER: US/10/067,800
```

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; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-60
```

```
Query Match      84.3%; Score 547; DB 14; Length 121;
Best Local Similarity 86.0%; Pred. No. 2.4e-41;
Matches 104; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYKSWIRQPPGKLEWIGYIYYTWTSNYN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYKSWIRQPPGKLEWIGYIYSGNTN 60
Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAIVYICARDQGWLLPDAFDIWGGQTMVT 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAIVYICARDGSSWYPDADFIDWGGQTMVT 120
Qy 121 S 121
Db 121 S 121
```

Search completed: November 9, 2005, 12:43:00  
Job time : 68.2222 secs

THE STATE OF TEXAS  
(COUNTY OF DALLAS)

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OM protein - protein search, using sw model

Run on: November 9, 2005, 12:25:58 ; Search time 13.0401 Seconds  
(without alignments)  
892.802 Million cell updates/sec

Title: US-10-660-357A-17

Perfect score: 649

Sequence: 1 QVQLQSGGPGLVKPSSETLSL.....WLLPDAFDIWGQGTMTVTS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543	83.7	140	2 I37782	Ig variable region
2	536	82.6	155	2 S31512	Ig heavy chain - h
3	533	82.1	130	2 S31690	Ig heavy chain - h
4	533	82.1	155	2 S31511	Ig heavy chain - h
5	526.5	81.1	139	2 S31586	Ig heavy chain - h
6	518.5	79.9	130	2 S30534	Ig heavy chain - h
7	512.5	79.0	137	2 S31676	Ig heavy chain - h
8	509.5	78.5	118	2 S20780	Ig heavy chain - h
9	505	77.8	147	2 S31519	Ig heavy chain - h
10	498.5	76.8	140	2 S78052	Ig heavy chain - h
11	495	76.3	135	2 S78051	Ig heavy chain - h
12	490	75.5	105	2 S44125	Ig lambda chain - h
13	489	75.3	97	2 S26906	Ig heavy chain - h
14	489	75.3	146	2 S09711	Ig heavy chain - h
15	488	75.2	116	2 B26340	Ig heavy chain - h
16	486	74.9	97	2 S12416	Ig heavy chain - h
17	486	74.9	121	2 S44113	Ig heavy chain - h
18	485	74.7	140	2 A49045	Ig heavy chain - h
19	481	74.1	123	2 S30530	Ig heavy chain - h
20	481	74.1	139	2 S31696	Ig heavy chain - h
21	477	73.5	118	2 A26340	Ig heavy chain - h
22	474.5	73.1	129	2 S44114	Ig heavy chain - h
23	473.5	73.0	126	2 S47010	Ig heavy chain - h
24	473.5	73.0	145	2 S78055	Ig heavy chain - h
25	468.5	72.2	118	2 S24443	Ig heavy chain - h
26	467	72.0	99	2 S26802	Ig heavy chain - h
27	467	72.0	99	2 S26803	Ig heavy chain - h
28	467	72.0	220	2 A49444	Ig heavy chain - h
29	466	71.8	97	2 PH0876	Ig heavy chain - h

30	465	71.6	99	2 S12412	Ig heavy chain - h
31	462	71.2	143	2 B49028	Ig heavy chain - h
32	460	70.9	97	2 S26804	Ig heavy chain - h
33	460	70.9	116	2 S18557	Ig heavy chain - h
34	459.5	70.8	122	2 D41287	Ig heavy chain - h
35	458	70.6	99	2 S26801	Ig heavy chain - h
36	458	70.6	134	2 S54906	Ig heavy chain - h
37	458	70.6	146	2 S09710	Ig heavy chain - h
38	455.5	70.2	110	2 S44110	Ig heavy chain - h
39	454.5	70.0	146	1 G1HUH2	Ig heavy chain - h
40	454	70.0	99	2 S12418	Ig heavy chain - h
41	453.5	69.9	122	2 S69912	Ig heavy chain - h
42	452	69.6	140	2 A24770	Ig heavy chain - h
43	451	69.5	109	2 PH1673	Ig heavy chain - h
44	451	69.5	135	2 S31604	Ig heavy chain - h
45	449	69.2	115	2 S57464	Ig heavy chain - h

ALIGNMENTS

RESULT 1

I37782

Ig variable region (VDJ) (clone T23-9) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999

C;Accession: I37782; S25476

R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A;Title: Somatic diversification in the heavy chain variable region genes expressed by

A;Reference number: A36876; MUID:94119917; PMID:8290556

A;Accession: I37782

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140 <RES>

A;Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;46-128/Domain: immunoglobulin homology <IMM>

Query Match 83.7%; Score 543; DB 2; Length 140;

Best Local Similarity 86.0%; Pred. No. 3.5e-41;

Matches 104; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 QVQLQSGGPGLVKPSSETLSLCTVSGSISYVSWIRQPPGKLEWIGIYYTWTN 60

Db 20 QVQLQSGGPGLVKPSSETLSLCTVSGSISYVSWIRQPPGKLEWIGIYYTWTN 79

QY 61 PSLKSRVTISVDTSKNQPSLRLSSVTAADTAVYYCARDDQQLLPDAFDIWGQGTMTVTS 120

Db 80 PSLKSRVTISVDTSKNQPSLRLSSVTAADTAVYYCARHNSSSWYGRYFDYWGQGTMTVTS 139

QY 121 S 121

Db 140 S 140

RESULT 2

S31512

Ig heavy chain - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999

C;Accession: S31512

R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.

submitted to the EMBL data library, December 1992

A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA aut

A;Reference number: S31509

A;Accession: S31512

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-155 <CHA>

A;Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;47-129/Domain: immunoglobulin homology &lt;IMM&gt;

	Query Match	82.6%;	Score 536;	DB 2;	Length 155;
	Best Local Similarity	82.9%;	Pred. NO. 1.6e-40;		
	Matches 102;	Conservative 7;	Mismatches 12;	Indels 2;	Gaps 1
Qy	1	OVLQESGGLVKPSETLSLCTVSGGSISSYKWSWIROPFGKLEWIGVIYYTWSNYN	60		
Db	33	OVLQESGGLVKPSETLSLCTVSGGSISSYKWSWIROPFGKLEWIGVIYYTGSATYN	92		
Qy	61	PSLKSRVTISVDTSKNQFSLRSSVTAADTAVVYCARDQG--QWLPLDAPFDIWGQGTWT	118		
Db	93	PIPKSRVTISVDTSKNQFSLKVSVTAADTAVVYCARGGGISSVYYYGNDWGQGTWT	152		
Qy	119	VSS 121			
Db	153	VSS 155			

RESULT 3

S31690  
19 heavy chain V region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S31690  
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.  
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A/Reference number: S31585  
A/Accession: S31690  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-130 <CDI>  
A/Cross-references: EMBL:D14199; NID:g30984; PIDN:CAA78568.1; PID:g30985  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/20-102/Domain: immunoglobulin homology <IMW>

Query Match	82.1%;	Score 533;	DB 2;	Length 130;
Best Local Similarity	84.0%;	Pred. No. 2.5e-40;		
Matches 105;	Conservative 5;	Mismatches 11;	Indels 4;	Gaps 1
Qy	1	OYQLESGLVKPSETLSLCTVSGSGSISSYVHSWIRPPGKLEWIGVYYTWSNTN	60	
Db	6	OYQLESGLVKPSETLSLCTVSGSGSISSYVHSWIRPPGKLEWIGVYYTWSNTN	65	
Qy	61	PSLKSRTVISVDTSKNQPSLKLSSVTAADTAVYICARDQGWL----	LPDAFDIMQGQTM	116
Db	66	PSLKSRTVISVDTSKNQPSLKLSSVTAADTAVYICARGSVLLWFGELLYYFDYWGQGL	125	
Qy	117	VTVSS	121	
Db	126	VTVSS	130	

RESULT 4  
S31511  
IG heavy chain - human  
S31511  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S31511  
R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A:Accession: S31511  
A:Reference number: S31509  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <CHA>  
A:Cross-references: EMBL:XG9866; NID:g33094; PIDN:CAA49500.1; PID:g33095  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:47-129/Domain: immunoglobulin homology <IMM>

Query Match	82.1%;	Score 533;	DB 2;	Length 155;
Best Local Similarity	83.7%;	Pred. No. 3e-40;		
Matches 103; Conservative	5;	Mismatches 13;	Indels 2;	Gaps 1
QY	1	QVQLQESGGPGLVKPSSETLSLTCTVSGGSISSYVSWIRQPPGKLEWIGYIYYTWTSNYN	60	
Db	33	QVQLQESGGPGLVKPSSETLSLTCTVSGGSISSYVSWIRQPPGKLEWIGYIYYTGSATYN	92	
QY	61	PSLKSRTVISVDTSKNQFSLRLSSVTAADTAVVYCARDQG--QWLLPDAFDIWGGQTMVT	118	
Db	93	PPLKSRTVISVDTSKNQFSLKLVSSVTAADTAVVYCARGGGISWYDYGMVDWGGQTMT	152	
QY	119	VSS 121		
Db	153	VSS 155		

```

RESULT 5
S31586
IG heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31586
R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31586
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-139 <CUI>
A/Cross-references: EMBL:Z14136; NID:G30978; PIDN:CAA78565.1; PID:G30979
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

```

	Query Match	81.1%	Score 526.5	DB 2	Length 139
	Best Local Similarity	86.0%	Pred. No. 1e-39		
	Matches 104	Conservative 6	Mismatches 10	Indels 1	Gaps 1
Qy	1	QVQLQSGGCLVVKPSETLSITCTVSGGISISSYVWSWIRQPPGKLEWIGYIYYTWS	60		
Db	20	QVQLQSGGCLVVKPSETLSITCTVSGGISISSYVWSWIRQPPGKLEWIGYIYYTWS	79		
Qy	61	PSLKSRTVISDVTSSKNQFSLRLSSVTAADTAVVYCARDQGWLLPDAFDIWGQGTMTVTS	120		
Db	80	PSLKSRTVMSDVTSSKNQFSLKLSVTAADTAVVYCARGLGIRRGAFDIWGQGTMTVTS	138		
Qy	121	S 121			
Db	139	S 139			

```

RESULT 6
S30534
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C:Accession: S30534
R:Marlette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30534
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <MAP>
A:Cross-references: EMBL:Z18320
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 79.9% Score 518.5 DB 2 Length 130;

```



Best Local Similarity 81.5%; Pred. No. 4.8e-39;  
Matches 106; Conservative 6; Mismatches 9; Indels 9; Gaps 3;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGYIYTWTSN 58  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGRIYTSNSTN 60

Qy 59 YNPSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCARDQGW-LPDAFDI 111  
Db 61 YNPSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCARDKGGFWSGYTNSRAAFDI 120

Qy 112 GQGTMTVTSS 121  
Db 121 GQGTMTVTSS 130

RESULT 7  
S31676  
Ig heavy chain V region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S31676  
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.  
submitted to the EMBL Data Library, June 1992  
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A/Reference number: S31585  
A/Accession: S31676  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-137 <CUI>  
A/Cross-references: EMBL:Z14182; NID:G31031; PIDN:CAA78551.1; PID:G31032  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 512.5; DB 2; Length 137;  
Best Local Similarity 83.5%; Pred. No. 1.7e-38;  
Matches 101; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGYIYTWTSN 60  
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGRIYTSNSTN 79

Qy 61 PSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDI 120  
Db 80 PSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCARDAP--LMYGMVDVWGQGTMTVS 136

Qy 121 S 121  
Db 137 S 137

RESULT 8  
S20780  
Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C/Accession: S20780  
R/Mortari, F.; Wang, J.; Schroeder, H.W.  
submitted to the EMBL Data Library, April 1992  
A/Description: Analysis of human cord blood Ig heavy chain Iga and Igg repertoire.  
A/Reference number: S20764  
A/Accession: S20780  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-118 <MOR>  
A/Cross-references: EMBL:Z11958; NID:G33893; PIDN:CAA78015.1; PID:G33894  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 78.5%; Score 509.5; DB 2; Length 118;  
Best Local Similarity 81.0%; Pred. No. 2.7e-38;

Matches 98; Conservative 11; Mismatches 9; Indels 3; Gaps 1;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGYIYTWTSN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIAFIRYTGSTHYN 60

Qy 61 PSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDI 120  
Db 61 PSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYSCARDGR---DGGFDI 117

Qy 121 S 121  
Db 118 S 118

RESULT 9  
S31519  
Ig heavy chain V region precursor - human  
C/Species: Homo sapiens (man)  
C/Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S31519  
R/Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.  
Nucleic Acids Res. 19, 673, 1991  
A/Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked  
A/Reference number: S31519; MUID:91187691; PMID:2011536  
A/Accession: S31519  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-147 <MOR>  
A/Cross-references: EMBL:X56158; NID:G37724; PIDN:CAA39626.1; PID:G37725  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F;41-125/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 505; DB 2; Length 147;  
Best Local Similarity 82.1%; Pred. No. 8.6e-38;  
Matches 101; Conservative 7; Mismatches 11; Indels 4; Gaps 3;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGYIYTWTSN 58  
Db 27 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGSIYSGSTY 86

Qy 59 YNPSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDI 118  
Db 87 YNPSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCARPL-LW-FCGLDFYWGQGTMTVS 144

Qy 119 VSS 121  
Db 145 VSS 147

RESULT 10  
S78052  
Ig heavy chain precursor V-D-J region (clone mAb 63VH) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C/Accession: S78052; S23717  
R/Harindranath, N.  
submitted to the EMBL Data Library, August 1990  
A/Reference number: S78051  
A/Accession: S78052  
A/Molecule type: mRNA  
A/Residues: 1-140 <HAR>  
A/Cross-references: EMBL:X54441; NID:G37815; PIDN:CAA38308.1; PID:G930118  
R/Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Nokin  
Int. Immunol. 3, 865-875, 1991  
A/Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and  
patient.  
A/Reference number: S23716; MUID:92031262; PMID:1718404  
A/Accession: S23717  
A/Molecule type: mRNA  
A/Residues: 15-111 <HAW>  
A/Cross-references: EMBL:X54441



Search completed: November 9, 2005, 13:08:03  
Job time : 14.0401 secs

## RESULT 14

S09711  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C:Accession: S09711  
R: Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.  
Biochem. J. 268, 135-140, 1990  
A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of human immunoglobulin heavy chain variable region  
A:Reference number: S09710; MUID: 90262535; PMID: 2111699  
A:Accession: S09711  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-146 <HUG>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-118/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 489; DB 2; Length 146;  
Best Local Similarity 74.0%; Pred. No. 2.2e-36;  
Matches 97; Conservative 11; Mismatches 9; Indels 14; Gaps 3;  
  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISS--YVSWIRPPGKLEWIGYIYYTWSN 58  
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISS--YVSWIRPPGKLEWIGYIYYTWSN 79  
  
Qy 59 YNPISKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCAR-----DQGWLLPDAFDI 110  
Db 80 YNPISKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCAR-----DQGWLLPDAFDI 135  
  
Qy 111 WGQGTMTVTVSS 121  
Db 136 WGQGTMTVTVSS 146

## RESULT 15

B26340  
Ig heavy chain precursor V-II region (71-4) - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Jun-1988 #sequence\_revision 30-Jun-1991 #text\_change 23-Jul-1999  
C:Accession: B26340  
R: Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo, T.  
J. Mol. Biol. 190, 529-541, 1986  
A:Title: Organization and evolution of variable region genes of the human immunoglobulin heavy chain variable region  
A:Reference number: A26340; MUID: 87061007; PMID: 3037326  
A:Accession: B26340  
A:Molecule type: DNA  
A:Residues: 1-116 <KOD>  
A:Cross-references: GB:X05711; NID:g33602; PIDN:CAA29183.1; PID:g296660  
A:Note: the authors translated the codon GAG for residue 25 as Gln  
C:Genetics:  
A:Introns: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-116/Product: Ig heavy chain V region 71-4 #status predicted <MAT>  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 75.2%; Score 488; DB 2; Length 116;  
Best Local Similarity 93.8%; Pred. No. 2.1e-36;  
Matches 91; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIRPPGKLEWIGYIYYTWSN 60  
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIRPPGKLEWIGYIYYTWSN 79  
  
Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCAR 97  
Db 80 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCAR 116

... ..

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:46:52 ; Search time 62.4712 Seconds  
(without alignments)  
991.843 Million cell updates/sec

Title: US-10-660-357A-17

Perfect score: 649

Sequence: 1 QVQLQESGPGVGLVPSSETLSL.....WLLPDAFDIWGQGTMTVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	516	79.5	476	2	Q6GMX1	Q6gm1 homo sapien
2	515	79.4	119	2	Q9UL73	Q9ul73 homo sapien
3	508.5	78.4	465	2	Q6GMX6	Q6gm6 homo sapien
4	501.5	77.3	620	2	Q9ERY0	Q9ey0 homo sapien
5	498.5	76.8	477	2	Q6GMX7	Q6gm7 homo sapien
6	495	76.3	139	2	Q86SX2	Q86sx2 homo sapien
7	493.5	76.0	478	2	Q72379	Q72379 homo sapien
8	482.5	74.3	150	2	Q95973	Q95973 homo sapien
9	472.5	72.8	576	2	Q6P418	Q6p418 homo sapien
10	472	72.7	492	2	Q72374	Q72374 homo sapien
11	460.5	71.0	496	2	Q96KX8	Q96kx8 homo sapien
12	454.5	70.0	146	1	HV21 HUMAN	P06331 homo sapien
13	451	69.5	595	2	Q8WUX4	Q8wux4 homo sapien
14	451	69.5	597	2	Q6GMX5	Q6gm5 homo sapien
15	451	69.5	597	2	Q9BU10	Q9bu10 homo sapien
16	451	69.5	625	2	Q96AA6	Q96aa6 homo sapien
17	450	69.3	478	2	Q6NYH3	Q6nyh3 homo sapien
18	449	69.2	597	2	Q9BQB8	Q9bqb8 homo sapien
19	445	68.6	117	1	HV2G HUMAN	P1825 homo sapien
20	444	68.4	129	1	HV2F HUMAN	P01824 homo sapien
21	435.5	67.1	130	2	Q81ZD7	Q81zd7 homo sapien
22	416.5	64.2	116	2	Q723Y6	Q723y6 homo sapien
23	411.5	63.4	122	2	Q9UL75	Q9ul75 homo sapien
24	407	62.7	479	2	Q99M22	Q99m22 mus musculus
25	398	61.3	476	2	Q6MZX7	Q6mzx7 homo sapien
26	394.5	60.8	136	2	Q6LB05	Q6lb05 mus musculus
27	394	60.7	137	1	HV46 MOUSE	P01822 mus musculus
28	390.5	60.2	473	2	Q8TC63	Q8tc63 homo sapien
29	375	57.8	113	1	HV47 MOUSE	P01823 mus musculus
30	372	57.3	262	2	Q65Z11	Q65z11 mus musculus
31	369.5	56.9	482	2	Q91X92	Q91x92 mus musculus

32	366.5	56.5	116	1	HV60 MOUSE	P18531 mus musculus
33	355	54.7	117	1	HV62 MOUSE	P18533 mus musculus
34	354.5	54.6	116	1	HV61 MOUSE	P18532 mus musculus
35	348	53.6	118	2	Q9UL74	Q9ul74 homo sapien
36	348	53.6	144	1	HV43 MOUSE	P01819 mus musculus
37	347.5	53.5	118	2	Q811U5	Q81lu5 mus musculus
38	345.5	53.2	121	1	Q99NG4	Q99ng4 mus musculus
39	343.5	52.9	135	1	HV02 XENLA	P20957 xenopus lae
40	333	51.3	121	2	Q9UL96	Q9ul96 homo sapien
41	332	51.2	470	2	Q6PJA4	Q6pja4 homo sapien
42	330.5	50.9	613	2	Q8WUK1	Q8wuk1 homo sapien
43	328.5	50.6	118	2	Q9UL91	Q9ul91 homo sapien
44	324.5	50.0	606	2	Q6GMV2	Q6gmv2 homo sapien
45	320	49.3	240	2	Q65ZC9	Q65zc9 homo sapien

## ALIGNMENTS

RESULT 1  
Q6GMX1 PRELIMINARY; PRT; 476 AA.  
ID Q6GMX1  
AC Q6GMX1;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Heltan E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RA "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
SEQUENCE FROM N.A.  
RP TISSUE=Spleen;  
RC Strausberg R.;  
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
EMBL: BC073773; AAH73773.1; -.  
DR InterPro; IPR003599; Ig-like.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00654; C1-set; 3.  
DR Pfam; PF00047; ig; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.

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KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 79.5%; Score 516; DB 2; Length 476;
Best Local Similarity 79.7%; Pred. No. 3.6e-43;
Matches 102; Conservative 10; Mismatches 8; Indels 8; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISS--YYNSWIROPKGLGWIGYIYYTWSN 58
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYYNSWIROPKGLGWIGYIYSGSTY 79
RN |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 59 YNPSLKSRTVISDVTSKNQFSLRLSSVTAADTAVYVCARDQGW-----LLPDAFDIWGQ 113
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 YNPSLKSRTVISDVTSKNQFSLRLSSVTAADTAVYFCAR-AGVWGSFRSWAIDGFNIWGQ 138
RN |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 114 GTWVTWSS 121
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
139 GTWVTWSS 146
RN |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 2
ID Q9UL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035041; AAD56277.1; -.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; P850835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BD886B6420EA0BE CRC64;

Query Match 79.4%; Score 515; DB 2; Length 119;
Best Local Similarity 82.6%; Pred. No. 1e-43;
Matches 100; Conservative 8; Mismatches 11; Indels 2; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYNSWIROPKGLGWIGYIYYTWSN 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYNSWIROPKGLGWIGYIYSGSTNYT 60
RN |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 PSLKSRVTISDVTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGQMTWTVS 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 PSLKSRVTISDVTSKNQFSLRLSSVTAADTAVYFCAR-LSNW-GPYFYDWGQGLTVTVS 118
RN |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 S 121
Db |
119 S 119

RESULT 3
Q6GMX6 PRELIMINARY; PRT; 465 AA.
ID Q6GMX6
```

```
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 78.4%; Score 508.5; DB 2; Length 465;
Best Local Similarity 81.8%; Pred. No. 2e-42;
Matches 99; Conservative 8; Mismatches 9; Indels 5; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYNSWIROPKGLGWIGYIYYTWSN 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYNSWIROPKGLGWIGRIYTSNSTYN 79
RN |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 PSLKSRVTISDVTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGQMTWTVS 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 PSLKSRVTISDVTSKNQFSLRLSSVTAADTAVYVCARGRTY-----FDYWGGTLTVTS 134
RN |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 S 121
Db |
135 S 135

RESULT 4
Q6EY0
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Q96EY0 PRELIMINARY; PRT; 620 AA.  
 AC Q96EY0; 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE IGHM protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC011857; AAH11857.2; --  
 DR PIR: S15590; S15590.  
 DR HSP: P01820; IGJ7.  
 DR InterPro: IPR003599; IG.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003597; IG cl.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam: PF07654; Cl-set; 4.  
 DR Pfam: PF00047; IG; 3.  
 DR SMART: SM00409; IG; 4.  
 DR SMART: SM00407; IGcl; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS00835; IG LIKE; 5.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN 3.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN 3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 620 AA; 58125 MW; 950A1A4A6E8FF27B CRC64;  
 Query Match 77.3%; Score 501.5; DB 2; Length 620;  
 Best Local Similarity 82.0%; Pred. No. 1.4e-41;  
 Matches 100; Conservative 6; Mismatches 13; Indels 3; Gaps 2;  
 Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIRQPPGKLEWIGYIYTWTSNYN 60  
 Db 27 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIRQPPGKLEWIGYIYTSN 86  
 Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAAYVYCARDQGWLLPDAFDWGQGTWTV 119  
 Db 87 PSLKSRVTMSVDTSKNQFSLRLSSVTAADTAAYVYCASQ--PWELPTVGLFYWGQGLTV 144  
 Qy 120 SS 121  
 Db 145 SS 146

RESULT 5

Q6GMX7 PRELIMINARY; PRT; 477 AA.  
 AC Q6GMX7; 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC073765; AAH73765.1; --  
 DR InterPro: IPR003599; IG.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003597; IG cl.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam: PF07654; Cl-set; 2.  
 DR Pfam: PF00047; IG; 3.  
 DR SMART: SM00409; IG; 4.  
 DR SMART: SM00407; IGcl; 3.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS00835; IG LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;  
 Query Match 76.8%; Score 498.5; DB 2; Length 477;  
 Best Local Similarity 81.0%; Pred. No. 2e-41;  
 Matches 98; Conservative 8; Mismatches 12; Indels 3; Gaps 2;  
 Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIRQPPGKLEWIGYIYTWTSNYN 60  
 Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIRQPPGKLEWIGYIYTSN 79  
 Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAAYVYCARDQGWLLPDAFDWGQGTWTV 120  
 Db 80 PSLKSRVTISLDTSKNQFSLRLSSVTAADTAAYVYCAHG--SSW--DFAFDYWGQGLTV 136  
 Qy 121 S 121  
 Db 137 S 137

```
RESULT 6
Q86SX2
ID Q86SX2 PRELIMINARY; PRT; 139 AA.
AC Q86SX2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line) of
DE Homo sapiens (human) (fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Li W.B., Gruber C., Jesse J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248300; CAD62627.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 76.3%; Score 495; DB 2; Length 139;
Best Local Similarity 94.9%; Pred. No. 1.2e-41;
Matches 93; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWYMWIRPPGKLEWIGYIYTWTSN 60
DB |||||
QY 33 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWYMWIRPPGKLEWIGYIYTSN 92
DB |||||

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARD 98
DB |||||
QY 93 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARD 130
DB |||||

RESULT 7
Q72379
ID Q72379 PRELIMINARY; PRT; 478 AA.
AC Q72379;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686K04218 (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Human rectum tumor;
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Robo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538066; CAD97996.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.

Query Match 76.3%; Score 495; DB 2; Length 139;
Best Local Similarity 94.9%; Pred. No. 1.2e-41;
Matches 93; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWYMWIRPPGKLEWIGYIYTWTSN 60
DB |||||
QY 33 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWYMWIRPPGKLEWIGYIYTSN 92
DB |||||

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARD 98
DB |||||
QY 93 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARD 130
DB |||||
```

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DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match 76.0%; Score 493.5; DB 2; Length 478;
Best Local Similarity 77.2%; Pred. No. 6.5e-41;
Matches 95; Conservative 15; Mismatches 8; Indels 5; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWYMWIRPPGKLEWIGYIYTWTSN 58
DB |||||
QY 19 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWYMWIRPPGKLEWIGYIYTSN 78
DB |||||
QY 59 YNP SLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDINGQGTVMVT 118
DB |||||
QY 79 YNP SLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDINGQGTVMVT 135
QY 119 VSS 121
DB |||||
QY 136 VSS 138
DB |||||

RESULT 8
O95973
ID O95973 PRELIMINARY; PRT; 150 AA.
AC O95973;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE VH4 heavy chain variable region precursor (Fragment).
GN Name=IGM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103795; AAC79084.1; -.
DR PIR; S31673; S31673.
DR PIR; S78056; S78056.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 19 Potential.
FT CHAIN 20 >150 VH4 heavy chain variable region.
FT NON TER 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 74.3%; Score 482.5; DB 2; Length 150;
Best Local Similarity 79.7%; Pred. No. 2.3e-40;
Matches 98; Conservative 6; Mismatches 12; Indels 7; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWYMWIRPPGKLEWIGYIYTWTSN 58
DB |||||
QY 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWYMWIRPPGKLEWIGYIYTSN 79
DB |||||
QY 59 YNP SLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDINGQGTVMVT 118
DB |||||
QY 80 YNP SLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDINGQGTVMVT 134
QY 119 VSS 121
DB |||||
QY 135 VSS 137
DB |||||

RESULT 9
Q6P418
ID Q6P418 PRELIMINARY; PRT; 576 AA.
```



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AC Q6P418;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHD protein.
GN Name=IGHD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Beak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Harte S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DE EMBL; BC063384; AAB63384.1;
DR HSP; P01820; I47N.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00407; IG; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00407; IGcl; 3.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;

Query Match 72.8%; Score 472.5; DB 2; Length 576;
Best Local Similarity 76.2%; Pred. No. 1e-38;
Matches 96; Conservative 9; Mismatches 10; Indels 11; Gaps 3;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSI--SSYYWSWIRQPPGKLEWIGIYYTTSNY 59
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSI--SSYYWSWIRQPPGKLEWIGIYYTTSNY 59
Qy 27 QVQLQESGPGLVKPSGTLTSLTCAVSGGSISSNNWWSVRQPPGKLEWIGIYHSGSTNY 86
Db 27 QVQLQESGPGLVKPSGTLTSLTCAVSGGSISSNNWWSVRQPPGKLEWIGIYHSGSTNY 86
Qy 60 NPSSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDGOWLLPAPF-----DIWQGT 115
Db 87 NPSSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDGOWLLPAPF-----DIWQGT 115
Qy 116 MVTVSS 121
Db 141 TVTVSS 146
RESULT 10

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Q7Z374
ID Q7Z374 PRELIMINARY; PRT; 492 AA.
AC Q7Z374;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686C02218 (Fragment).
GN Name=DKFZp686C02218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Pobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DE EMBL; BX538077; CAD98001.1;
DR HSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 72.7%; Score 472; DB 2; Length 492;
Best Local Similarity 75.4%; Pred. No. 9.5e-39;
Matches 95; Conservative 9; Mismatches 12; Indels 10; Gaps 4;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSI--SSYYWSWIRQPPGKLEWIGIYYTTSN 58
Db 32 QVQLQESGPGLVKPSSETLSLTCTVSGGSI--SSYYWSWIRQPPGKLEWIGIYYTTSN 58
Qy 59 YNPSLKSRTISVDTSKNQFSLRLSSVTAADTAVYVCARD--QGO--WLLPAPFDIWQGT 115
Db 92 YNPSLKSRLTIFVDTSKNHFSLRLTSVTAADTAVYVCVRHVEGPGYGV-----FDPWQGT 146
Qy 116 MVTVSS 121
Db 147 LVTVSS 152
RESULT 11
Q96KX8
ID Q96KX8 PRELIMINARY; PRT; 496 AA.
AC Q96KX8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MG27165 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

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DR Pfam; PF07654; Cl-set; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 4.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
KW Hypothetical protein.  
SQ SEQUENCE 595 AA; 0D4B50776545714E CRC64;

Query Match 69.5%; Score 451; DB 2; Length 595;  
Best Local Similarity 69.8%; Pred. No. 1.5e-36;  
Matches 90; Conservative 10; Mismatches 17; Indels 12; Gaps 2;

Qy 1 QVQLQESGPGGLVKKPSSETLSLTCTVSGSISYYWYWIQQPGKLEWIGYIYTWTSNYN 60  
Db 27 QVQLQWAGAGLLKPSSETLSLTCTGVYGSFGYWYWIQQPGKLEWIGEINHSNSTNYN 86  
Qy 61 PSLKSRVTISVDTSKQFSLRLSVTAADTAVYYCAR-----DQGWLLPDAFDIWG 112  
Db 87 PSLKSRVTISVDTSKQSLKSLSSVNAADTAVYYCARVITRASPQTDGRY----GMDVWG 142  
Qy 113 QGTMTVTSS 121  
Db 143 QGTIVTVSS 151

RESULT 14  
Q6GMX5  
ID Q6GMX5 PRELIMINARY; PRT; 597 AA.  
AC Q6GMX5;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Richards S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,  
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC073767; AAH73767.1; -  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF07654; Cl-set; 4.  
DR SMART; SM00409; IG; 4.  
DR SMART; SM00407; IGc1; 2.  
DR SMART; SM00406; IGv; 4.  
DR PROSITE; PS00835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
KW Hypothetical protein.  
SQ SEQUENCE 597 AA; 2A1E75F6AED85230 CRC64;

Query Match 69.5%; Score 451; DB 2; Length 597;  
Best Local Similarity 69.8%; Pred. No. 1.5e-36;  
Matches 90; Conservative 10; Mismatches 17; Indels 12; Gaps 2;

Qy 1 QVQLQESGPGGLVKKPSSETLSLTCTVSGSISYYWYWIQQPGKLEWIGYIYTWTSNYN 60  
Db 20 QVQLQWAGAGLLKPSSETLSLTCTGVYGSFGYWYWIQQPGKLEWIGEINHSNSTNYN 79  
Qy 61 PSLKSRVTISVDTSKQFSLRLSVTAADTAVYYCAR-----DQGWLLPDAFDIWG 112  
Db 80 PSLKSRVTISVDTSKQSLKSLSSVNAADTAVYYCARVITRASPQTDGRY----GMDVWG 135  
Qy 113 QGTMTVTSS 121  
Db 136 QGTIVTVSS 144

RESULT 15  
Q9BU10  
ID Q9BU10 PRELIMINARY; PRT; 597 AA.  
AC Q9BU10;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE IGHM protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Richards S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,  
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC002963; AAH02963.1; -  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.



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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:43:32 ; Search time 75.8346 Seconds  
(without alignments)  
627.306 Million cell updates/sec

Title: US-10-660-357A-21

Perfect score: 653

Sequence: 1 QVQLVQSGAEVKKPGASVKV.....GVHYIGMDVWGQTTVTVSS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	653	100.0	123	7	Adc99792 Anti-huma
2	653	100.0	123	7	Ado05396 Anti-MUC1
3	653	100.0	123	7	Adf09834 Human ant
4	593	90.8	125	6	Abr55813 Heavy cha
5	587.5	90.0	251	5	Abp45910 Human Bly
6	587.5	90.0	251	7	Adg96737 Single ch
7	576	88.2	127	7	Adk18819 Anti-huma
8	576	88.2	127	7	Adk18901 Anti-huma
9	576	88.2	127	7	Adk18607 Anti-huma
10	576	88.2	127	8	Adl25432 Human mAb
11	565	86.5	121	4	Aau02549 Anti-adip
12	561	85.9	125	7	Adk18783 Anti-huma
13	561	85.9	125	7	Adk18618 Anti-huma
14	561	85.9	125	8	Adl25452 Human mAb
15	558.5	85.5	126	7	Adk18930 Anti-huma
16	557	85.3	251	5	Abp45551 Human Bly
17	557	85.3	251	7	Adg96378 Single ch
18	556	85.1	123	6	Abr55819 Heavy cha
19	554.5	84.9	247	5	Abp45862 Human Bly
20	554.5	84.9	247	7	Adg96689 Single ch
21	552	84.5	257	5	Abp45599 Human Bly
22	552	84.5	257	7	Adg96426 Single ch
23	551.5	84.5	249	8	Adi58070 Reg IV-sp
24	551	84.4	248	5	Abp45461 Human Bly
25	551	84.4	248	7	Adg96288 Single ch

## ALIGNMENTS

## RESULT 1

ADC99792  
ID ADC99792 standard; protein; 123 AA.

XX AC ADC99792;

XX AC  
DT 01-JAN-2004 (first entry)

XX DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 21.

XX KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.

XX OS Homo sapiens.

XX PN WO2003057838-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041581.

XX PR 28-DEC-2001; 2001US-0346299P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J;

XX DR WPI; 2003-587113/55.

XX DR N-PSDB; ADC99794.

XX PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
or condition associated with expression of MUC18 in a patient, e.g.  
tumors, cancers, and other malignancies.

XX PS Claim 1; SEQ ID NO 21; 78pp; English.

XX CC The invention relates to a novel isolated monoclonal antibody comprising  
a heavy or light chain amino acid or a heavy or light chain variable  
domain where the antibody binds to MUC18. The monoclonal antibody of the  
invention demonstrates cytostatic activity and may be useful for treating  
a disease or condition associated with the expression of MUC18 on the  
cell surface such as tumors, specifically melanoma, oesophageal,  
pancreatic or colorectal tumours, carcinomas, particularly cervical  
carcinomas and cervical intraepithelial neoplasia and cancers including  
colorectal, breast or lung cancer, as well as other malignancies. The  
current sequence is that of the anti-human MUC18 monoclonal antibody

26	551	84.4	255	5	ABP45179	Abp45179 Human Bly
27	551	84.4	255	7	ADG96006	Adg96006 Single ch
28	551	84.4	257	5	ABP45343	Abp45343 Human Bly
29	551	84.4	257	7	ADG96170	Adg96170 Single ch
30	550.5	84.3	251	5	ABP45304	Abp45304 Human Bly
31	550.5	84.3	251	7	ADG96131	Adg96131 Single ch
32	550	84.2	248	5	ABP45435	Abp45435 Human Bly
33	550	84.2	248	7	ADG96262	Adg96262 Single ch
34	549.5	84.2	132	7	ADP40567	Adp40567 4G11 heav
35	549	84.1	248	5	ABP45767	Abp45767 Human Bly
36	549	84.1	248	7	ADG96594	Adg96594 Single ch
37	547.5	83.8	249	5	ABP45414	Abp45414 Human Bly
38	547.5	83.8	249	7	ADG96241	Adg96241 Single ch
39	547.5	83.8	252	5	ABP45663	Abp45663 Human Bly
40	547.5	83.8	252	7	ADG96490	Adg96490 Single ch
41	547	83.8	251	5	ABP45861	Abp45861 Human Bly
42	547	83.8	251	7	ADG96402	Adg96402 Single ch
43	547	83.8	251	7	ADG96688	Adg96688 Single ch
44	547	83.8	251	7	ADG96688	Adg96688 Single ch
45	547	83.8	257	5	ABP45568	Abp45568 Human Bly

```
CC heavy chain protein of the invention.
XX
SQ Sequence 123 AA;
    Query Match      100.0%; Score 653; DB 7; Length 123;
    Best Local Similarity 100.0%; Pred. No. 7.3e-53;
    Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVOLVOSGAEVKKPGASVKVSKASGYTFFSYGFSWVRQAPQGLEWLGWISAYNGNTNY 60
Db 1 QVOLVOSGAEVKKPGASVKVSKASGYTFFSYGFSWVRQAPQGLEWLGWISAYNGNTNY 60
QY 61 AQKLGQGRVTMTTDTSTSTAYMELSLRSDDTAVVYVCARETKVGVHYHGYMDVWGQGT'TVT 120
Db 61 AQKLGQGRVTMTTDTSTSTAYMELSLRSDDTAVVYVCARETKVGVHYHGYMDVWGQGT'TVT 120
QY 121 VSS 123
Db 121 VSS 123

RESULT 3
ADD05396
ID ADD05396 standard; protein; 123 AA.
XX
AC ADD05396;
XX
DT 01-JAN-2004 (first entry)
DE
DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 21.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
XX
OS Homo sapiens.
XX
PN WO2003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
PI WPI: 2003-577496/54.
XX
DR N-PSDB; ADD05398.
XX
PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
PS Claim 1; SEQ ID NO 21; 87pp; English.
XX
XX The invention relates to a novel monoclonal antibody used for inhibiting
XX tumour growth in an animal. The tumour inhibition process comprises
XX selecting an animal in need of treatment for a tumour, providing a
XX monoclonal antibody comprising a heavy chain amino acid, where the
XX antibody consists of any one of 10 fully defined sequences of 117-123
XX amino acids given in the specification, and where the monoclonal antibody
XX binds MUC18, and contacting the tumour with the antibody resulting in
XX inhibited proliferation of the cells. The monoclonal antibody has
XX cytostatic and can be used in the production of a vaccine. The monoclonal
XX antibodies against the MUC18 antigen are useful for diagnosing and
XX treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
XX tumour metastasis), inhibiting cell invasion associated with melanoma, or
XX increasing survival of an animal having a metastatic tumour. This
XX sequence represents an anti-MUC18 antibody heavy chain, variable region,
XX protein of the invention.

CC heavy chain protein of the invention.
XX
SQ Sequence 123 AA;
    Query Match      100.0%; Score 653; DB 7; Length 123;
    Best Local Similarity 100.0%; Pred. No. 7.3e-53;
    Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVOLVOSGAEVKKPGASVKVSKASGYTFFSYGFSWVRQAPQGLEWLGWISAYNGNTNY 60
Db 1 QVOLVOSGAEVKKPGASVKVSKASGYTFFSYGFSWVRQAPQGLEWLGWISAYNGNTNY 60
QY 61 AQKLGQGRVTMTTDTSTSTAYMELSLRSDDTAVVYVCARETKVGVHYHGYMDVWGQGT'TVT 120
Db 61 AQKLGQGRVTMTTDTSTSTAYMELSLRSDDTAVVYVCARETKVGVHYHGYMDVWGQGT'TVT 120
QY 121 VSS 123
Db 121 VSS 123

RESULT 3
ADD05396
ID ADD05396 standard; protein; 123 AA.
XX
AC ADD05396;
XX
DT 12-FEB-2004 (first entry)
DE
DE Human anti-MUC18 monoclonal antibody heavy chain #6.
XX
KW cell proliferation inhibition; MUC18 tumour antigen;
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; heavy chain; human.
XX
OS Homo sapiens.
XX
PN WO2003057837-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041580.
XX
PR 28-DEC-2001; 2001US-0346414P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
PI WPI: 2003-598367/56.
XX
DR N-PSDB; ADF09836.
XX
PT Inhibiting cell proliferation associated with expression of MUC18 tumor
PT antigen, involves incubating and inhibiting cell by administering anti-
PT MUC18 monoclonal antibody.
XX
PS Claim 1; SEQ ID NO 21; 83pp; English.
XX
XX The invention comprises a method for inhibiting cell proliferation
XX associated with expression of MUC18 tumour antigen. The method involves
XX administering anti-MUC18 monoclonal antibody. The method of the invention
XX is useful for inhibiting cell (e.g. melanoma or tumour cell)
XX proliferation associated with the expression of MUC18 tumour antigen, the
XX method is preferably useful for inhibiting tumour metastasis. The method
XX is useful for inhibiting cell proliferation in patients with tumours,
XX carcinomas, cancer and other malignancies. The present amino acid
XX sequence represents a heavy chain from an MUC18 tumour antigen-specific
XX monoclonal antibody.

CC heavy chain protein of the invention.
XX
SQ Sequence 123 AA;
    Query Match      100.0%; Score 653; DB 7; Length 123;
    Best Local Similarity 100.0%; Pred. No. 7.3e-53;
    Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSSYGFSGVSRQAPGGQGLEWLGWISAYNGNTNY 60  
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSSYGFSGVSRQAPGGQGLEWLGWISAYNGNTNY 60  
Qy 61 AQKLGQRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRRGVHHYGMVMDVWGQGT 120  
Db 61 AQKLGQRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRRGVHHYGMVMDVWGQGT 120  
Qy 121 VSS 123  
Db 121 VSS 123  
RESULT 4  
ID ABR55813 standard; protein; 125 AA.  
XX ABR55813;  
XX 02-SEP-2003 (first entry)  
XX Heavy chain variable region of anti-Ang-2 antibody FJ-G11 HC.  
XX  
XX Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;  
XX gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;  
XX angiogenesis; antibody.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX FT Region 26..36  
XX FT /note= "complementarity determining region (CDR) 1"  
XX FT 50..56  
XX FT /note= "complementarity determining region (CDR) 2"  
XX FT 96..115  
XX FT /note= "complementarity determining region (CDR) 3"  
XX  
XX WO2003030833-A2.  
XX  
XX 17-APR-2003.  
XX  
XX 11-OCT-2002; 2002WO-US032613.  
XX  
XX 11-OCT-2001; 2001US-0328604P.  
XX 10-OCT-2002; 2002US-00269805.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Oliner JD;  
XX  
XX WPI; 2003-504963/47.  
XX  
XX New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful  
XX for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,  
XX hemangioma, arteriosclerosis, atherosclerosis or endometriosis.  
XX  
XX Claim 1; Page 92; 161pp; English.  
XX  
XX The invention relates to a specific binding agent, which comprises at  
XX least one peptide selected from any of 62 peptides (ABR55769-830) or its  
XX fragment. The binding agents are antibodies that recognize and bind to  
XX angiopoietin-2 (Ang-2). The specific binding agent, particularly the  
XX antibody, is useful for inhibiting undesired angiogenesis, treating  
XX cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-  
XX 2 activity, modulating vascular permeability or plasma leakage, or  
XX treating a disease (e.g. ocular neovascular disease, obesity,  
XX haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,  
XX inflammatory disorders, atherosclerosis, endometriosis, neoplastic  
XX disease, bone-related disease, or psoriasis) in a mammal. The present  
XX sequence represents a heavy chain variable region of an anti-Ang-2  
XX antibody

SQ Sequence 125 AA;

Query Match 90.8%; Score 593; DB 6; Length 125;  
Best Local Similarity 90.4%; Pred. No. 2.7e-47;  
Matches 113; Conservative 4; Mismatches 6; Indels 2; Gaps 1;  
Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSSYGFSGVSRQAPGGQGLEWLGWISAYNGNTNY 60  
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSSYGFSGVSRQAPGGQGLEWLGWISAYNGNTNY 60  
Qy 61 AQKLGQRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKV--RGVHHYGMVMDVWGQGT 118  
Db 61 AQKLGQRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKV--RGVHHYGMVMDVWGQGT 120  
Qy 119 VTVSS 123  
Db 121 VTVSS 125

RESULT 5

ABP45910  
ID ABP45910 standard; protein; 251 AA.  
XX  
XX AC ABP45910;  
XX  
XX DT 19-AUG-2002 (first entry)  
XX  
XX DE Human BlyS binding scFv SEQ ID 1921.  
XX  
XX KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200202641-A1.  
XX  
XX PD 10-JAN-2002.  
XX  
XX PF 15-JUN-2001; 2001WO-US019110.  
XX  
XX PR 16-JUN-2000; 2000US-0212210P.  
XX 17-OCT-2000; 2000US-0240816P.  
XX PR 16-MAR-2001; 2001US-0276248P.  
XX 21-MAR-2001; 2001US-0277379P.  
XX PR 25-MAY-2001; 2001US-0293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX  
XX DR  
XX  
XX PT Antibodies against B lymphocyte stimulating polypeptides, useful for the  
XX diagnosis and treatment of cancers and immune disorders.  
XX  
XX PS Claim 1; Page 2693-2694; 3148pp; English.  
XX  
XX CC This invention describes novel antibodies that immunospecifically bind to  
XX B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the  
XX tumour necrosis factor (TNF) super family and induces B cell  
XX proliferation and differentiation. The antibodies of the invention have  
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
XX antirheumatic and antiAIDS activity and can be used in vaccines to  
XX inhibit the expression and activity of BlyS. The antibodies bind to BlyS  
XX and so may be used to detect and quantitate the presence of BlyS in  
XX biological samples and may be used in this way to diagnose disease  
XX associated with aberrant expression of BlyS. They may also be  
XX administered to treat diseases associated with aberrant BlyS expression

CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 251 AA;

Query Match 90.0%; Score 587.5; DB 5; Length 251;  
Best Local Similarity 88.3%; Pred. No. 1.9e-46;  
Matches 113; Conservative 4; Mismatches 6; Indels 5; Gaps 1;

QY 1 QVQLVQSGAEVKKPKGASVKVCKASGYTFYSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60  
DB 1 QVQLVQSGAEVKKPKGASVKVCKASGYTFYSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60

QY 61 AQKLGQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKV-----RGVHYGYMDVMGQ 115  
DB 61 AQKLGQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKV-----RGVHYGYMDVMGQ 120

QY 116 GTTIVTVSS 123  
DB 121 GTTIVTVSS 128

RESULT 6  
ADG96737  
ID ADG96737 standard; protein; 251 AA.

AC ADG96737;

DT 11-MAR-2004 (first entry)

XX Single chain antibody that immunospecifically binds BlyS SeqID 1921.  
XX antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;  
KW B cell proliferation; differentiation; scFv; myasthenia gravis;  
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;  
KW carcinoma; lymphoma; anti-rheumatic; antiarthritic; neuroprotective;  
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.  
XX

OS Unidentified.

XX WO2003055979-A2.

XX 10-JUL-2003.

XX 14-NOV-2002; 2002WO-US036496.

XX 16-NOV-2001; 2001US-0331469P.

PR 19-DEC-2001; 2001US-0340817P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX WPI; 2003-505530/47.

XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator  
PT (BlyS), useful for detecting and treating diseases or disorders e.g.  
PT rheumatoid arthritis, asthma and leukemia.  
XX

XX Example 1; SEQ ID NO 1921; 394pp; English.

XX This invention relates to novel antibodies that immunospecifically bind  
CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to  
CC chromosome 13q34 and encodes a protein that is a member of the tumour  
CC necrosis factor superfamily and induces both in vivo and in vitro B cell  
CC proliferation and differentiation. Specifically, it refers to single  
CC chain antibody molecules (scFvs) derived, preferably, from the variable  
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or  
CC fragment thereof, of either human, murine, rat or monkey BlyS. The

CC present invention refers to the use of such antibodies in various methods  
CC for the detection, diagnosis and prognosis of diseases related to the  
CC aberrant expression or inappropriate function of BlyS or its receptor. As  
CC such, these compositions are useful for identifying immune disorders  
CC including myasthenia gravis and multiple sclerosis, inflammatory  
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such  
CC as AIDS and proliferative disorders including leukaemia, carcinoma and  
CC lymphoma. Accordingly, they can be described as exhibiting various  
CC activities such as antirheumatic, antiallergic, neuroprotective,  
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This  
CC polypeptide sequence is a single chain antibody that binds BlyS of the  
CC invention. NOTE: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published pct\_sequences.

XX Sequence 251 AA;

Query Match 90.0%; Score 587.5; DB 7; Length 251;  
Best Local Similarity 88.3%; Pred. No. 1.9e-46;  
Matches 113; Conservative 4; Mismatches 6; Indels 5; Gaps 1;

QY 1 QVQLVQSGAEVKKPKGASVKVCKASGYTFYSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60  
DB 1 QVQLVQSGAEVKKPKGASVKVCKASGYTFYSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60

QY 61 AQKLGQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKV-----RGVHYGYMDVMGQ 115  
DB 61 AQKLGQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKV-----RGVHYGYMDVMGQ 120

QY 116 GTTIVTVSS 123  
DB 121 GTTIVTVSS 128

RESULT 7

ADK18819  
ID ADK18819 standard; protein; 127 AA.

XX ADK18819;

XX 06-MAY-2004 (first entry)

DE Anti-human PDGF-D antibody protein related sequence #45.

XX antiinflammatory; immunomodulator; cytostatic; gene therapy.

XX Homo sapiens.

XX WO2003057857-A2.

XX 17-JUL-2003.

XX 06-JAN-2003; 2003WO-US000398.

XX 07-JAN-2002; 2002US-00041860.

XX (ABGE-) ABGENIX INC.

XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
PI Bezabeh B;

XX WPI; 2003-587119/55.

XX New human monoclonal antibody that binds to platelet-derived growth  
PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
PT diseases, such as inflammation, autoimmunity and cancer.  
XX

PS Disclosure; SEQ ID NO 243; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to  
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
CC treating chronic and recurrent human diseases, such as inflammation,  
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are



CC useful for modulating collagen formation, and for staging various  
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
 CC generated using an active protein fragment of the gene product from the  
 CC clone 30664188.0.99 arising in the conditioned medium obtained when  
 CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
 CC sequence corresponds to a protein used in the invention.

SQ Sequence 127 AA;

Query Match 88.2%; Score 576; DB 7; Length 127;  
 Best Local Similarity 87.4%; Pred. No. 1.1e-45;  
 Matches 111; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVCKASGYTFYSGFSGWVRQAPGGQLEWLGWISAYNGNTNY 60  
 Db 1 QVQLVQSGAEVKKPGASVKVCKASGYTFYSGFSGWVRQAPGGQLEWLGWISAYNGNTNY 60  
 Qy 61 AQKLGKRVMTTDTSTAYMELSLRSDDTAVYYCARETKVRG-----VHYGMDVWGQG 116  
 Db 61 AQKLGKRVMTTDTSTAYMELSLRSDDTAVYYCARETKVRG-----VHYGMDVWGQG 120  
 Qy 117 TTVTVSS 123  
 Db 121 TTVTVSS 127

RESULT 8

ADK18901  
 ID ADK18901 standard; protein; 127 AA.

AC ADK18901;

DT 06-MAY-2004 (first entry)

DE Anti-human PDGF-D antibody protein related sequence #127.

KW antiinflammatory; immunomodulator; cytostatic; gene therapy.

OS Homo sapiens.

PN W02003057857-A2.

XX 17-JUL-2003.

XX 06-JAN-2003; 2003WO-US000398.

XX 07-JAN-2002; 2002US-00041860.

XX (ABGE-) ABGENIX INC.

XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 PI Bezabeh B;

XX WPI; 2003-587119/55.

XX New human monoclonal antibody that binds to platelet-derived growth  
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
 PT diseases, such as inflammation, autoimmunity and cancer.

PS Disclosure; SEQ ID NO 325; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to  
 CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
 CC treating chronic and recurrent human diseases, such as inflammation,  
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
 CC useful for modulating collagen formation, and for staging various  
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
 CC generated using an active protein fragment of the gene product from the  
 CC clone 30664188.0.99 arising in the conditioned medium obtained when  
 CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
 CC sequence corresponds to a protein used in the invention.

XX Sequence 127 AA;

Query Match 88.2%; Score 576; DB 7; Length 127;  
 Best Local Similarity 87.4%; Pred. No. 1.1e-45;  
 Matches 111; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVCKASGYTFYSGFSGWVRQAPGGQLEWLGWISAYNGNTNY 60  
 Db 1 QVQLVQSGAEVKKPGASVKVCKASGYTFYSGFSGWVRQAPGGQLEWLGWISAYNGNTNY 60  
 Qy 61 AQKLGKRVMTTDTSTAYMELSLRSDDTAVYYCARETKVRG-----VHYGMDVWGQG 116  
 Db 61 AQKLGKRVMTTDTSTAYMELSLRSDDTAVYYCARETKVRG-----VHYGMDVWGQG 120  
 Qy 117 TTVTVSS 123  
 Db 121 TTVTVSS 127

RESULT 9

ADK18607

ID ADK18607 standard; protein; 127 AA.

AC ADK18607;

DT 06-MAY-2004 (first entry)

DE Anti-human PDGF-D antibody heavy chain protein sequence.

KW antiinflammatory; immunomodulator; cytostatic; gene therapy.

OS Homo sapiens.

PN W02003057857-A2.

XX 17-JUL-2003.

XX 06-JAN-2003; 2003WO-US000398.

XX 07-JAN-2002; 2002US-00041860.

XX (ABGE-) ABGENIX INC.

XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 PI Bezabeh B;

XX WPI; 2003-587119/55.

XX New human monoclonal antibody that binds to platelet-derived growth  
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
 PT diseases, such as inflammation, autoimmunity and cancer.

PS Disclosure; SEQ ID NO 31; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to  
 CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
 CC treating chronic and recurrent human diseases, such as inflammation,  
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
 CC useful for modulating collagen formation, and for staging various  
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
 CC generated using an active protein fragment of the gene product from the  
 CC clone 30664188.0.99 arising in the conditioned medium obtained when  
 CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
 CC sequence corresponds to a protein used in the invention.

SQ Sequence 127 AA;

Query Match 88.2%; Score 576; DB 7; Length 127;  
 Best Local Similarity 87.4%; Pred. No. 1.1e-45;  
 Matches 111; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVCKASGYTFYSGFSGWVRQAPGGQLEWLGWISAYNGNTNY 60  
 Db 1 QVQLVQSGAEVKKPGASVKVCKASGYTFYSGFSGWVRQAPGGQLEWLGWISAYNGNTNY 60

QY 61 AQLQGRVTMTTSTSTAYMELSLRSDDTAVYVCARETKVRG-----VHYGMQVWGQG 116  
DB 61 AQLQGRVTMTTSTSTAYMELSLRSDDTAVYVCARETKVRG-----VHYGMQVWGQG 120  
QY 117 TTVTVSS 123  
DB 121 TTVTVSS 127

RESULT 10  
ADL25432  
ID ADL25432 standard; protein; 127 AA.  
XX  
AC ADL25432;  
DT 17-JUN-2004 (first entry)  
XX  
DE Human mAb 1.33 heavy chain variable region protein SEQ ID NO:42.  
XX  
KW antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;  
KW nephritis; mesangial cell proliferation inhibition;  
KW mesangial proliferative glomerulonephritis; nephrotropic;  
KW antiinflammatory; dermatological; immunosuppressive; antidiabetic;  
KW gene therapy; human; monoclonal antibody; mAb.  
XX  
OS Homo sapiens.  
XX  
PN WO2004024098-A2.  
XX  
PD 25-MAR-2004.  
XX  
PF 16-SEP-2003; 2003WO-US029414.  
XX  
PR 16-SEP-2002; 2002US-0411137P.  
XX  
XX (ABGE-) ABGENIX INC.  
PA (CURA-) CURAGEN CORP.  
XX  
PI Floege J, Gazit-Bornstein G, Keyt B, Larochele WJ, Lichenstein H;  
XX  
XX WPI: 2004-269881/25.  
DR N-PSDB; ADL25431.  
XX  
PT Use of an antibody or its binding fragment that binds platelet derived  
PT growth factor-DD (PDGF-DD) for preparing a medicament for treating  
PT nephritis.

PS Disclosure; SEQ ID NO 42; 115pp; English.  
XX  
CC The present invention describes an antibody or its binding fragment that  
CC binds platelet derived growth factor-DD (PDGF-DD), where the antibody is  
CC useful in preparing a medicament for treating nephritis. Also described:  
CC (1) a method of detecting nephritis; (2) a method of treating nephritis;  
CC (3) a method of inhibiting mesangial cell proliferation; and (4) a method  
CC of treating mesangial proliferative glomerulonephritis. The antibody has  
CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and  
CC antidiabetic activities, and can be used in gene therapy. The antibody or  
CC its binding fragment, that binds PDGF-DD, can be used in preparing a  
CC medicament for treating nephritis and related disorders, e.g., mesangial  
CC proliferative glomerulonephritis. The present sequence represents a human  
CC monoclonal antibody (mAb) variable region sequence, which is used in the  
CC exemplification of the present invention.  
XX  
SQ Sequence 127 AA;

Query Match 88.2%; Score 576; DB 8; Length 127;  
Best Local Similarity 87.4%; Pred. No. 1.1e-45;  
Matches 111; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY 1 QVOLVSGAEVKKPGASVKVSKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60  
DB 1 QVOLVSGAEVKKPGASVKVSKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60

QY 61 AQLQGRVTMTTSTSTAYMELSLRSDDTAVYVCARETKVRG-----VHYGMQVWGQG 116  
DB 61 AQLQGRVTMTTSTSTAYMELSLRSDDTAVYVCARETKVRG-----VHYGMQVWGQG 120  
QY 117 TTVTVSS 123  
DB 121 TTVTVSS 127

RESULT 11  
AAU02549  
ID AAU02549 standard; protein; 121 AA.  
XX  
AC AAU02549;  
DT 29-AUG-2001 (first entry)  
XX  
DE Anti-adipocyte monoclonal antibody heavy chain, FAT 36.  
XX  
KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;  
KW heart disease; complementarity determining region; CDR.  
XX  
OS Homo sapiens.  
XX  
PN WO200127279-A1.  
XX  
PD 19-APR-2001.  
XX  
PF 11-OCT-2000; 2000WO-CB003900.  
XX  
PR 12-OCT-1999; 99US-0158812P.  
XX  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Edwards BM, Main SH, Vaughan TJ;  
XX  
XX WPI: 2001-282031/29.  
DR N-PSDB; AAS03449.  
XX  
PT Panel of specific binding members of antibody molecules which bind to  
PT whole adipocytes is used in the treatment of obesity and obesity related  
PT diseases.

PS Claim 1; Page 123; 182pp; English.  
XX  
CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid  
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,  
CC and heavy chain complementarity determining regions (CDR) of the  
CC invention. The antibodies can be used in the treatment of obesity and  
CC obesity related diseases. The antibodies can be used to deliver drugs or  
CC pro-drugs directly to the fat mass of an obese patient or the antibody  
CC can be used as a therapeutic itself. Antibodies binding specifically to  
CC adipocytes can be used to activate the immune system to destroy the cells  
CC by complement mediated lysis. The antibodies may be labeled with a  
CC detectable label such as radiolabel, fluorescent or chemical group and  
CC used in methods of diagnosis in human subjects e.g. to determine the  
CC presence of adipocyte antigen on the surface of an adipocyte to detect or  
CC determine the presence or level of adipocytes in a cell or tissue sample.  
CC The antibodies can be used as an alternative means of treatment for obese  
CC patients other than undergoing surgery to remove excess fat. Antibodies  
CC for different types of fat deposits can also be produced e.g. intra-  
CC abdominal fat associated with heart disease  
XX  
SQ Sequence 121 AA;

Query Match 86.5%; Score 565; DB 4; Length 121;  
Best Local Similarity 87.2%; Pred. No. 1.1e-44;  
Matches 109; Conservative 6; Mismatches 4; Indels 6; Gaps 2;

QY 1 QVOLVSGAEVKKPGASVKVSKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60  
DB 1 EQVLVESGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQGLEWLGWISAYNGNTNY 60

Qy	61	AQKLGRTVMTTDTSTAYMELSLRSDDTAVYYCARETKVRGV--HYYGMDVMGCGTT	118
		:               :	
Db	61	ABKLGRTVMTTDTSTAYMELSLRSDDTAVYYCARD---GVLDYYGMDVMGCGTTL	116

Qy	119	VTVSS	123
	.		
Db	117	VTVSS	121

RESULT	12
ADK18783	
ID	ADK18783 standard; protein; 125 AA.
XX	
XX	ADK18783;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	Anti-human PDGF-D antibody protein related sequence #9.
XX	
KW	antiinflammatory; immunomodulator; cytostatic; gene therapy.

	119	VT	VSS	123
Qy				
D <sub>b</sub>	121	VT	VSS	125

RESULT 14  
ADL25452  
ID ADL25452 standard; protein; 125 AA.  
XX  
AC ADL25452;



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55 ; Search time 19.1128 Seconds  
(without alignments)  
480.403 Million cell updates/sec

Title: US-10-660-357A-21

Perfect score: 653

Sequence: 1 QVQLVQSGAEVKKPGASVKV.....GVHYGMDVWGQGTITVTVSS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCFUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	521.5	79.9	118	4	US-09-726-219A-165
2	517	79.2	121	1	Sequence 165, App
3	501	76.7	117	3	Sequence 3, Appli
4	499.5	76.5	120	2	Sequence 105, App
5	491	75.2	129	2	Sequence 19, Appl
6	491	75.2	129	3	Sequence 45, Appl
7	491	75.2	129	5	Sequence 77, Appl
8	490.5	75.1	120	3	Sequence 45, Appl
9	490.5	75.1	120	3	Sequence 36, Appl
10	490.5	75.1	120	4	Sequence 59, Appl
11	490.5	75.1	120	4	Sequence 36, Appl
12	490.5	75.1	120	4	Sequence 59, Appl
13	490.5	75.1	120	4	Sequence 36, Appl
14	490.5	75.1	120	4	Sequence 36, Appl
15	490.5	75.1	120	4	Sequence 59, Appl
16	490	75.0	117	3	Sequence 22, Appl
17	490	75.0	117	4	Sequence 22, Appl
18	490	75.0	117	4	Sequence 22, Appl
19	490	75.0	117	4	Sequence 22, Appl
20	489.5	75.0	128	1	Sequence 22, Appl
21	489.5	75.0	128	3	Sequence 22, Appl
22	485	74.3	470	4	Sequence 28, Appl
23	481	73.7	125	3	Sequence 3, Appli
24	480	73.5	140	3	Sequence 63, Appl
25	480	73.5	140	4	Sequence 63, Appl
26	477	73.0	119	2	Sequence 10, Appl
27	477	73.0	119	5	Sequence 10, Appl

28	474	72.6	119	4	US-09-438-954-41	Sequence 41, Appl
29	473	72.4	139	3	US-08-933-983-21	Sequence 21, Appl
30	472.5	72.4	139	1	US-08-233-877C-19	Sequence 19, Appl
31	472.5	72.4	139	2	US-08-452-164A-19	Sequence 19, Appl
32	472.5	72.4	139	3	US-08-603-024-18	Sequence 18, Appl
33	472.5	72.4	139	4	US-08-450-809-14	Sequence 14, Appl
34	470	72.0	119	2	US-08-561-521-12	Sequence 12, Appl
35	470	72.0	119	5	PCT-US95-01219-12	Sequence 12, Appl
36	469	71.8	132	4	US-09-513-999C-4112	Sequence 4112, Ap
37	468.5	71.7	139	4	US-09-289-921-123	Sequence 123, App
38	468	71.7	140	3	US-08-836-561-74	Sequence 74, Appl
39	468	71.7	140	4	US-09-434-122-74	Sequence 74, Appl
40	466	71.4	119	1	US-08-300-386A-65	Sequence 65, Appl
41	466	71.4	119	3	US-08-931-645-65	Sequence 65, Appl
42	466	71.4	119	5	PCT-US95-11235-65	Sequence 65, Appl
43	466	71.4	134	4	US-09-471-276-849	Sequence 849, App
44	464.5	71.1	139	4	US-09-269-921-108	Sequence 108, App
45	463	70.9	121	1	US-08-202-047-23	Sequence 23, Appl

#### ALIGNMENTS

#### RESULT 1

US-09-726-219A-165  
; Sequence 165, Application US/09726219A  
; Patent No. 6806079

; GENERAL INFORMATION:  
; APPLICANT: Cambridge Antibody Technology Limited

; APPLICANT: Medical Research Council

; APPLICANT: McCafferty, John

; APPLICANT: Pope, Anthony

; APPLICANT: Johnson, Kevin

; APPLICANT: Hoogenboom, Hendricus

; APPLICANT: Griffiths, Andrew

; APPLICANT: Jackson, Ronald

; APPLICANT: Holliger, Kasper

; APPLICANT: Marks, James

; APPLICANT: Clarkson, Timothy

; APPLICANT: Chiswell, David

; APPLICANT: Winter, Gregory

; APPLICANT: Bonert, Timothy

; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs

; FILE REFERENCE: 213839-00013

; CURRENT APPLICATION NUMBER: US/09/726,219A

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: GB 9015198.6

; PRIOR FILING DATE: 1990-07-10

; PRIOR APPLICATION NUMBER: GB 9022845.3

; PRIOR FILING DATE: 1990-10-19

; PRIOR APPLICATION NUMBER: GB 9022845.3

; PRIOR FILING DATE: 1990-10-19

; PRIOR APPLICATION NUMBER: GB 9024503.6

; PRIOR FILING DATE: 1990-11-12

; PRIOR APPLICATION NUMBER: GB 9104744.9

; PRIOR FILING DATE: 1991-03-06

; PRIOR APPLICATION NUMBER: GB 9110549.4

; PRIOR FILING DATE: 1991-05-15

; PRIOR APPLICATION NUMBER: PCT/GB91/01134

; PRIOR FILING DATE: 1991-07-10

; PRIOR APPLICATION NUMBER: US 07/971,857

; PRIOR FILING DATE: 1993-01-08

; PRIOR APPLICATION NUMBER: US 08/484,893

; PRIOR FILING DATE: 1995-06-07

; NUMBER OF SEQ ID NOS: 272

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 165

; LENGTH: 118

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-726-219A-165

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Query Match          79.9%; Score 521.5; DB 4; Length 118;
Best Local Similarity 84.0%; Pred. No. 2.1e-43; Indels 3; Gaps 2;
Matches 100; Conservative 6; Mismatches 10; Indels 3; Gaps 2;

QY 1 QVOLVSGAEVKKPGASVKVCKASGYTFYSYGFSGWVRQAPGGLEWLGWISAYNGNTNY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLVSGAEVKKPGASVKVCKASGYTFYSYGFSGWVRQAPGGLEWLGWISAYNGNTKY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AQKLGQRTVMTTDTSTSTAYMELRSDDTAVYYCAR--ETKRVGHYHGMVWGQGT 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AQKLGQRTVMTTDTSTSTAYMELRSDDTAVYYCVRLLPKRTATLHY--IDVWGKGT 118
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 2
US-08-264-093-3
; Sequence 3, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ridout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,093
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: No. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 868-1482
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS: not applicable
; TOPOLOGY: linear
US-08-264-093-3

Query Match          79.2%; Score 517; DB 1; Length 121;
Best Local Similarity 82.1%; Pred. No. 5.8e-43;
Matches 101; Conservative 8; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVOLVSGAEVKKPGASVKVCKASGYTFYSYGFSGWVRQAPGGLEWLGWISAYNGNTNY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLVSGAEVKKPGASVKVCKASGYTFYTGISWVRQAPGGLEWLGWISAHNGNTNS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AQKLGQRTVMTTDTSTSTAYMELRSDDTAVYYCARETKRVGHYHGMVWGQGT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AQKFGQRTVMTTDTSTSTAYMEVRSDDTAVYYCARVGVWDLNLF--DYWGQGLT 118
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 VSS 123
   |||
Db 119 VSS 121
   |||
```

```
RESULT 3
US-08-545-809A-105
; Sequence 105, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-105

Query Match          76.7%; Score 501; DB 3; Length 117;
Best Local Similarity 96.9%; Pred. No. 2e-41;
Matches 95; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVOLVSGAEVKKPGASVKVCKASGYTFYSYGFSGWVRQAPGGLEWLGWISAYNGNTNY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVOLVSGAEVKKPGASVKVCKASGYTFTSYGISWVRQAPGGLEWLGWISAYNGNTNY 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AQKLGQRTVMTTDTSTSTAYMELRSDDTAVYYCAR 98
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 AQKLGQRTVMTTDTSTSTAYMELRSDDTAVYYCAR 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
US-08-652-816A-19
; Sequence 19, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; TITLE OF INVENTION: methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
```

COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652.816A  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.4  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.8  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 23-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9535004.9  
FILING DATE: 07-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9610824.6  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/02240  
FILING DATE: 02-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/244,597  
FILING DATE: 01-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/33308  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-652-816A-19

Query Match 76.5%; Score 499.5; DB 2; Length 120;  
Best Local Similarity 80.5%; Pred. No. 2.9e-41;  
Matches 99; Conservative 7; Mismatches 14; Indels 3; Gaps 2;  
QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFYSGFSGWVRQAPGQGLEWLGWISAYNGNTNY 60  
DB 1 QVTLQSGAEVKKPGSPKVKVSKASGYTFYAGFNWVRQAPGQGLEWM-WISAYSGNTKY 59  
QY 61 AQLQGRVTMTTDTSTSTAYMELSLRSDDTAVYICARETKKVRGHHYGMVNGQGTVT 120  
DB 60 AQLQGRVTMTTDTSTSTAYMELSLRSDDTAVYICARETKKVRGHHYGMVNGQGTMT 117  
QY 121 VSS 123  
DB 118 VSS 120

RESULT 5  
US-08-561-521-45  
Sequence 45, Application US/08561521  
Patent No. 5840299  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Leger, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte

TITLE OF INVENTION: Adhesion Molecule VLA-4  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/561,521  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/186,269A  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 129 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-561-521-45

Query Match 75.2%; Score 491; DB 2; Length 129;  
Best Local Similarity 76.3%; Pred. No. 2.1e-40;  
Matches 100; Conservative 5; Mismatches 16; Indels 10; Gaps 3;  
QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFYSGFSGWVRQAPGQGLEWLGWISAY-NGNTN 59  
DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFYTSYAISWVRQAPGQGLEWGMWNPYNGDNTN 60  
QY 60 YAKLQGRVTMTTDTSTSTAYMELSLRSDDTAVYICARETK-----VRGHHYGMV 112  
DB 61 YAKLQGRVTMTTDTSTSTAYMELSLRSDDTAVYICARETK-----DYXFDY 118  
QY 113 WGQGTTLTVSS 123  
DB 119 WGQGTTLTVSS 129

RESULT 6  
US-08-525-539A-77  
Sequence 77, Application US/08525539A  
Patent No. 6309636  
GENERAL INFORMATION:  
APPLICANT: DO COUTO, FERNANDO J.R.  
APPLICANT: CERIANI, ROBERTO L.  
APPLICANT: PETERSON, JERRY A.  
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE  
TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND  
TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FORSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 77:
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; QUERY MATCH 75.2%; Score 491; DB 3; Length 129;
; Best Local Similarity 76.3%; Pred. No. 2.1e-40;
; Matches 100; Conservative 5; Mismatches 16; Indels 10; Gaps 3;
;
; QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFPSYGFSGVVRQAPQGGLWLGWISAY-NGNTN 59
; Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFPSYGFSGVVRQAPQGGLWLGWISAY-NGNTN 59
;
; QY 60 YAKLQGRVTMTDTSTSTAYMELSLRSDDTAVYYCARETK-----VRGVHYYGMDV 112
; Db 61 YAKLQGRVTMTDTSTSTAYMELSLRSDDTAVYYCARETK-----VRGVHYYGMDV 112
;
; QY 113 WQGQTTVTVSS 123
; Db 119 WQGQTLVTVSS 129
;
; RESULT 7
; PCT-US95-01219-45
; Sequence 45, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Legier, Olivier J.
; APPLICANT: Saidanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-01219-45
;
; Query Match 75.2%; Score 491; DB 5; Length 129;
; Best Local Similarity 76.3%; Pred. No. 2.1e-40;
; Matches 100; Conservative 5; Mismatches 16; Indels 10; Gaps 3;
;
; QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFPSYGFSGVVRQAPQGGLWLGWISAY-NGNTN 59
; Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFPSYGFSGVVRQAPQGGLWLGWISAY-NGNTN 59
;
; QY 60 YAKLQGRVTMTDTSTSTAYMELSLRSDDTAVYYCARETK-----VRGVHYYGMDV 112
; Db 61 YAKLQGRVTMTDTSTSTAYMELSLRSDDTAVYYCARETK-----VRGVHYYGMDV 112
;
; QY 113 WQGQTTVTVSS 123
; Db 119 WQGQTLVTVSS 129
;
; RESULT 8
; US-09-025-769B-36
; Sequence 36, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
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;  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-025-769B-36

Query Match 75.1%; Score 490.5; DB 3; Length 120;  
Best Local Similarity 78.9%; Pred. No. 2.2e-40;  
Matches 97; Conservative 5; Mismatches 18; Indels 3; Gaps 1;

Qy 1 QVOLVSGAEVKKPGASVKVSCKASGYTFSSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60  
Db 1 QVOLVSGAEVKKPGASVKVSCKASGYTFSSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60

Qy 61 AQKLGKRVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTFTV 120  
Db 61 AQKLGKRVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTFTV 120

Qy 121 VSS 123  
Db 118 VSS 120

RESULT 9  
US-09-025-769B-59  
; Sequence 59, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-025-769B-59

Query Match 75.1%; Score 490.5; DB 3; Length 120;  
Best Local Similarity 78.9%; Pred. No. 2.2e-40;  
Matches 97; Conservative 5; Mismatches 18; Indels 3; Gaps 1;

Qy 1 QVOLVSGAEVKKPGASVKVSCKASGYTFSSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60  
Db 1 QVOLVSGAEVKKPGASVKVSCKASGYTFSSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60  
Qy 61 AQKLGKRVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTFTV 120  
Db 61 AQKLGKRVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTFTV 120  
Qy 121 VSS 123  
Db 118 VSS 120

RESULT 10  
US-09-490-070A-36  
; Sequence 36, Application US/09490070A  
; Patent No. 6696248  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
; White & McAuliffe  
; STREET: 1666 K Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,070A  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Colin G. Sandercock, Esq.  
; REGISTRATION NUMBER: 31,298  
; REFERENCE/DOCKET NUMBER: 37629-0005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 912-2000  
; TELEFAX: (202) 912-2020  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-09-490-070A-36

Query Match 75.1%; Score 490.5; DB 4; Length 120;  
Best Local Similarity 78.9%; Pred. No. 2.2e-40;  
Matches 97; Conservative 5; Mismatches 18; Indels 3; Gaps 1;

Qy 1 QVOLVSGAEVKKPGASVKVSCKASGYTFSSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60  
Db 1 QVOLVSGAEVKKPGASVKVSCKASGYTFSSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60

Qy 61 AQKLGKRVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTFTV 120  
Db 61 AQKLGKRVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTFTV 120

QY 121 VSS 123  
|||  
Db 118 VSS 120

## RESULT 11

US-09-490-070A-59  
; Sequence 59, Application US/09490070A  
; Patent No. 6696248

## GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter  
Ilag, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman

White & McAuliffe

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 59:

US-09-490-070A-59

Query Match 75.1%; Score 490.5; DB 4; Length 120;  
Best Local Similarity 78.9%; Pred. No. 2.2e-40;  
Matches 97; Conservative 5; Mismatches 18; Indels 3; Gaps 1;

QY 1 QVOLVSGAEVKKPGASVKVSKASGYTFPSYGFVSRQAPGQGLWLGWISAYNGNTNY 60  
|||||  
Db 1 QVOLVSGAEVKKPGASVKVSKASGYTFPSYGFVSRQAPGQGLWLGWISAYNGNTNY 60  
|||||

QY 61 AQLQGRVTMTTSTSTAYMELSLRSDTAVYYCARETKVGRVHYGMDVWGQGTFTVT 120  
|||||  
Db 61 AQLQGRVTMTTSTSTAYMELSLRSDTAVYYCARETKVGRVHYGMDVWGQGTFTVT 120  
|||||

QY 121 VSS 123  
|||  
Db 118 VSS 120

## RESULT 12

US-09-490-153-36

; Sequence 36, Application US/09490153

; Patent No. 6706484

; GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 36:

US-09-490-153-36

Query Match 75.1%; Score 490.5; DB 4; Length 120;  
Best Local Similarity 78.9%; Pred. No. 2.2e-40;  
Matches 97; Conservative 5; Mismatches 18; Indels 3; Gaps 1;

QY 1 QVOLVSGAEVKKPGASVKVSKASGYTFPSYGFVSRQAPGQGLWLGWISAYNGNTNY 60  
|||||  
Db 1 QVOLVSGAEVKKPGASVKVSKASGYTFPSYGFVSRQAPGQGLWLGWISAYNGNTNY 60  
|||||

QY 61 AQLQGRVTMTTSTSTAYMELSLRSDTAVYYCARETKVGRVHYGMDVWGQGTFTVT 120  
|||||  
Db 61 AQLQGRVTMTTSTSTAYMELSLRSDTAVYYCARETKVGRVHYGMDVWGQGTFTVT 120  
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QY 121 VSS 123  
|||  
Db 118 VSS 120

## RESULT 13

US-09-490-153-59

; Sequence 59, Application US/09490153

; Patent No. 6706484

; GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilag, Vic

Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
US-09-490-153-59

Query Match 75.1%; Score 490.5; DB 4; Length 120;  
Best Local Similarity 78.9%; Pred. No. 2.2e-40;  
Matches 97; Conservative 5; Mismatches 18; Indels 3; Gaps 1;  
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Db 1 QVQLVQSGAEVKKPGASVKVCKASGYTFSSYHWHVRQAPGQGLEWGWINPNSGNTNY 60  
QY 61 AQKLQGRVTMTDTSTSTAYMELSLRSDDTAVVYVCARETKVRGVHYGMDVWGQGTTLT 120  
Db 61 AQKFGQRTVTRDTSTISATYMWELSLRSDDTAVVYCAR---WGDDGFYANDYWGQGTTLT 117  
QY 121 VSS 123  
Db 118 VSS 120

RESULT 14  
US-09-490-324-36  
Sequence 36, Application US/09490324  
Patent No. 6828422  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,324  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-09-490-324-36

Query Match 75.1%; Score 490.5; DB 4; Length 120;  
Best Local Similarity 78.9%; Pred. No. 2.2e-40;  
Matches 97; Conservative 5; Mismatches 18; Indels 3; Gaps 1;  
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Db 1 QVQLVQSGAEVKKPGASVKVCKASGYTFSSYHWHVRQAPGQGLEWGWINPNSGNTNY 60  
QY 61 AQKLQGRVTMTDTSTSTAYMELSLRSDDTAVVYVCARETKVRGVHYGMDVWGQGTTLT 120  
Db 61 AQKFGQRTVTRDTSTISATYMWELSLRSDDTAVVYCAR---WGDDGFYANDYWGQGTTLT 117  
QY 121 VSS 123  
Db 118 VSS 120

RESULT 15  
US-09-490-324-59  
Sequence 59, Application US/09490324  
Patent No. 6828422  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,324  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769  
; FILING DATE: 18-FEB-1998  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
US-09-490-324-59

Query Match 75.1%; Score 490.5; DB 4; Length 120;  
Best Local Similarity 78.9%; Pred. No. 2.2e-40;  
Matches 97; Conservative 5; Mismatches 18; Indels 3; Gaps 1;  
  
Qy 1 QVQLVSGAEVKKPGASVKVSKASGYTFESYGFSGVVRQAPGQGLEWLGWISAYNGNTNY 60  
Db 1 QVQLVSGAEVKKPGASVKVSKASGYTFESYGFSGVVRQAPGQGLEWLGWISAYNGNTNY 60  
  
Qy 61 AQLKQGRVTMTDTSTAYMELSLRSDDTAVYVCARETKVGVHHYGVNDVWGQGTYYT 120  
Db 61 AQLKQGRVTMTDTSTAYMELSLRSDDTAVYVCARETKVGVHHYGVNDVWGQGTYYT 120  
  
Qy 121 VSS 123  
Db 118 VSS 120

Search completed: November 9, 2005, 11:46:39  
Job time : 20.1128 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2005, 11:40:37 ; Search time 68.3333 Seconds  
(without alignments)  
753.137 Million cell updates/sec

Title: US-10-660-357A-21

Perfect score: 653

Sequence: 1 QVQLVQSGAEVKPGASVKV.....GVHYGMDVWGQGTITVSS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
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- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	653	100.0	123	14	US-10-330-613-21
2	653	100.0	123	14	US-10-330-530-21
3	653	100.0	123	16	US-10-660-357-21
4	593	90.8	125	14	US-10-269-805-45
5	587.5	90.0	251	10	US-09-880-748-1921
6	587.5	90.0	251	15	US-10-293-418-1921
7	584.5	89.5	121	20	US-11-031-485-120
8	576	88.2	127	14	US-10-041-860-31
9	576	88.2	127	14	US-10-041-860-243
10	576	88.2	127	14	US-10-041-860-325
11	576	88.2	127	16	US-10-665-383-42
Sequence 21, Appl					
Sequence 21, Appl					
Sequence 21, Appl					
Sequence 45, Appl					
Sequence 1921, Ap					
Sequence 1921, Ap					
Sequence 120, App					
Sequence 31, Appl					
Sequence 243, App					
Sequence 325, App					
Sequence 42, Appl					

12	571.5	87.5	469	20	US-11-031-485-42	Sequence 42, Appl
13	569.5	87.2	469	20	US-11-031-485-34	Sequence 34, Appl
14	561	85.9	125	14	US-10-041-860-42	Sequence 42, Appl
15	561	85.9	125	14	US-10-041-860-207	Sequence 207, App
16	561	85.9	125	16	US-10-665-383-62	Sequence 62, Appl
17	558.5	85.5	126	14	US-10-041-860-354	Sequence 354, App
18	557	85.3	251	10	US-09-880-748-1562	Sequence 1562, Ap
19	557	85.3	251	15	US-10-293-418-1562	Sequence 1562, Ap
20	556	85.1	123	14	US-10-269-805-51	Sequence 51, Appl
21	554.5	84.9	125	20	US-11-031-485-133	Sequence 133, App
22	554.5	84.9	247	10	US-09-880-748-1873	Sequence 1873, Ap
23	554.5	84.9	247	15	US-10-293-418-1873	Sequence 1873, Ap
24	552	84.5	257	10	US-09-880-748-1610	Sequence 1610, Ap
25	552	84.5	257	15	US-10-293-418-1610	Sequence 1610, Ap
26	551.5	84.5	249	20	US-11-017-030-30	Sequence 30, Appl
27	551	84.4	248	10	US-09-880-748-1472	Sequence 1472, Ap
28	551	84.4	248	15	US-10-293-418-1472	Sequence 1472, Ap
29	551	84.4	255	10	US-09-880-748-1190	Sequence 1190, Ap
30	551	84.4	255	15	US-10-293-418-1190	Sequence 1190, Ap
31	551	84.4	257	10	US-09-880-748-1354	Sequence 1354, Ap
32	551	84.4	257	15	US-10-293-418-1354	Sequence 1354, Ap
33	550.5	84.3	251	10	US-09-880-748-1315	Sequence 1315, Ap
34	550.5	84.3	251	15	US-10-293-418-1315	Sequence 1315, Ap
35	550	84.2	248	10	US-09-880-748-1446	Sequence 1446, Ap
36	550	84.2	248	15	US-10-293-418-1446	Sequence 1446, Ap
37	549.5	84.2	132	17	US-10-506-743-18	Sequence 18, Appl
38	549	84.1	248	10	US-09-880-748-1778	Sequence 1778, Ap
39	549	84.1	248	15	US-10-293-418-1778	Sequence 1778, Ap
40	547.5	83.8	249	10	US-09-880-748-1425	Sequence 1425, Ap
41	547.5	83.8	249	15	US-10-293-418-1425	Sequence 1425, Ap
42	547.5	83.8	252	10	US-09-880-748-1674	Sequence 1674, Ap
43	547.5	83.8	252	15	US-10-293-418-1674	Sequence 1674, Ap
44	547	83.8	251	10	US-09-880-748-1586	Sequence 1586, Ap
45	547	83.8	251	10	US-09-880-748-1872	Sequence 1872, Ap

#### ALIGNMENTS

RESULT 1  
US-10-330-613-21  
; Sequence 21, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ARGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330.613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-21

Query Match 100.0%; Score 653; DB 14; Length 123;  
Best Local Similarity 100.0%; Pred. No. 1e-54;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPGASVKVCKASGYTFFSYGFSWVRQAPGGQLEWLGWISAYNGNTNY 60  
Db 1 QVQLVQSGAEVKPGASVKVCKASGYTFFSYGFSWVRQAPGGQLEWLGWISAYNGNTNY 60

Qy 61 AQKLGQGVNTTDTSTSTAYMELRSRSDDTATVYTCARETKVGRGVHYGHVWGQGTITVT 120  
Db 61 AQKLGQGVNTTDTSTSTAYMELRSRSDDTATVYTCARETKVGRGVHYGHVWGQGTITVT 120

Qy 121 VSS 123  
|||

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Db      121 VSS 123

RESULT 2
US-10-330-530-21
; Sequence 21, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ARGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-21

Query Match      100.0%; Score 653; DB 14; Length 123;
Best Local Similarity 100.0%; Pred. No. 1e-54;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QVQLVQSGAEVKKPGASVKVCKASGYTFYSGFSGWVRQAPGGGLEWLGWISAYNGNTNY 60
Db      1 QVQLVQSGAEVKKPGASVKVCKASGYTFYSGFSGWVRQAPGGGLEWLGWISAYNGNTNY 60
Qy      61 AQLQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKVGRGVHYGMDVWGQGT 120
Db      61 AQLQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKVGRGVHYGMDVWGQGT 120
Qy      121 VSS 123
Db      121 VSS 123

RESULT 3
US-10-660-357-21
; Sequence 21, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ARGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-21

Query Match      100.0%; Score 653; DB 16; Length 123;
Best Local Similarity 100.0%; Pred. No. 1e-54;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QVQLVQSGAEVKKPGASVKVCKASGYTFYSGFSGWVRQAPGGGLEWLGWISAYNGNTNY 60
Db      1 QVQLVQSGAEVKKPGASVKVCKASGYTFYSGFSGWVRQAPGGGLEWLGWISAYNGNTNY 60
Qy      61 AQLQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKVGRGVHYGMDVWGQGT 120
Db      61 AQLQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKVGRGVHYGMDVWGQGT 120
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Qy      121 VSS 123
Db      121 VSS 123

RESULT 4
US-10-269-805-45
; Sequence 45, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-45

Query Match      90.8%; Score 593; DB 14; Length 125;
Best Local Similarity 90.4%; Pred. No. 5.8e-49;
Matches 113; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

Qy      1 QVQLVQSGAEVKKPGASVKVCKASGYTFYSGFSGWVRQAPGGGLEWLGWISAYNGNTNY 60
Db      1 QVQLVQSGAEVKKPGASVKVCKASGYTFYSGFSGWVRQAPGGGLEWLGWISAYNGNTNY 60
Qy      61 AQLQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKV--RGVHYGMDVWGQGT 118
Db      61 AQLQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKV--RGVHYGMDVWGQGT 120
Qy      119 VTVSS 123
Db      121 VTVSS 125

RESULT 5
US-09-880-748-1921
; Sequence 1921, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1921
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1921

Query Match      90.0%; Score 587.5; DB 10; Length 251;
Best Local Similarity 88.3%; Pred. No. 4e-48;
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Matches 113; Conservative 4; Mismatches 6; Indels 5; Gaps 1;

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Qy 1 QVQLVQSGAEVKKPGASVKSCASGYTFYSGFSGWRQAPGQGLEWLGWISAYNGNTNY 60
Db 1 QVQLVQSGAEVKKPGASVKSCASGYTFYSGFSGWRQAPGQGLEWLGWISAYNGNTNY 60
Qy 61 AQLQGRVTMTTDTSTAYMELSLRSDDTAVYICARETKV-----RGVHYGMDVWGQ 115
Db 61 AQLQGRVTMTTDTSTAYMELSLRSDDTAVYICARETKV-----RGVHYGMDVWGQ 120
Qy 116 GTTVTVSS 123
Db 121 GTTVTVSS 128
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## RESULT 6

US-10-293-418-1921  
; Sequence 1921, Application US/10293418  
; Publication No. US20030223996A1  
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: P523P2  
; CURRENT APPLICATION NUMBER: US/10/293,418  
; CURRENT FILING DATE: 2002-11-27

; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 03/880,748  
; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 1921

; LENGTH: 251

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-293-418-1921

Query Match 90.0%; Score 587.5; DB 15; Length 251;  
Best Local Similarity 88.3%; Pred. No. 4e-48;  
Matches 113; Conservative 4; Mismatches 6; Indels 5; Gaps 1;

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Qy 1 QVQLVQSGAEVKKPGASVKSCASGYTFYSGFSGWRQAPGQGLEWLGWISAYNGNTNY 60
Db 1 QVQLVQSGAEVKKPGASVKSCASGYTFYSGFSGWRQAPGQGLEWLGWISAYNGNTNY 60
Qy 61 AQLQGRVTMTTDTSTAYMELSLRSDDTAVYICARETKV-----RGVHYGMDVWGQ 115
Db 61 AQLQGRVTMTTDTSTAYMELSLRSDDTAVYICARETKV-----RGVHYGMDVWGQ 120
Qy 116 GTTVTVSS 123
Db 121 GTTVTVSS 128
```

## RESULT 7

US-11-031-485-120  
; Sequence 120, Application US/11031485  
; Publication No. US20050232917A1  
; GENERAL INFORMATION:

; APPLICANT: PULLEN, NICHOLAS

; APPLICANT: MOLLOY, ELIZABETH

; APPLICANT: KELLERMANN, SIRID-AIMEE

; APPLICANT: GREEN, LARRY L.

; TITLE OF INVENTION: ANTIBODIES TO MACCAM

; FILE REFERENCE: ABX-PP6

; CURRENT APPLICATION NUMBER: US/11/031,485

; CURRENT FILING DATE: 2005-01-07

; PRIOR APPLICATION NUMBER: 60/535,490

; PRIOR FILING DATE: 2004-01-09

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 120

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-031-485-120

Query Match 89.5%; Score 584.5; DB 20; Length 121;  
Best Local Similarity 91.1%; Pred. No. 3.6e-48;  
Matches 112; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

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Qy 1 QVQLVQSGAEVKKPGASVKSCASGYTFYSGFSGWRQAPGQGLEWLGWISAYNGNTNY 60
Db 1 QVQLVQSGAEVKKPGASVKSCASGYTFYSGFSGWRQAPGQGLEWLGWISAYNGNTNY 60
Qy 61 AQLQGRVTMTTDTSTAYMELSLRSDDTAVYICARETKVGVHYGMDVWGQGTITV 120
Db 61 AQLQGRVTMTTDTSTAYMELSLRSDDTAVYICARETKVGVHYGMDVWGQGTITV 117
Qy 121 VSS 123
Db 118 VSS 120
```

## RESULT 8

US-10-041-860-31

; Sequence 31, Application US/10041860

; Publication No. US20030157109A1

; GENERAL INFORMATION:

; APPLICANT: Corvalan, Jose R.F.

; APPLICANT: Jia, Xiao-Chi

; APPLICANT: Feng, Xiao

; APPLICANT: Yang, Xiao-Dong

; APPLICANT: Chen, Francine

; APPLICANT: Gazit, Gadi

; APPLICANT: Weber, Richard

; APPLICANT: Bezabeh, Binyam

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES

; FILE REFERENCE: ABGENIX.051A

; CURRENT APPLICATION NUMBER: US/10/041,860

; CURRENT FILING DATE: 2002-01-07

; NUMBER OF SEQ ID NOS: 377

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 31

; LENGTH: 127

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-041-860-31

Query Match 88.2%; Score 576; DB 14; Length 127;  
Best Local Similarity 87.4%; Pred. No. 2.5e-47;  
Matches 111; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

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Qy 1 QVQLVQSGAEVKKPGASVKSCASGYTFYSGFSGWRQAPGQGLEWLGWISAYNGNTNY 60
Db 1 QVQLVQSGAEVKKPGASVKSCASGYTFYSGFSGWRQAPGQGLEWLGWISAYNGNTNY 60
Qy 61 AQLQGRVTMTTDTSTAYMELSLRSDDTAVYICARETKV-----VHYGMDVWGQ 116
Db 61 AQLQGRVTMTTDTSTAYMELSLRSDDTAVYICARETKV-----VHYGMDVWGQ 120
Qy 117 TTVTVSS 123
Db 118 TTVTVSS 123
```

```
Db      121 TTVTVSS 127

RESULT 9
US-10-041-860-243
; Sequence 325, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 243
; LENGTH: 127
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-243

Query Match      88.2%; Score 576; DB 14; Length 127;
Best Local Similarity 87.4%; Pred. No. 2.5e-47;
Matches 111; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY      1 QVQLVQSGAEVKKPGASVKVCKASGYTFYSGFSGWVRQAPGQGLEWLGWISAYNGNTNY 60
Db      1 QVQLVQSGAEVKKPGASVKVCKASGYTFYSGFSGWVRQAPGQGLEWLGWISAYNGNTNY 60

QY      61 AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRG----VHYIGMDVWGQ 116
Db      61 AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRG----VHYIGMDVWGQ 116

QY      117 TTVTVSS 123
Db      121 TTVTVSS 127

RESULT 10
US-10-041-860-325
; Sequence 325, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 127
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-325

Query Match      88.2%; Score 576; DB 14; Length 127;
Best Local Similarity 87.4%; Pred. No. 2.5e-47;
Matches 111; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY      1 QVQLVQSGAEVKKPGASVKVCKASGYTFYSGFSGWVRQAPGQGLEWLGWISAYNGNTNY 60
Db      1 QVQLVQSGAEVKKPGASVKVCKASGYTFYSGFSGWVRQAPGQGLEWLGWISAYNGNTNY 60

QY      61 AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRG----VHYIGMDVWGQ 116
Db      61 AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRG----VHYIGMDVWGQ 116

QY      117 TTVTVSS 123
Db      121 TTVTVSS 127

RESULT 11
US-10-665-383-42
; Sequence 42, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRochele, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 127
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-42

Query Match      88.2%; Score 576; DB 16; Length 127;
Best Local Similarity 87.4%; Pred. No. 2.5e-47;
Matches 111; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY      1 QVQLVQSGAEVKKPGASVKVCKASGYTFYSGFSGWVRQAPGQGLEWLGWISAYNGNTNY 60
Db      1 QVQLVQSGAEVKKPGASVKVCKASGYTFYSGFSGWVRQAPGQGLEWLGWISAYNGNTNY 60

QY      61 AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRG----VHYIGMDVWGQ 116
Db      61 AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRG----VHYIGMDVWGQ 116

QY      117 TTVTVSS 123
Db      121 TTVTVSS 127

RESULT 12
US-11-031-485-42
; Sequence 42, Application US/11031485
; Publication No. US20050232917A1
; GENERAL INFORMATION:
; APPLICANT: PULLEN, NICHOLAS
; APPLICANT: MOLLOY, ELIZABETH
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: GREEN, LARRY L.
; APPLICANT: HAAS-FRENDSCHO, MARY
; TITLE OF INVENTION: ANTIBODIES TO MAGCAM
; FILE REFERENCE: ABX-PF6
; CURRENT APPLICATION NUMBER: US/11/031,485
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 60/535,490
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Db 61 AQLQGRVTMTTDTSTAYMELRSLRSDDTAVYICARDVEYYDGSYYFFDYWGQGTl 120

Qy 119 VTVSS 123

|||

Db 121 VTVSS 125

Search completed: November 9, 2005, 12:43:01  
Job time : 69.3333 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: . November 9, 2005, 12:25:58 ; Search time 13.2556 Seconds  
(without alignments)  
892.802 Million cell updates/sec

Title: US-10-660-357A-21  
Perfect score: 653  
Sequence: 1 QVOLVSGAEVKKPGASVKV.....GVHYGMDVWGQTTVTVSS 123  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	559	85.6	129	2 S36260	Ig heavy chain V r
2	549.5	84.2	124	2 S19665	Ig heavy chain V r
3	533	81.6	122	2 S36271	Ig heavy chain V r
4	521	79.8	160	2 PLO105	anti-PR2 erythrocy
5	501	76.7	98	2 S26919	Ig heavy chain V r
6	486.5	74.5	118	2 PH1666	Ig heavy chain V r
7	483	74.0	127	2 S34014	Ig heavy chain V r
8	481	73.7	129	2 S46393	Ig heavy chain V r
9	480	73.5	119	2 PH0961	Ig heavy chain V r
10	477	73.0	131	2 S21924	Ig heavy chain V r
11	477	73.0	133	2 C33548	Ig heavy chain V-1
12	477	73.0	627	2 S14683	Ig mu chain precu
13	475.5	72.8	136	2 PH0960	Ig heavy chain V r
14	474.5	72.7	132	2 PH0954	Ig heavy chain V r
15	474	72.6	125	2 S68170	Ig heavy chain V r
16	473	72.4	142	2 A32483	Ig heavy chain V r
17	472.5	72.4	135	2 B32274	Ig heavy chain pre
18	471	72.1	127	2 PH0955	Ig heavy chain V r
19	469.5	71.9	135	2 S49530	anti-Sm antibody V
20	468.5	71.7	118	2 S36265	Ig heavy chain V r
21	468.5	71.7	126	2 B33548	Ig heavy chain V-1
22	465	71.2	111	2 S21925	Ig heavy chain V r
23	464	71.1	123	2 D33548	Ig heavy chain V-1
24	461.5	70.7	122	2 PH0958	Ig heavy chain V r
25	461.5	70.7	136	2 S31600	Ig heavy chain V r
26	453.5	69.4	114	2 PH1667	Ig heavy chain V r
27	452.5	69.3	132	2 S46394	Ig heavy chain V r
28	451	69.1	131	2 S26792	Ig heavy chain V r
29	449.5	68.8	120	2 S31999	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S36260  
Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999  
C;Accession: S36260  
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J  
EMBO J. 12, 725-734, 1993  
A;Title: Human anti-self antibodies with high specificity from phage display libraries.  
A;Reference number: S36256; MUID:93178448; PMID:7679990  
A;Accession: S36260  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-129 <GRI>  
A;Cross-references: EMBL:Z18851; NID:g33124; PIDN:CAA79303.1; PID:g939903  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMW>

Query Match 85.6%; Score 559; DB 2; Length 129;  
Best Local Similarity 84.5%; Pred. No. 1.le-44;  
Matches 109; Conservative 5; Mismatches 9; Indels 6; Gaps 1;

Qy	1	QVOLVSGAEVKKPGASVKSCASGYTFPSYGFSVVRQAPGGGLEWLGWISAYNGNTNY	60
Db	1	QVOLQSGAEVKKPGASVKSCASGYTFPSYGFISVVRQAPGGGLEWLGWISAYNGNTNY	60
Qy	61	AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVVYICARE-----TKVRGVHYGYMDVWG	114
Db	61	AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVVYICARDSFGYCSSTSCPFYIYMDVWG	120
Qy	115	QGTFTVTSS 123	
Db	121	KGTTVTSS 129	

RESULT 2

S19665  
Ig heavy chain V region (alpha-phOx15) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 20-Jun-2000  
C;Accession: S19665; S24442  
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter  
J. Mol. Biol. 222, 581-597, 1991  
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on p  
A;Reference number: S19663; MUID:92085276; PMID:1748994  
A;Accession: S19665  
A;Molecule type: mRNA  
A;Residues: 1-124 <MAR>  
R;Jones, P.T.  
submitted to the EMBL Data Library, October 1991

```
A;Reference number: S24442
A;Accession: S24442
A;Molecule type: mRNA
A;Residues: 1-40,'GUSGWDGSAALMTVQSIIDK',61-118,'T',120-124 <JON>
A;Cross-references: EMBL:X61647; NID:g37667; PIDN:CAA43828.1; PID:g1335368
A;Note: the difference for residues 41-60 results from misplacement of 10 bases in the s
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match      84.2%; Score 549.5; DB 2; Length 124;
Best Local Similarity 85.6%; Pred. No. 8.1e-44;
Matches 107; Conservative 5; Mismatches 10; Indels 3; Gaps 2;

QY 1 QVQLVSGAEVKKPKGASVKVSKASGYTFPSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60
Db 1 QVQLVSGAEVKKPKGASVKVSKASGYTFPSYGFSWVRQAPGQGLEWLGWISAYNGNTKY 60

QY 61 AOKLQGRVTMTTDTSTSTAYMELRSDDTAVYYCAR--ETKVRGVHYHYGMDVWGQGIT 118
Db 61 AOKLQGRVTMTTDTSTSTAYMELRSDDTAVYYCYVRLLPKRATLHY--IDVWGKGTL 119

QY 119 VTVSS 123
Db 120 VTVSS 124

RESULT 3
S36271
IG heavy chain V region (clone alpha-THV-29) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36271
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36271
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-122 <GRI>
A;Cross-references: EMBL:Z18832; NID:g33115; PIDN:CAA79284.1; PID:g939895
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match      81.6%; Score 533; DB 2; Length 122;
Best Local Similarity 85.2%; Pred. No. 2.7e-42;
Matches 104; Conservative 3; Mismatches 13; Indels 2; Gaps 1;

QY 1 QVQLVSGAEVKKPKGASVKVSKASGYTFPSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60
Db 1 QVQLVSGAEVKKPKGASVKVSKASGYTFPSYGFSWVRQAPGQGLEWLGWISAYNGNTY 60

QY 61 AOKLQGRVTMTTDTSTSTAYMELRSDDTAVYYCARETKVRGVHY--YGMVDVWGQGIT 118
Db 61 AOKLQGRVTMTTDTSTSTAYMELRSDDTAVYYCAADTGRIDDFWGSYFNFDVWGQGL 120

QY 119 VT 120
Db 121 VT 122

RESULT 4
PL0105
anti-PR2 erythrocyte autoantibody heavy chain precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 26-Apr-1996
C;Accession: PL0105
R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A;Title: Relationship of variable region genes expressed by a human B cell lymphoma secd
A;Reference number: PL0106; MUID:89235583; PMID:2541221
```

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A;Accession: PL0105
A;Molecule type: mRNA
A;Residues: 1-160 <SIL>
A;Note: the authors translated the codon GAC for residues 108 and 109 as Glu
C;Comment: The antibody is one of the cold agglutinins that preferentially bind red blo
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: autoantibody; hemagglutinin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;34-117/Domain: immunoglobulin homology <IMM>
F;49-54/Region: complementarity-determining 1
F;69-84/Region: complementarity-determining 2
F;118-131/Domain: D region <DRG>
F;132-144/Domain: J4 segment <JSG>
F;145-160/Domain: C region <CRG>

Query Match      79.8%; Score 521; DB 2; Length 160;
Best Local Similarity 82.4%; Pred. No. 4.6e-41;
Matches 103; Conservative 3; Mismatches 17; Indels 2; Gaps 1;

QY 1 QVQLVSGAEVKKPKGASVKVSKASGYTFPSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60
Db 20 QVQLVASGAENVKPKGASVKVSKASGYTFPSYGFSWVRQAPGQGLEWGMGWSYNGDTNY 79

QY 61 AOKLQGRVTMTTDTSTSTAYMELRSDDTAVYYCARETKV--RGVHYHYGMDVWGQGIT 118
Db 80 AOKLQGRVTMTTDTSTSTAYMELNRSDDTAVYYCARAPGYCSGGCGYRGDDYWGQGL 139

QY 119 VTVSS 123
Db 140 VTVSS 144

RESULT 5
S26919
IG heavy chain V region (DP-14) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26919
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26919
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12316; NID:g32855; PIDN:CAA78186.1; PID:g32856
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match      76.7%; Score 501; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.9e-39;
Matches 95; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKPKGASVKVSKASGYTFPSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60
Db 1 QVQLVSGAEVKKPKGASVKVSKASGYTFPSYGFSWVRQAPGQGLEWGMGWSYNGNTNY 60

QY 61 AOKLQGRVTMTTDTSTSTAYMELRSDDTAVYYCAR 98
Db 61 AOKLQGRVTMTTDTSTSTAYMELNRSDDTAVYYCAR 98

RESULT 6
PH1666
IG heavy chain V region (clone 6C9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1666
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyl.
```

A;Reference number: PH1642; MUID:93301610; PMID:8315388  
A;Accession: PH1666  
A;Molecule type: mRNA  
A;Residues: 1-118 <HIL>  
A;Experimental source: B cell  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 74.5%; Score 486.5; DB 2; Length 118;  
Best Local Similarity 79.7%; Pred. No. 5e-38;  
Matches 94; Conservative 6; Mismatches 15; Indels 3; Gaps 1;

Qy 9 AEVKKPGASVKSCASGYTFPSYFSGSWVRQAPGQGLEWLGWISAYNGNTNYAQKQGRV 68  
Db 1 AEVKKPGASVKSCASGYTFPSYFSGSWVRQAPGQGLEWLGWISAYNGNTNYAQKQGRV 60

Qy 69 TWITDSTSTAYMELSLRSDDTAVYVCARETKVRGV---HYGMDVWGQTTVTVSS 123  
Db 61 TITRDTASTAYMELSLRSDDTAVYVCARETKVRGV---HYGMDVWGQTTVTVSS 118

## RESULT 7

S34014  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C;Accession: S34014; S30535  
R;Mariette, X.; Tsapis, A.; Brouet, J.C.  
Eur. J. Immunol. 23, 846-851, 1993  
A;Title: Nucleotide sequence analysis of the variable domains of four human monoclonal  
A;Reference number: S34001; MUID:9320281; PMID:7681398  
A;Accession: S34014  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-127 <MAR>  
A;Cross-references: EMBL:Z18321  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 483; DB 2; Length 127;  
Best Local Similarity 72.7%; Pred. No. 1.1e-37;  
Matches 93; Conservative 14; Mismatches 15; Indels 6; Gaps 2;

Qy 1 QVOLVSGAEVKKPGASVKSCASGYTFPSYFSGSWVRQAPGQGLEWLGWISAYNGNTNY 60  
Db 1 QVOLVSGAEVKKPGASVKSCASGYTFPSYFSGSWVRQAPGQGLEWLGWISAYNGNTNY 60

Qy 61 AQKQGRVTMTTDTSTAYMELSLRSDDTAVYVCARETK-----VRGVHYGMDVWGQ 115  
Db 61 AQKQGRVTMTTDTSTAYMELSLRSDDTAVYVCARETK-----VRGVHYGMDVWGQ 119

Qy 116 GTTTVTSS 123  
Db 120 GTTTVS 127

## RESULT 8

S46393  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000  
C;Accession: S46393  
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.  
J. Mol. Biol. 239, 68-78, 1994  
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by  
A;Reference number: S46390; MUID:94254092; PMID:8196048  
A;Accession: S46393  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-129 <FIG>  
A;Cross-references: EMBL:Z31680; NID:g509786; PIDN:CAA83485.1; PID:g1335146

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.7%; Score 481; DB 2; Length 129;  
Best Local Similarity 72.2%; Pred. No. 1.8e-37;  
Matches 96; Conservative 7; Mismatches 16; Indels 14; Gaps 2;

Qy 1 QVOLVSGAEVKKPGASVKSCASGYTFPSYFSGSWVRQAPGQGLEWLGWISAYNGNTNY 60  
Db 1 QVOLVSGAEVKKPGASVKSCASGYTFPSYFSGSWVRQAPGQGLEWLGWISAYNGNTNY 60

Qy 61 AQKQGRVTMTTDTSTAYMELSLRSDDTAVYVCARETKVRGVHYG-----M 110  
Db 61 AQKQGRVTMTTDTSTAYMELSLRSDDTAVYVCARETKVRGVHYG-----M 116

Qy 111 DVWGQTTVTSS 123  
Db 117 DVWGQTTVTSS 129

## RESULT 9

PH0961  
Ig heavy chain V region (G6+ T-L33) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
C;Accession: PH0961  
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A;Title: Evidence for somatic selection of natural autoantibodies.  
A;Reference number: PH0952; MUID:9220280; PMID:1552291  
A;Accession: PH0961  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-119 <MAR>

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-30/Region: framework 1  
F;15-98/Domain: immunoglobulin homology <IMM>  
F;31-35/Region: complementarity-determining 1  
F;36-50/Region: framework 2  
F;51-67/Region: complementarity-determining 2  
F;68-98/Region: framework 3  
F;99-107/Region: complementarity-determining 3

Query Match 73.5%; Score 480; DB 2; Length 119;  
Best Local Similarity 78.0%; Pred. No. 2e-37;  
Matches 96; Conservative 5; Mismatches 18; Indels 4; Gaps 1;

Qy 1 QVOLVSGAEVKKPGASVKSCASGYTFPSYFSGSWVRQAPGQGLEWLGWISAYNGNTNY 60  
Db 1 QVOLVSGAEVKKPGASVKSCASGYTFPSYFSGSWVRQAPGQGLEWLGWISAYNGNTNY 60

Qy 61 AQKQGRVTMTTDTSTAYMELSLRSDDTAVYVCARETKVRGVHYGMDVWGQTTVT 120  
Db 61 AQKQGRVTMTTDTSTAYMELSLRSDDTAVYVCARETKVRGVHYGMDVWGQTTVT 116

Qy 121 VSS 123  
Db 117 VSS 119

## RESULT 10

S21924  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C;Accession: S21924; S21923  
R;Friedman, D.F.  
submitted to the EMBL Data Library, July 1991  
A;Reference number: S21923  
A;Accession: S21924  
A;Status: preliminary

A;Molecule type: DNA  
A;Residues: 1-131 <PRI>  
A;Cross-references: EMBL:X60505; NID:g33565; PIDN:CAA43025.1; PID:g33566; EMBL:X60504; N  
C;Genetics:  
A;Introns: 16/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>  
  
Query Match 73.0%; Score 477; DB 2; Length 131;  
Best Local Similarity 91.8%; Pred. No. 4.2e-37;  
Matches 90; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 QVOLVSGAEVKKPGASVKVCKASGYTFSSYGFSGFVSVRQAPGGLEWLGWISAYNGNTNY 60  
DB 20 QVOLVSGAEVKKPGASVKVCKASGYTFSSYGFSGFVSVRQAPGGLEWLGWISAYNGNTNY 79  
  
QY 61 AOKLQGRVTMTTDTSTAYMELSLRSDDTAVYCAR 98  
DB 80 AOKLQGRVTMTTDTSTAYMELSLRSDDTAVYCAR 117  
  
RESULT 11  
C33548  
Ig heavy chain V-1 region (783) - human  
C;Species: Homo sapiens (man)  
C;Date: 17-Jan-1990 #sequence\_revision 17-Jan-1990 #text\_change 16-Aug-1996  
C;Accession: C33548  
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.  
Proc. Natl. Acad. Sci. U.S.A. 86: 5913-5917, 1989  
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr  
A;Reference number: A33548; MUID:89345575; PMID:2503826  
A;Accession: C33548  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A;Molecule type: DNA  
A;Residues: 1-133 <KIP>  
A;Experimental source: the sequence was determined from the differentiated gene  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>  
  
Query Match 73.0%; Score 477; DB 2; Length 133;  
Best Local Similarity 72.4%; Pred. No. 4.3e-37;  
Matches 97; Conservative 7; Mismatches 18; Indels 12; Gaps 2;  
  
QY 1 QVOLVSGAEVKKPGASVKVCKASGYTFSSYGFSGFVSVRQAPGGLEWLGWISAYNGNTNY 60  
DB 1 QVOLVSGAEVKKPGASVKVCKASGYTFSSYGFSGFVSVRQAPGGLEWLGWISAYNGNTNY 60  
  
QY 61 AOKLQGRVTMTTDTSTAYMELSLRSDDTAVYCAR 109  
DB 61 AOKLQGRVTMTTDTSTAYMELSLRSDDTAVYCAR 119  
  
QY 110 MDVWGQGTITVTVSS 123  
DB 120 MDVWGQGTITVTVSS 133  
  
RESULT 12  
S14683  
Ig mu chain precursor, membrane-bound (clone 201) - human  
C;Species: Homo sapiens (man)  
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 23-Jul-1999  
C;Accession: S14683; S08047  
R;Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.  
Nucleic Acids Res. 18, 4278, 1990  
A;Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.  
A;Reference number: S14683; MUID:90332450; PMID:2115996  
A;Accession: S14683  
A;Molecule type: mRNA  
A;Residues: 1-627 <PRI>  
A;Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451  
C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin; membrane protein  
F;1-15/Domain: signal sequence #status predicted <SIG>  
F;16-627/Product: Ig mu chain #status predicted <MAT>  
F;34-117/Domain: immunoglobulin homology <IMM>  
  
Query Match 73.0%; Score 477; DB 2; Length 627;  
Best Local Similarity 72.4%; Pred. No. 2.2e-36;  
Matches 97; Conservative 7; Mismatches 18; Indels 12; Gaps 2;  
  
QY 1 QVOLVSGAEVKKPGASVKVCKASGYTFSSYGFSGFVSVRQAPGGLEWLGWISAYNGNTNY 60  
DB 20 QVOLVSGAEVKKPGASVKVCKASGYTFSSYGFSGFVSVRQAPGGLEWLGWISAYNGNTNY 79  
  
QY 61 AOKLQGRVTMTTDTSTAYMELSLRSDDTAVYCAR 109  
DB 80 AOKLQGRVTMTTDTSTAYMELSLRSDDTAVYCAR 138  
  
QY 110 MDVWGQGTITVTVSS 123  
DB 139 MDVWGQGTITVTVSS 152  
  
RESULT 13  
PH0960  
Ig heavy chain V region (G6+ T-L30) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
C;Accession: PH0960  
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A;Title: Evidence for somatic selection of natural autoantibodies.  
A;Reference number: PH0952; MUID:92202880; PMID:1552291  
A;Accession: PH0960  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-136 <MAR>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;1-30/Region: framework 1  
F;15-98/Domain: immunoglobulin homology <IMM>  
F;31-35/Region: complementarity-determining 1  
F;36-50/Region: framework 2  
F;51-67/Region: complementarity-determining 2  
F;68-98/Region: framework 3  
F;99-124/Region: complementarity-determining 3  
  
Query Match 72.8%; Score 475.5; DB 2; Length 136;  
Best Local Similarity 72.8%; Pred. No. 6e-37;  
Matches 99; Conservative 6; Mismatches 18; Indels 13; Gaps 3;  
  
QY 1 QVOLVSGAEVKKPGASVKVCKASGYTFSSYGFSGFVSVRQAPGGLEWLGWISAYNGNTNY 60  
DB 1 QVOLVSGAEVKKPGASVKVCKASGYTFSSYGFSGFVSVRQAPGGLEWLGWISAYNGNTNY 60  
  
QY 61 AOKLQGRVTMTTDTSTAYMELSLRSDDTAVYCAR 107  
DB 61 AOKLQGRVTMTTDTSTAYMELSLRSDDTAVYCAR 120  
  
QY 108 YGMDVWGQGTITVTVSS 123  
DB 121 YGMDVWGQGTITVTVSS 136  
  
RESULT 14  
PH0954  
Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
C;Accession: PH0954  
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A;Title: Evidence for somatic selection of natural autoantibodies.  
A;Reference number: PH0952; MUID:92202880; PMID:1552291



THIS PAGE (1450) XRAY 10 1974 SHL



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:46:52 ; Search time 63.5038 Seconds  
(without alignments)  
991.843 Million cell updates/sec

Title: US-10-660-357A-21

Perfect score: 653

Sequence: 1 QVQLVSGAEVKKPGASVKV.....GVHYGMDVWGQGTITVSS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501	76.7	500	Q6N091	Q6N091 homo sapien
2	490.5	75.1	159	Q96Q50	Q96Q50 homo sapien
3	474	72.6	244	Q65ZC8	Q65ZC8 homo sapien
4	472.5	72.4	500	Q2BRV0	Q2BRV0 homo sapien
5	469.5	71.9	469	Q2Z7P5	Q2Z7P5 homo sapien
6	464	71.1	125	Q9UL95	Q9UL95 homo sapien
7	453	69.4	119	Q9UL94	Q9UL94 homo sapien
8	450.5	69.0	124	Q9UL92	Q9UL92 homo sapien
9	449.5	68.8	147	HVIC HUMAN	P01744 homo sapien
10	440.5	67.5	518	Q6N030	Q6N030 homo sapien
11	438.5	67.2	498	Q6N041	Q6N041 homo sapien
12	436	66.8	119	Q9GY22	Q9GY22 schistosoma
13	419.5	64.2	116	Q9UL89	Q9UL89 homo sapien
14	417	63.9	480	Q6P089	Q6P089 homo sapien
15	416	63.9	480	Q6PJF1	Q6PJF1 homo sapien
16	416	63.7	497	Q8WY24	Q8WY24 homo sapien
17	415	63.6	117	HVIC HUMAN	P01743 homo sapien
18	412	63.1	208	Q6ZP87	Q6ZP87 homo sapien
19	409.5	62.7	465	Q6PJB2	Q6PJB2 mus musculus
20	409	62.6	120	HV03 MOUSE	P01747 mus musculus
21	408	62.5	140	HV02 MOUSE	P01746 mus musculus
22	406.5	62.3	143	Q924F9	Q924F9 mus musculus
23	405	62.0	120	Q6NSA4	Q6NSA4 homo sapien
24	404	61.9	117	HVIC HUMAN	P23083 homo sapien
25	403.5	61.8	145	Q924O6	Q924O6 mus musculus
26	402.5	61.6	475	Q6N095	Q6N095 homo sapien
27	398.5	61.0	613	Q8VCX7	Q8VCX7 mus musculus
28	396	60.6	117	Q9QXE9	Q9QXE9 mus musculus
29	396	60.6	142	Q924Q1	Q924Q1 mus musculus
30	393.5	60.3	241	Q921A6	Q921A6 mus musculus
31	391	59.9	134	Q652R6	Q652R6 mus musculus

32	390.5	59.8	145	2	Q924R1	Q924R1 mus musculus
33	390.5	59.8	463	2	Q99LC4	Q99LC4 mus musculus
34	389.5	59.6	145	2	Q924Q9	Q924Q9 mus musculus
35	389	59.6	142	2	Q924Q2	Q924Q2 mus musculus
36	389	59.6	147	2	Q925S3	Q925S3 mus musculus
37	389	59.6	150	2	Q9Y298	Q9Y298 homo sapien
38	388.5	59.5	109	2	Q9JL75	Q9JL75 mus musculus
39	387.5	59.3	145	2	Q924P7	Q924P7 mus musculus
40	387	59.3	470	2	Q7TMK1	Q7TMK1 mus musculus
41	387	59.3	481	2	Q91WT1	Q91WT1 mus musculus
42	386	59.1	117	1	HV13 MOUSE	P01757 mus musculus
43	386	59.1	170	2	Q925S2	Q925S2 mus musculus
44	385.5	59.0	118	1	HV51 MOUSE	P06330 mus musculus
45	384.5	58.9	118	2	Q9Z1C4	Q9Z1C4 mus musculus

ALIGNMENTS

RESULT 1

Q6N091 PRELIMINARY; PRT; 500 AA.  
AC Q6N091;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFp686C02220 (Fragment).  
GN Name=DKFp686C02220;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RG The German Human cDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640625; CAB45779.1; -  
DR HSSP; P01751; 1A6W.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 2.  
DR SMART; SM00409; IG; 4.  
DR SMART; SM00407; IGc1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 500 AA; 54160 MW; 3C423A17D65A41E4 CRC64;

Query Match 76.7%; Score 501; DB 2; Length 500;  
Best Local Similarity 77.2%; Pred. No. 5.6e-45;  
Matches 95; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

Qy 1 QVQLVSGAEVKKPGASVKVSKASGYTFPSYGVFVSRQAPGQGLEWIGWISAYNGNTNY 60

Db 38 QVQLVSGAEVKKPGASVKVSKASGYTFSDHITWLRQAPGQGLEWIGWISAYSGQTY 97

Qy 61 AQKLQGRVTMTDTSTSTAYMELRSDDTAVYVCARETKVRGVHYGMDVWGQGTFTV 120

Db 98 AQNLQGRVTMTDTSTSTAYMELRSDDTAVYVCARDQSYTTIPNDAPHINGQGTMT 157

Qy 121 VSS 123

Db 158 VSS 160

```
RESULT 2
Q96QSO PRELIMINARY; PRT; 159 AA.
ID Q96QSO
AC Q96QSO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative matrix cell adhesion molecule-3.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tilson M.D.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; AY039025; AAK82649.1; -.
DR HSSP; P01869; IAE6.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537B881FAF02 CRC64;

Query Match 75.1%; Score 490.5; DB 2; Length 159;
Best Local Similarity 72.3%; Pred. No. 2.1e-44;
Matches 94; Conservative 13; Mismatches 16; Indels 7; Gaps 1;

QY 1 QVQLVSGAEVKKPGASVKSCASGYTFSPYSGFVSRVQAPGQGLEWLGWISAYNGTNY 60
DB 20 QVQLVSGAEVKKPGASVKSCASGYTFSPYSGFVSRVQAPGQPEWVGINSGSARY 79
QY 61 AQKLQGRVTMTDTSTSTAYMELRSDDTAVVYCARETKV-----RGVHYGMDVW 113
DB 80 SQKFGRLTMTDRTSTSTVYMDLSRLSDDTAVVFCAREMEITFGGAVSKGFFYYGMDVW 139
QY 114 GQGTVTVTSS 123
DB 140 GQGTVTVTSS 149

RESULT 3
Q65ZC8 PRELIMINARY; PRT; 244 AA.
ID Q65ZC8
AC Q65ZC8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR ENBL; Y13057; CAA73500.1; -.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
FT NON_TER 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match 72.6%; Score 474; DB 2; Length 244;
Best Local Similarity 71.1%; Pred. No. 6.3e-42;
Matches 91; Conservative 10; Mismatches 22; Indels 5; Gaps 1;
```

```
Best Local Similarity 75.6%; Pred. No. 2e-42;
Matches 93; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

QY 1 QVQLVSGAEVKKPGASVKSCASGYTFSPYSGFVSRVQAPGQGLEWLGWISAYNGTNY 60
DB 1 QVQLVSGAEVKKPGASVKSCASGYTFSDHYMHVVRQAPGQGLEWMDPNNGDTRF 60
QY 61 AQKLQGRVTMTDTSTSTAYMELRSDDTAVVYCARETKVGRVHYGMDVWGQGTVT 120
DB 61 AQRFQGRVTMTDRTSTISAAAYMEVSRLSDDTAVVYCAREG--TGSAIYGMVWGQGLT 118
QY 121 VSS 123
DB 119 VSS 121

RESULT 4
Q9BRV0 PRELIMINARY; PRT; 500 AA.
ID Q9BRV0
AC Q9BRV0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC27165 protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleto M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC005951; AA05951.1; -.
DR HSSP; P01876; IOWO.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 72.4%; Score 472.5; DB 2; Length 500;
Best Local Similarity 71.1%; Pred. No. 6.3e-42;
Matches 91; Conservative 10; Mismatches 22; Indels 5; Gaps 1;
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QY 1 QVOLVSGAEVKKPGASVKVSKASGYTFYFGFSGVSRVQAPGQGLEWIGWISAYNGNTNY 60
|||
D 20 QVHLVSGAEVMSFGASVRVSKTSGYAFHYYSIIWVRQAPGQGLEWNGWISPSDDTRF 79
|||
QY 61 AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCAR-----ETKVRGVHYYGMDVWGQ 115
|||
D 80 AKFPQGRVTLTDTSTSTVYVMEVSLRSDDTAVYYCARRYSYSSQNDYVYVMDVWGK 139
|||
QY 116 GTTVTVSS 123
|||
D 140 GTTVTVSS 147
|||

RESULT 5
Q727P5 PRELIMINARY; PRT; 469 AA.
AC Q727P5
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGH1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL SUBMITTED (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -.
DR HSSP; P01857; 1HZH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IG_LIKE; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;

Query Match 71.9%; Score 469.5; DB 2; Length 469;
Best Local Similarity 74.88; Pred. No. 1.2e-41;
Matches 92; Conservative 9; Mismatches 19; Indels 3; Gaps 2;

QY 1 QVOLVSGAEVKKPGASVKVSKASGYTFYFGFSGVSRVQAPGQGLEWIGWISAYNGNTNY 60
|||
D 20 QVHLVSGAEVMSFGASVRVSKTSGYAFHYYSIIWVRQAPGQGLEWNGWISPSDDTRF 79
|||
QY 61 AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCAR-----ETKVRGVHYYGMDVWGQ 115
|||
D 80 AKFPQGRVTLTDTSTSTVYVMEVSLRSDDTAVYYCARRYSYSSQNDYVYVMDVWGK 139
|||
QY 116 GTTVTVSS 123
|||
D 140 GTTVTVSS 147
|||

RESULT 6
Q9UL95 PRELIMINARY; PRT; 125 AA.
AC Q9UL95
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035019; AAD56255.1; -.
DR HSSP; P01751; INQB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER 125
FT NON_TER 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 71.1%; Score 464; DB 2; Length 125;
Best Local Similarity 72.8%; Pred. No. 1.1e-41;
Matches 91; Conservative 9; Mismatches 23; Indels 2; Gaps 1;

QY 1 QVOLVSGAEVKKPGASVKVSKASGYTFYFGFSGVSRVQAPGQGLEWIGWISAYNGNTNY 60
|||
D 1 EVLVESGAEVKKPGASVKVSKASGYTFYFGFSGVSRVQAPGQGLEWNGWISPSGNTY 60
|||
QY 61 AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRGVHYYGMDVWGQTT 118
|||
D 61 AQKVGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRGVHYYGMDVWGQTT 120
|||
QY 119 VTVSS 123
|||
D 121 VTVSS 125
|||

RESULT 7
Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetuses";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR ENBL; AF03020; AAD56256.1; -;  
DR HSSP; P01751; INQB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
FT NON\_TER 1 119  
FT NON\_TER 124 124  
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match 69.4%; Score 453; DB 2; Length 119;  
Best Local Similarity 74.0%; Pred. No. 1.6e-40; Indels 4; Gaps 2;  
Matches 91; Conservative 8; Mismatches 20; Indels 4; Gaps 2;

QY 1 QVQLVSGAEVKKPGASVKVSCKASGYTFSSYGFSSVRQAPGQGLEWLGWISAYNGNTNY 60  
Db 1 EVQLVESGAEVKKPGASVKVSCKASGYTFGYTHVVRQAPGQGLEWMGWINPNSWTNY 60

QY 61 AQKLGQRTVMTTDTSTSTAYMELSLRSDTAVYVCARETKVRGVH-----YGMVDVWG 114  
Db 61 AQKFGQRTVMTTDTSTSTAYMELSLRSDTAVYVCARETKVRGVH-----YGMVDVWG 115

QY 121 VSS 123  
Db 117 VSS 119

RESULT 8  
Q9UL92 PRELIMINARY; PRT; 124 AA.  
AC Q9UL92;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
(Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetuses";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR ENBL; AF03020; AAD56256.1; -;  
DR HSSP; P01751; INQB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
FT NON\_TER 1 124  
FT NON\_TER 124 124  
SQ SEQUENCE 124 AA; 13580 MW; 1BAACB9D6ACD2A2 CRC64;

Query Match 69.0%; Score 450.5; DB 2; Length 124;  
Best Local Similarity 70.5%; Pred. No. 3.1e-40; Indels 11; Gaps 2;  
Matches 91; Conservative 10; Mismatches 17; Indels 11; Gaps 2;

QY 1 QVQLVSGAEVKKPGASVKVSCKASGYTFSSYGFSSVRQAPGQGLEWLGWISAYNGNTNY 60  
Db 1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYGMHVRQAPGQGLEWMGINPNSGGTSY 60

QY 61 AQKLGQRTVMTTDTSTSTAYMELSLRSDTAVYVCARETKVRGVH-----YGMVDVWG 114  
Db 61 AQKFGQRTVMTTDTSTSTAYMELSLRSDTAVYVCARETKVRGVH-----YGMVDVWG 115

QY 115 QGTTVTVSS 123  
Db 116 QGTLVTVSS 124

RESULT 9  
HV1C HUMAN STANDARD; PRT; 147 AA.  
ID HV1C HUMAN  
AC P01744;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig heavy chain V-I region ND precursor (Fragments).  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83065234; PubMed=6815656;  
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,  
Bell L.O., Gould H.J.;  
RT "Cloning and sequence determination of the gene for the human  
immunoglobulin epsilon chain expressed in a myeloma cell line.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).  
RN [2]  
RP SEQUENCE OF 20-147.  
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;  
RL (in) Bach M.K. (eds.);  
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,  
Marcel Dekker, New York (1978).  
CC -I- MISCELLANEOUS: This epsilon chain was isolated from a myeloma  
protein.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR HSSP; P01751; INQB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin V region;  
KW Pyrrolidone carboxylic acid; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 147 Ig heavy chain V-I region ND.  
FT DOMAIN 20 131 Ig-like.  
FT MOD\_RES 20 20 Pyrrolidone carboxylic acid.  
FT DISULFID 41 115  
FT CONFLICT 21 21 T -> V (in Ref. 2).  
FT CONFLICT 53 54 IH -> HI (in Ref. 2).  
FT CONFLICT 67 68 GV -> GV (in Ref. 2).  
FT CONFLICT 125 125 Missing (in Ref. 2).  
FT NON\_TER 147 147  
SQ SEQUENCE 147 AA; 16491 MW; 948P9F72A5366C20 CRC64;

Query Match 68.8%; Score 449.5; DB 1; Length 147;  
Best Local Similarity 67.2%; Pred. No. 4.8e-40;  
Matches 86; Conservative 13; Mismatches 24; Indels 5; Gaps 1;

QY 1 QVQLVSGAEVKKPGASVKVSCKASGYTFSSYGFSSVRQAPGQGLEWLGWISAYNGNTNY 60  
Db 20 QQLVSGAEVKKPGASVKVSCKASGYTFIDSVIHWIRQAPGQGLEWGINPNSGNTNY 79

QY 61 AQKLGQRTVMTTDTSTSTAYMELSLRSDTAVYVCARETKVRGVH-----YGMVDVWG 115  
Db 80 APRFGQRTVMTDASPTAYMDLRLSRSDSAVFYCAKSPDPSYDFSYTLVDVWG 139

QY 116 GTTIVTSS 123

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Db      140 GTTIVTSS 147
|||||
RESULT 10
Q6N030 PRELIMINARY; PRT; 518 AA.
ID Q6N030
AC Q6N030
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686l15212.
GN Name=DKFZp686l15212;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640724; CAE45841.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR000005; HTHAcC.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein_
FT NON_TER 1
SQ SEQUENCE 518 AA; 57019 MW; 93B5F98613BF6382 CRC64;

Query Match 67.5%; Score 440.5; DB 2; Length 518;
Best Local Similarity 69.9%; Pred. No. 1.8e-38;
Matches 86; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFYSGFVSWVRQAPGQGLEWIGWISAYNGNTNY 60
Db 20 QVHLVQSGAEVKKPGASVKVSCTASGYPFTNHFINWVRQAPGQGLEWGWINTGNGTKY 79
|||||
Qy 61 AQKLQGRVTMTDTSTAYMELSLRSDDTAVVYCARETKVRG--VHYYGMDVWGQTTVT 120
Db 80 SQKFGQGVITRTDTTWTTAYMDLSSLASEDTAVVYWCARDAP-QGVTTTYFDYWGQGLVT 138
|||||
Qy 121 VSS 123
Db 139 VSS 141
|||||

RESULT 11
Q6N041 PRELIMINARY; PRT; 498 AA.
ID Q6N041
AC Q6N041
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686O16217 (Fragment).
GN Name=DKFZp686O16217;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640724; CAE45841.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR000005; HTHAcC.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein_
FT NON_TER 1
SQ SEQUENCE 498 AA; 54125 MW; 40B3208A84E03B46 CRC64;

Query Match 67.2%; Score 438.5; DB 2; Length 498;
Best Local Similarity 70.4%; Pred. No. 2.8e-38;
Matches 88; Conservative 12; Mismatches 22; Indels 3; Gaps 2;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFYSGFVSWVRQAPGQGLEWIGWISAYNGNTNY 60
Db 35 QVQLVQSGADVKKPGASVKVSCKASGYTFNTFFHWVRQAPGQGPWGMINPRDGSSTKY 94
|||||
Qy 61 AQKLQGRVTMTDTSTAYMELSLRSDDTAVVYCARETKVRG--VHYYGMDVWGQTT 118
Db 95 AQRFGQGVSWTRDTSTSTIYMWLSSLASEDTAMFFCARAGPGYGTSSAY--FDYWGQGLT 153
|||||
Qy 119 VTVSS 123
Db 154 VTVSS 158
|||||

RESULT 12
Q9GYZ2 PRELIMINARY; PRT; 119 AA.
ID Q9GYZ2
AC Q9GYZ2
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoida; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RC Song X.T., Feng X.O., Guan X.H.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAG01452.1; -.
DR HSSP; P01751; IA6W.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FDSFA6AB CRC64;

Query Match 66.8%; Score 436; DB 2; Length 119;
Best Local Similarity 69.9%; Pred. No. 1.1e-38;
Matches 86; Conservative 12; Mismatches 21; Indels 4; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFYSGFVSWVRQAPGQGLEWIGWISAYNGNTNY 60
|||||

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Db      1 QVQLVSGAEVRKPGASVVRVCKASGYTFGGYYMWRQAPGCHLEWIGYINPSRGYTNV 60
QY      61 AQKLQGRVTMTDTSTSTAYMELSLRSDTAVYYCARETKVGRGVHYGMDVWGQGTVT 120
Db      61 NQKFKDRVTMTDTKSPSTAYMDLRLSLRSADSAVVYCARYYD----DHYCLDYGWQGTVT 116
QY      121 VSS 123
Db      117 VSS 119

RESULT 13
Q9UL89 PRELIMINARY; PRT; 116 AA.
AC Q9UL89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=982717139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Bernay S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035025; AAD56261.1; -.
DR PIR; PH0870; PH0870.
DR PIR; PH1671; PH1671.
DR HSP; P01751; INQB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

Query Match 64.2%; Score 419.5; DB 2; Length 116;
Best Local Similarity 72.3%; Pred. No. 6e-37;
Matches 86; Conservative 8; Mismatches 22; Indels 3; Gaps 2;

QY      5 VQSGAEVKKPGASVKVSKASGYTFSSYGFSGVSRQAPGQGLEWLGWISAYNGNTYAOKL 64
Db      1 VQSGAEVKKPGSSVKVSKASGGTFSSYAI-SVWRQAPGQGLEWGRIPILGIANYAQKF 60
QY      65 QGRVTMTDTSTSTAYMELSLRSDTAVYYCARETKVGRGVHYGMDVWGQGTVTVSS 123
Db      61 QGRVTITADKSTSTAYMELSLRSDTAVYYCASSN--WGPIWY-PDLWGRGLTVTVSS 116

RESULT 14
Q6P089 PRELIMINARY; PRT; 480 AA.
AC Q6P089;
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner F.S., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleck J., Schmutz J., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065733; AAH65733.1; -.
DR HSP; P01751; IA6W.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 51997 MW; 2E286C57E4F0ED65 CRC64;

Query Match 63.9%; Score 417; DB 2; Length 480;
Best Local Similarity 68.3%; Pred. No. 5.3e-36;
Matches 84; Conservative 9; Mismatches 28; Indels 2; Gaps 1;

QY      1 QVQLVSGAEVRKPGASVKVSKASGYTFSSYGFSGVSRQAPGQGLEWLGWISAYNGNTNY 60
Db      20 QVQLVSGAEVRKPGASVKVSKASGYSDNYIHWRQAPGQGLEWMAIRPQNGTVS 79
QY      61 AQKLQGRVTMTDTSTSTAYMELSLRSDTAVYYCARETKVGRGVHYGMDVWGQGTVT 120
Db      80 AEKFGQVRVTTIDTSLNTAYMELTSLKSDDTALYYCARGHSDWSSYF--DYWGQGLTVT 137
QY      121 VSS 123
Db      138 VSS 140

RESULT 15
Q6PJF1 PRELIMINARY; PRT; 480 AA.
AC Q6PJF1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;

```



(also) 11/17/19 11:11 AM



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:43:32 ; Search time 73.3684 Seconds  
(without alignments)  
627.306 Million cell updates/sec

Title: US-10-660-357A-25

Perfect score: 636

Sequence: 1 QVQLQESGPGVLRPSQTL...DRETAGFDYWGQGLTVTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 396760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_16Dec04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001s:\*

5: Geneseq2002s:\*

6: Geneseq2003as:\*

7: Geneseq2003bs:\*

8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	636	100.0	119	7	ADQ9796 Anti-huma
2	636	100.0	119	7	ADQ9796 Anti-MUC1
3	636	100.0	119	7	ADQ9796 Human ant
4	561	88.2	117	7	ADQ9784 Anti-huma
5	561	88.2	117	7	ADQ9784 Anti-MUC1
6	561	88.2	117	7	ADQ9784 Human ant
7	558	87.7	122	4	AAB62765 Human HIV
8	554.5	87.2	123	4	AAB62745 Human HIV
9	553.5	87.0	118	7	ADQ9796 Murine-ex
10	552	86.8	123	7	ADQ9796 Murine-ex
11	551	86.6	119	7	ADQ9796 Murine-ex
12	549	86.3	123	7	ADQ9796 Murine-ex
13	549	86.3	123	7	ADQ9796 Murine-ex
14	548	86.2	120	4	AAB62775 Human HIV
15	547.5	86.1	121	7	ADQ9796 Antibody
16	547	86.0	119	7	ADQ9796 Murine-ex
17	547	86.0	446	8	ADK52356 Human ant
18	546.5	85.9	120	7	ADQ9796 Murine-ex
19	546.5	85.9	120	7	ADQ9796 Murine-ex
20	545.5	85.8	252	5	ADP45983 Human Bly
21	545.5	85.8	252	7	ADG96810 Single ch
22	545	85.7	119	2	AAR30143 MAB GAH v
23	545	85.7	119	6	ABP98691 Human GAH
24	545	85.7	119	6	ABP98683 Human GAH
25	545	85.7	119	7	ADG43869 Human pro

26	545	85.7	119	8	ADQ28266	ADQ28266 Method of
27	545	85.7	127	7	ADP03874	ADP03874 Murine-ex
28	544.5	85.6	124	7	ADP03935	ADP03935 Murine-ex
29	544	85.5	123	2	AAW78433	AAW78433 Antibody
30	544	85.5	123	5	ABB97976	ABB97976 Heavy cha
31	544	85.5	123	5	ADG88414	ADG88414 anti-Ob-R
32	542	85.2	117	7	ADQ9796	ADQ9796 Anti-huma
33	542	85.2	117	7	ADQ9796	ADQ9796 Anti-huma
34	542	85.2	117	7	ADQ9796	ADQ9796 Anti-huma
35	542	85.2	117	7	ADQ9796	ADQ9796 Anti-huma
36	541.5	85.1	122	7	ADP03869	ADP03869 Murine-ex
37	541	85.1	125	7	ADP03871	ADP03871 Murine-ex
38	540	84.9	121	7	ADP03882	ADP03882 Murine-ex
39	540	84.9	125	7	ADP03868	ADP03868 Murine-ex
40	540	84.9	125	7	ADP03876	ADP03876 Murine-ex
41	540	84.9	129	5	AAU81275	AAU81275 Human trk
42	540	84.9	129	5	AAU81276	AAU81276 Human trk
43	540	84.9	251	6	ABJ19829	ABJ19829 Human VEG
44	540	84.9	251	8	ADH13871	ADH13871 Human vas
45	539.5	84.8	120	7	ADP03969	ADP03969 Murine-ex

## ALIGNMENTS

RESULT 1

ADQ9796  
ID ADC9796 standard; protein; 119 AA.

XX AC ADC9796;

XX AC

XX 01-JAN-2004 (first entry)

XX DE

XX DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 25.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;

XX cytotostatic; melanoma; oesophageal; pancreatic; colorectal tumour;

XX cervical carcinoma; intraepithelial neoplasia; colorectal; breast;

XX lung cancer; human.

XX Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

XX N-PSDB; ADC9796.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease

XX or condition associated with expression of MUC18 in a patient, e.g.

XX tumors, cancers, and other malignancies.

XX Claim 1; SEQ ID NO 25; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising

XX a heavy or light chain amino acid or a heavy or light chain variable

XX domain where the antibody binds to MUC18. The monoclonal antibody of the

XX invention demonstrates cytostatic activity and may be useful for treating

XX a disease or condition associated with the expression of MUC18 on the

XX cell surface such as tumours, specifically melanoma, oesophageal,

XX pancreatic or colorectal tumours, carcinomas, particularly cervical

XX carcinomas and cervical intraepithelial neoplasia and cancers including

XX colorectal, breast or lung cancer, as well as other malignancies. The

XX current sequence is that of the anti-human MUC18 monoclonal antibody

CC heavy chain protein of the invention.

XX  
SQ Sequence 119 AA;  
Query Match 100.0%; Score 636; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.1e-48;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKLEWIGIYSSGSTY 60  
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKLEWIGIYSSGSTY 60  
QY 61 YNPISLKRITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGFDYWGQGTLTIVSS 119  
DB 61 YNPISLKRITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGFDYWGQGTLTIVSS 119

## RESULT 2

ADDF09838  
ID ADF09838 standard; protein; 119 AA.  
XX  
AC ADF09838;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human anti-MUC18 monoclonal antibody heavy chain #7.  
XX  
KW cell proliferation inhibition; MUC18 tumour antigen;  
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
KW carcinoma; cancer; malignancy; heavy chain; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003057837-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 26-DEC-2002; 2002WO-US041580.  
XX  
PR 28-DEC-2001; 2001US-0346414P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J;  
XX  
DR WPI; 2003-577496/54.  
DR N-PSDB; ADD05402.  
XX  
PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
PT associated with melanoma, or increasing survival of an animal having a  
PT metastatic tumor.

Claim 1; SEQ ID NO 25; 87pp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting  
CC tumour growth in an animal. The tumour inhibition process comprises  
CC selecting an animal in need of treatment for a tumour, providing a  
CC monoclonal antibody comprising a heavy chain amino acid, where the  
CC antibody consists of any one of 10 fully defined sequences of 117-123  
CC amino acids given in the specification, and where the monoclonal antibody  
CC binds MUC18, and contacting the tumour with the antibody resulting in  
CC inhibited proliferation of the cells. The monoclonal antibody has  
CC cytostatic and can be used in the production of a vaccine. The monoclonal  
CC antibodies against the MUC18 antigen are useful for diagnosing and  
CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or  
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
CC increasing survival of an animal having a metastatic tumour. This  
CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
CC protein of the invention.

XX  
SQ Sequence 119 AA;  
Query Match 100.0%; Score 636; DB 7; Length 119;

Best Local Similarity 100.0%; Pred. No. 1.1e-48;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKLEWIGIYSSGSTY 60  
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKLEWIGIYSSGSTY 60  
QY 61 YNPISLKRITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGFDYWGQGTLTIVSS 119  
DB 61 YNPISLKRITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGFDYWGQGTLTIVSS 119

## RESULT 3

ADDF09838  
ID ADF09838 standard; protein; 119 AA.  
XX  
AC ADF09838;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human anti-MUC18 monoclonal antibody heavy chain #7.  
XX  
KW cell proliferation inhibition; MUC18 tumour antigen;  
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
KW carcinoma; cancer; malignancy; heavy chain; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003057837-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 26-DEC-2002; 2002WO-US041580.  
XX  
PR 28-DEC-2001; 2001US-0346414P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J;  
XX  
DR WPI; 2003-598367/56.  
DR N-PSDB; ADF09840.  
XX  
PT Inhibiting cell proliferation associated with expression of MUC18 tumour  
PT antigen, involves incubating and inhibiting cell by administering anti-  
PT MUC18 monoclonal antibody.

Claim 1; SEQ ID NO 25; 83pp; English.

XX The invention comprises a method for inhibiting cell proliferation  
CC associated with expression of MUC18 tumour antigen. The method involves  
CC administering anti-MUC18 monoclonal antibody. The method of the invention  
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
CC proliferation associated with the expression of MUC18 tumour antigen, the  
CC method is preferably useful for inhibiting tumour metastasis. The method  
CC is useful for inhibiting cell proliferation in patients with tumours,  
CC carcinomas, cancer and other malignancies. The present amino acid  
CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
CC monoclonal antibody.

XX Sequence 119 AA;

Query Match 100.0%; Score 636; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.1e-48;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKLEWIGIYSSGSTY 60  
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKLEWIGIYSSGSTY 60  
QY 61 YNPISLKRITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGFDYWGQGTLTIVSS 119  
DB 61 YNPISLKRITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGFDYWGQGTLTIVSS 119

RESULT 4  
ID ADC99784 standard; protein; 117 AA.  
XX  
AC ADC99784;  
DT  
XX  
XX  
DE  
XX  
XX  
KW anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 13.  
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytosolic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.  
XX  
OS Homo sapiens.  
XX  
XX WO2003057838-A2.  
XX  
XX  
PD 17-JUL-2003.  
XX  
XX  
PF 26-DEC-2002; 2002WO-US041581.  
XX  
XX  
PR 28-DEC-2001; 2001US-0346299P.  
XX  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
XX  
PI Gudas J;  
XX  
XX WPI; 2003-587113/55.  
XX  
XX N-PSDB; ADC99786.  
XX  
XX  
PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
PT or condition associated with expression of MUC18 in a patient, e.g.  
PT tumors, cancers, and other malignancies.  
XX  
XX  
PS Claim 1; SEQ ID NO 13; 78pp; English.  
XX  
XX  
CC The invention relates to a novel isolated monoclonal antibody comprising  
CC a heavy or light chain amino acid or a heavy or light chain variable  
CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
CC invention demonstrates cytostatic activity and may be useful for treating  
CC a disease or condition associated with the expression of MUC18 on the  
CC cell surface such as tumours, specifically melanoma, oesophageal,  
CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
CC carcinomas and cervical intraepithelial neoplasia and cancers including  
CC colorectal, breast or lung cancer, as well as other malignancies. The  
CC current sequence is that of the anti-human MUC18 monoclonal antibody  
CC heavy chain protein of the invention.  
XX  
XX  
SQ Sequence 117 AA;  
Query Match 88.2%; Score 561; DB 7; Length 117;  
Best Local Similarity 88.2%; Pred. No. 4.9e-42;  
Matches 105; Conservative 9; Mismatches 3; Indels 2; Gaps 1;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSINSGCCYWSWIQHPKGLGWIGFIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSINSGCCYWSWIQHPKGLGWIGFIYSGSTY 60  
QY 61 YNPSLKSRITLSVDTSKNQPSLKLNSMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119  
Db 61 YNPSLKSRVITISVDTSKNQPSLKLSSVTAADTAVYYCAREGD--GFDYWGQGLTVTVSS 117  
QY 61 YNPSLKSRITLSVDTSKNQPSLKLNSMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119  
Db 61 YNPSLKSRVITISVDTSKNQPSLKLSSVTAADTAVYYCAREGD--GFDYWGQGLTVTVSS 117  
RESULT 5  
ID ADD05388 standard; protein; 117 AA.  
XX  
XX ADD05388  
XX  
XX ADD05388;  
XX

01-JAN-2004 (first entry)  
Anti-MUC18 antibody heavy chain variable region protein, SEQ ID NO 13.  
monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
Homo sapiens.  
WO2003057006-A2.  
17-JUL-2003.  
26-DEC-2002; 2002WO-US041582.  
28-DEC-2001; 2001US-0346460P.  
(ABGE-) ABGENIX INC.  
Gudas J, Bar-Eli M;  
WPI; 2003-577496/54.  
N-PSDB; ADD05390.  
Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
treating tumors, inhibiting tumor growth, inhibiting cell invasion  
associated with melanoma, or increasing survival of an animal having a  
metastatic tumor.  
Claim 1; SEQ ID NO 13; 87pp; English.  
The invention relates to a novel monoclonal antibody used for inhibiting  
tumour growth in an animal. The tumour inhibition process comprises  
selecting an animal in need of treatment for a tumour, providing a  
monoclonal antibody comprising a heavy chain amino acid, where the  
antibody consists of any one of 10 fully defined sequences of 117-123  
amino acids given in the specification, and where the monoclonal antibody  
binds MUC18, and contacting the tumour with the antibody resulting in  
inhibited proliferation of the cells. The monoclonal antibody has  
cytostatic and can be used in the production of a vaccine. The monoclonal  
antibodies against the MUC18 antigen are useful for diagnosing and  
treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or  
tumour metastasis), inhibiting cell invasion associated with melanoma, or  
increasing survival of an animal having a metastatic tumour. This  
sequence represents an anti-MUC18 antibody heavy chain, variable region,  
protein of the invention.  
SQ Sequence 117 AA;  
Query Match 88.2%; Score 561; DB 7; Length 117;  
Best Local Similarity 88.2%; Pred. No. 4.9e-42;  
Matches 105; Conservative 9; Mismatches 3; Indels 2; Gaps 1;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSINSGCCYWSWIQHPKGLGWIGFIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSINSGCCYWSWIQHPKGLGWIGFIYSGSTY 60  
QY 61 YNPSLKSRITLSVDTSKNQPSLKLNSMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119  
Db 61 YNPSLKSRVITISVDTSKNQPSLKLSSVTAADTAVYYCAREGD--GFDYWGQGLTVTVSS 117  
RESULT 6  
ID ADF09826 standard; protein; 117 AA.  
XX  
XX ADF09826;  
XX  
XX  
DT 12-FEB-2004 (first entry)  
XX  
XX Human anti-MUC18 monoclonal antibody heavy chain #4.  
XX cell proliferation inhibition; MUC18 tumour antigen;

KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
 KW carcinoma; cancer; malignancy; heavy chain; human.  
 XX Homo sapiens.  
 OS  
 XX WO2003057837-A2.  
 PN  
 XX 17-JUL-2003.  
 PD  
 XX  
 XX 26-DEC-2002; 2002WO-US041580.  
 PF  
 XX  
 XX 28-DEC-2001; 2001US-0346414P.  
 PR  
 XX (ABGE-) ABGENIX INC.  
 PA  
 XX Gudas J;  
 XX  
 PI  
 XX WPI; 2003-598367/56.  
 DR  
 DR N-PSDB; ADF09828.  
 XX  
 XX Inhibiting cell proliferation associated with expression of MUC18 tumor  
 PT antigen, involves incubating and inhibiting cell by administering anti-  
 PT MUC18 monoclonal antibody.  
 PT  
 XX  
 XX Claim 1; SEQ ID NO 13; 83pp; English.  
 PS  
 XX The invention comprises a method for inhibiting cell proliferation  
 CC associated with expression of MUC18 tumour antigen. The method involves  
 CC administering anti-MUC18 monoclonal antibody. The method of the invention  
 CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
 CC proliferation associated with the expression of MUC18 tumour antigen, the  
 CC method is preferably useful for inhibiting tumour metastasis. The method  
 CC is useful for inhibiting cell proliferation in patients with tumours,  
 CC carcinomas, cancer and other malignancies. The present amino acid  
 CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
 CC monoclonal antibody.  
 CC  
 XX Sequence 117 AA;  
 SQ

Query Match 88.2%; Score 561; DB 7; Length 117;  
 Best Local Similarity 88.2%; Pred. No. 4.9e-42;  
 Matches 105; Conservative 9; Mismatches 3; Indels 2; Gaps 1;  
 QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGCYMSWIRQHPGKLEWIGYIYSGSTY 60  
 Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGYVYTWIRQHPGKLEWIGFYISGSTY 60  
 QY 61 YNPSLKSRLTSLVDTSKNQFSLKNSMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119  
 Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 61 YNPSLKSRLTSLVDTSKNQFSLKNSMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 117  
 RESULT 7  
 AAB62765  
 ID AAB62765 standard; protein; 122 AA.  
 AC  
 XX AAB62765;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE Human HIV-1 monoclonal antibody SEQ ID NO: 64.  
 XX  
 KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;  
 KW envelope glycoprotein; gp120; diagnosis.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200100678-A1.  
 PN  
 XX 04-JAN-2001.  
 PD  
 XX 23-JUN-2000; 2000WO-US017327.  
 PF  
 XX  
 XX 30-JUN-1999; 99US-0141701P.  
 PR  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 XX Watkins BA, Reitz MS;  
 XX WPI; 2001-112438/12.  
 DR  
 DR N-PSDB; AAF29046.  
 XX  
 XX Novel human monoclonal antibody immunoreactive with human  
 PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1  
 PT in biological sample and providing passive immunotherapy to HIV-1  
 PT

PR 30-JUN-1999; 99US-0141701P.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 XX Watkins BA, Reitz MS;  
 XX WPI; 2001-112438/12.  
 DR  
 DR N-PSDB; AAF29066.  
 XX  
 XX Novel human monoclonal antibody immunoreactive with human  
 PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1  
 PT in biological sample and providing passive immunotherapy to HIV-1  
 PT infected mammal.  
 XX  
 XX Claim 1; Page 63; 81pp; English.  
 PS  
 XX The present invention provides the protein and coding sequences for the  
 CC variable regions of human monoclonal antibodies which are immunoreactive  
 CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.  
 CC These can be used in diagnosis and therapy of HIV-1 infection  
 XX  
 XX Sequence 122 AA;  
 SQ

Query Match 87.7%; Score 558; DB 4; Length 122;  
 Best Local Similarity 86.8%; Pred. No. 9.5e-42;  
 Matches 105; Conservative 9; Mismatches 5; Indels 2; Gaps 1;  
 QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGCYMSWIRQHPGKLEWIGYIYSGSTY 60  
 Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 2 EVQLQESGPGLVKPSQTLSTCTVSGGSINSGGYVYTWIRQHPGKLEWIGYIYSGSTY 61  
 QY 61 YNPSLKSRLTSLVDTSKNQFSLKNSMTAADTAVYYCARD--RETAGFDYWGQGLTVTVSS 118  
 Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 62 YNPSLKSRLTSLVDTSKNQFSLKNSMTAADTAVYYCARDMLRDSGLCYWGKGLTVTVSS 121  
 QY 119 S 119  
 Db 122 S 122  
 RESULT 8  
 AAB62745  
 ID AAB62745 standard; protein; 123 AA.  
 AC  
 XX AAB62745;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE Human HIV-1 monoclonal antibody SEQ ID NO: 44.  
 XX  
 KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;  
 KW envelope glycoprotein; gp120; diagnosis.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200100678-A1.  
 PN  
 XX 04-JAN-2001.  
 PD  
 XX 23-JUN-2000; 2000WO-US017327.  
 PF  
 XX  
 XX 30-JUN-1999; 99US-0141701P.  
 PR  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 XX Watkins BA, Reitz MS;  
 XX WPI; 2001-112438/12.  
 DR  
 DR N-PSDB; AAF29046.  
 XX  
 XX Novel human monoclonal antibody immunoreactive with human  
 PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1  
 PT in biological sample and providing passive immunotherapy to HIV-1  
 PT

PT infected mammal.

XX Claim 1; Page 50; 81pp; English.

XX The present invention provides the protein and coding sequences for the  
 CC variable regions of human monoclonal antibodies which are immunoreactive  
 CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.  
 CC These can be used in diagnosis and therapy of HIV-1 infection  
 XX

SQ Sequence 123 AA;

Query Match 87.2%; Score 554.5; DB 4; Length 123;

Best Local Similarity 85.2%; Pred. No. 2e-41;

Matches 104; Conservative 9; Mismatches 6; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLTLCTVSGGINSGGYWSWIROHPGKLEWIGVIYSSGTY 60

DB 2 EVQLQESGPGLVKPSQTLTLCTVSGGINSGGYWSWIROHPGKLEWIGVIYNSGTY 61

QY 61 YNPSLKSRITLSVDTSKNQFSLKLSMTAADTAVYVCARDRETAG---FDYWGQGLTVTV 117

DB 62 YNPSLKSRVTISIDTSKNKFSKLSSVTAADTAVYVCARAAYCGDCSFDYWGQGLTVTV 121

QY 118 SS 119

DB 122 SS 123

RESULT 9

ADP03968

ID ADP03968 standard; protein; 118 AA.

XX

AC ADP03968;

XX

DT 29-JUL-2004 (first entry)

XX

DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138.

XX

KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;

KW cytosolic; colorectal neoplasm; renal cell carcinoma;

KW cervical intraepithelial squamous neoplasia;

KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;

KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX

OS Unidentified.

XX

PN WO2003048328-A2.

XX

PD 12-JUN-2003.

XX

PF 02-DEC-2002; 2002WO-US038550.

XX

PR 03-DEC-2001; 2001US-0337275P.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Gudas J, Foltz I, Handa M, Gallo M;

XX

DR WPT; 2003-523295/49.

XX

PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,

PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical

PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX

PS Example 2; SEQ ID NO 138; 89pp; English.

XX

CC The invention relates to a novel isolated monoclonal antibody (mAb)

CC comprising a heavy chain polypeptide and light chain polypeptide having a

CC sequence chosen from one of 53 fully defined amino acid sequences given

CC in the specification, where the antibody specifically binds carbonic

CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention

CC demonstrates cytostatic activity and may be useful for treating a tumour,

CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,

CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.

SQ Sequence 118 AA;

Query Match 87.0%; Score 553.5; DB 7; Length 118;

Best Local Similarity 89.1%; Pred. No. 2.3e-41;

Matches 106; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLTLCTVSGGINSGGYWSWIROHPGKLEWIGVIYSSGTY 60

DB 1 QVQLQESGPGLVKPSQTLTLCTVSGGINSGGYWSWIROHPGKLEWIGVIYSSGTY 60

QY 61 YNPSLKSRITLSVDTSKNQFSLKLSMTAADTAVYVCARDRETAGFDYWGQGLTVTVSS 119

DB 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCAR-YYGSGSDYWGQGLTVTVSS 118

RESULT 10

ADP03870

ID ADP03870 standard; protein; 123 AA.

XX

AC ADP03870;

XX

DT 29-JUL-2004 (first entry)

XX

DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 10.

XX

KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;

KW cytosolic; colorectal neoplasm; renal cell carcinoma;

KW cervical intraepithelial squamous neoplasia;

KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;

KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX

OS Unidentified.

XX

PN WO2003048328-A2.

XX

PD 12-JUN-2003.

XX

PF 02-DEC-2002; 2002WO-US038550.

XX

PR 03-DEC-2001; 2001US-0337275P.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Gudas J, Foltz I, Handa M, Gallo M;

XX

DR WPT; 2003-523295/49.

XX

PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX Claim 1; SEQ ID NO 10; 89pp; English.

CC The invention relates to a novel isolated monoclonal antibody (mAb)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytostatic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.

```
XX SQ Sequence 123 AA;
Query Match 86.8%; Score 552; DB 7; Length 123;
Best Local Similarity 86.2%; Pred. No. 3.3e-41;
Matches 106; Conservative 6; Mismatches 7; Indels 4; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWMSWIRQHPGKGLEWIGYIYSSGSTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWMSWIRQHPGKGLEWIGYIYSSGSTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 YNPSLKSRIITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAG---PDYWGQGTLYVT 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 YNPSLKSRIITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAG---PDYWGQGTLYVT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 117 VSS 119
   |||
Db 121 VSS 123
   |||

RESULT 11
ADP03970
ID ADP03970 standard; protein; 119 AA.
XX AC ADP03970;
XX DT 29-JUL-2004 (first entry)
XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 140.
XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX KW cytotatic; colorectal neoplasm; renal cell carcinoma;
XX KW cervical intraepithelial squamous neoplasia;
XX KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX KW gene therapy; murine; mouse; human; heavy chain variable domain.
XX OS Unidentified.
XX PN WO2003048328-A2.
XX PD 12-JUN-2003.
XX PF 02-DEC-2002; 2002WO-US038550.
XX PR 03-DEC-2001; 2001US-0337275P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas J, Foltz I, Handa M, Gallo M;
XX PS WPI; 2003-523295/49.
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Example 2; SEQ ID NO 140; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
XX sequence chosen from one of 53 fully defined amino acid sequences given
XX in the specification, where the antibody specifically binds carbonic
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX demonstrates cytostatic activity and may be useful for treating a tumour,
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX tumour or breast cancer, possibly via gene therapy. The current sequence
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX (heavy chain variable domain) protein of the invention. The protein was
XX generated via the introduction of the human CA IX protein into a
XX transgenic mouse strain.
XX
XX Sequence 119 AA;
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Query Match 86.6%; Score 551; DB 7; Length 119;
Best Local Similarity 87.4%; Pred. No. 3.9e-41;
Matches 104; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWMSWIRQHPGKGLEWIGYIYSSGSTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWMSWIRQHPGKGLEWIGYIYSSGSTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 YNPSLKSRIITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGFDYWGQGTLYTVSS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 YNPSLKSRIITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGFDYWGQGTLYTVSS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
ADP03879
ID ADP03879 standard; protein; 123 AA.
XX AC ADP03879;
XX DT 29-JUL-2004 (first entry)
XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 19.
XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX KW cytotatic; colorectal neoplasm; renal cell carcinoma;
XX KW cervical intraepithelial squamous neoplasia;
XX KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX KW gene therapy; murine; mouse; human; heavy chain variable domain.
XX OS Unidentified.
XX PN WO2003048328-A2.
XX PD 12-JUN-2003.
XX PF 02-DEC-2002; 2002WO-US038550.
XX PR 03-DEC-2001; 2001US-0337275P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas J, Foltz I, Handa M, Gallo M;
XX PS WPI; 2003-523295/49.
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Claim 1; SEQ ID NO 19; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
XX sequence chosen from one of 53 fully defined amino acid sequences given
XX in the specification, where the antibody specifically binds carbonic
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX demonstrates cytostatic activity and may be useful for treating a tumour,
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX tumour or breast cancer, possibly via gene therapy. The current sequence
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX (heavy chain variable domain) protein of the invention. The protein was
XX generated via the introduction of the human CA IX protein into a
XX transgenic mouse strain.
XX
XX Sequence 123 AA;
Query Match 86.3%; Score 549; DB 7; Length 123;
Best Local Similarity 85.4%; Pred. No. 6e-41;
Matches 105; Conservative 6; Mismatches 8; Indels 4; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWMSWIRQHPGKGLEWIGYIYSSGSTY 60
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Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGYWIRQHPGKGLEWIGYIYSGSTY 60  
 QY 61 YNPSLKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRET---AGFDYWGQGLT 116  
 Db 61 YNPSLKSRVLIISVDTSENQFSLKLSVTAADTAVYYCARERTDYIYYGLDVGQGT 120  
 QY 117 VSS 119  
 Db 121 VSS 123

## RESULT 13

ADP03878  
 ID ADF03878 standard; protein; 123 AA.

XX  
 AC ADP03878;

DT 29-JUL-2004 (first entry)

XX Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 18.  
 DE monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytostatic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX  
 OS Unidentified.

XX W02003048328-A2.

PN 12-JUN-2003.

XX 02-DEC-2002; 2002WO-US038550.

XX 03-DEC-2001; 2001US-0337275P.

XX (ABGE-) ABGENIX INC.

XX Gudas J, Foltz I, Handa M, Gallo M;

XX WPI; 2003-523295/49.

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

PS Claim 1; SEQ ID NO 18; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mAb)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytostatic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.

XX Sequence 123 AA;

Query Match 86.3%; Score 549; DB 7; Length 123;

Best Local Similarity 85.4%; Pred. No. 6e-41;

Matches 105; Conservative 6; Mismatches 8; Indels 4; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGYWIRQHPGKGLEWIGYIYSGSTY 60

Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGYWIRQHPGKGLEWIGYIYSGSTY 60

QY 61 YNPSLKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRET---AGFDYWGQGLT 116  
 Db 61 YNPSLKSRVLIISVDTSENQFSLKLSVTAADTAVYYCARERTDYIYYGLDVGQGT 120  
 QY 117 VSS 119  
 Db 121 VSS 123

## RESULT 14

AAB62775  
 ID AAB62775 standard; protein; 120 AA.

XX  
 AC AAB62775;

DT 03-APR-2001 (first entry)

XX Human HIV-1 monoclonal antibody SEQ ID NO: 74.

XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;  
 KW envelope glycoprotein; gp120; diagnosis.

XX Homo sapiens.

PN W0200100678-A1.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-US017327.

XX 30-JUN-1999; 99US-0141701P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Watkins BA, Reitz MS;

XX WPI; 2001-112438/12.

XX N-PSDB; AAF29076.

XX Novel human monoclonal antibody immunoreactive with human

PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1

PT in biological sample and providing passive immunotherapy to HIV-1

PT infected mammal.

XX Claim 1; Page 69; 81pp; English.

CC The present invention provides the protein and coding sequences for the  
 CC variable regions of human monoclonal antibodies which are immunoreactive  
 CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.  
 CC These can be used in diagnosis and therapy of HIV-1 infection

XX Sequence 120 AA;

Query Match 86.2%; Score 548; DB 4; Length 120;

Best Local Similarity 87.4%; Pred. No. 7.2e-41;

Matches 104; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGYWIRQHPGKGLEWIGYIYSGSTY 60

Db 2 EVQLQESGPGLVKPSQTLSTCTVSGGSINSGGYWIRQHPGKGLEWIGYIYSGSTY 61

QY 61 YNPSLKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRETAGFDYWGQGLT 119

Db 62 YNPSLKSRVLIISVDTSKNQFSLKLSVTAADTAVYYCARVWVDFPDWGQGLT 120

## RESULT 15

ADJ80377

ID ADJ80377 standard; protein; 121 AA.

XX  
 AC ADJ80377;

XX





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55 ; Search time 18.4912 Seconds  
(without alignments)  
480.403 Million cell updates/sec

Title: US-10-660-357A-25

Perfect score: 636

Sequence: 1 QVQLQESGPGLVKPSQTL.....DRETAGFDYWGQGLTVTSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTCUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	545	85.7	119	1	US-08-360-125-5
2	545	85.7	119	2	US-08-450-578-5
3	545	85.7	119	2	US-09-017-628-5
4	545	85.7	119	2	US-09-014-880-5
5	545	85.7	119	4	US-08-450-363-5
6	545	85.7	119	4	US-09-467-903-5
7	532.5	83.7	487	4	US-09-800-729-145
8	523.5	82.3	473	3	US-09-049-672A-4
9	513.5	80.7	118	3	US-09-025-769B-25
10	513.5	80.7	118	4	US-09-490-070A-25
11	513.5	80.7	118	4	US-09-490-153-25
12	513.5	80.7	118	4	US-09-490-324-25
13	506.5	79.6	172	4	US-09-472-087-7
14	506.5	79.6	172	4	US-09-472-087-86
15	503	79.1	117	4	US-09-720-493-2
16	503	79.1	119	3	US-09-025-769B-39
17	503	79.1	119	3	US-09-025-769B-65
18	503	79.1	119	4	US-09-490-070A-39
19	503	79.1	119	4	US-09-490-070A-65
20	503	79.1	119	4	US-09-490-153-39
21	503	79.1	119	4	US-09-490-153-65
22	503	79.1	119	4	US-09-490-324-39
23	503	79.1	119	4	US-09-490-324-65
24	499.5	78.5	122	1	US-08-360-125-11
25	499.5	78.5	122	2	US-08-450-578-11
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27	499.5	78.5	122	2	US-09-014-880-11

28 499.5 78.5 122 4 US-08-450-363-11 Sequence 11, Appl  
29 499.5 78.5 122 4 US-09-467-903-11 Sequence 11, Appl  
30 494 77.7 118 3 US-08-545-809A-116 Sequence 116, App  
31 490 77.0 142 2 US-08-480-774A-2 Sequence 2, Appli  
32 488 76.7 155 4 US-09-471-276-888 Sequence 888, App  
33 487.5 76.7 244 3 US-08-918-148-79 Sequence 79, Appl  
34 487.5 76.7 244 4 US-09-138-091A-77 Sequence 77, Appl  
35 485.5 76.3 120 4 US-09-424-840B-20 Sequence 20, Appl  
36 478 75.2 476 3 US-08-487-550-12 Sequence 12, Appl  
37 478 75.2 476 4 US-09-526-098-12 Sequence 12, Appl  
38 478 75.2 476 4 US-09-383-916-12 Sequence 12, Appl  
39 473.5 74.4 139 4 US-09-471-276-837 Sequence 837, App  
40 468.5 73.7 278 3 US-09-260-527-3 Sequence 3, Appli  
41 465 73.1 118 3 US-08-545-809A-142 Sequence 142, App  
42 463.5 72.9 139 4 US-09-203-768A-2 Sequence 2, Appli  
43 463.5 72.9 143 4 US-09-471-276-839 Sequence 839, App  
44 459.5 72.2 118 2 US-08-652-816A-13 Sequence 13, Appl  
45 458.5 72.1 150 4 US-09-582-337-14 Sequence 14, Appl

#### ALIGNMENTS

RESULT 1  
US-08-360-125-5  
; Sequence 5, Application US/08360125  
; Patent No. 5767246  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA  
; APPLICANT: Toshiaki TAGAWA  
; APPLICANT: Yoko HIRAKAWA  
; APPLICANT: No. 5767246hiko ITO  
; APPLICANT: Kazuhiro NAGAIKE  
; TITLE OF INVENTION: Human Monoclonal Antibody  
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
; TITLE OF INVENTION: Cell Membrane  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/360,125  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/905,534  
; FILING DATE: June 29, 1992  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

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; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
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; US-08-360-125-5
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; Query Match 85.7%; Score 545; DB 1; Length 119;
; Best Local Similarity 84.9%; Pred. No. 5e-47;
; Matches 101; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
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; QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSYGVSWIRQHPKGLGWIGYIYSGSTY 60
; DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSYGVSWIRQHPKGLGWIGYIYSGSTY 60
;
; QY 61 YNPSLKSRLTSLVDTSKNQFSLKNSMTAADTAVYYCARDRETAGPDYWGQGLTVTVSS 119
; DB 61 YNPSLKSRLTSLVDTSKNQFSLKNSMTAADTAVYYCARDRETAGPDYWGQGLTVTVSS 119
;
; RESULT 2
; US-08-450-578-5
; Sequence 5, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5837845ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
;
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,578
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
;
; US-08-450-578-5
;
; Query Match 85.7%; Score 545; DB 2; Length 119;
; Best Local Similarity 84.9%; Pred. No. 5e-47;
; Matches 101; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
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IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
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IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-467-903-5

Query Match 85.7%; Score 545; DB 4; Length 119;  
Best Local Similarity 84.9%; Pred. No. 5e-47;  
Matches 101; Conservative 9; Mismatches 9; Indels 0; Gaps 0;  
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Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGGYMSWIRQHPGKGLWIGYIYSSGSTY 60  
Qy 61 YNPSLKSRLTSLVDTSKNQFSLKLSMTAATAVYYCARDRETAGFDYWGQGLTVTVSS 119  
Db 61 YNPSLKSRLTSLVDTSKNQFSLKLSMTAATAVYYCARDRETAGFDYWGQGLTVTVSS 119

RESULT 7  
US-09-800-729-145  
Sequence 145, Application US/09800729  
Patent No. 6605592  
GENERAL INFORMATION:  
APPLICANT: Ni et al.  
TITLE OF INVENTION: 32 Human secreted proteins  
FILE REFERENCE: P2044P1  
CURRENT APPLICATION NUMBER: US/09/800,729  
CURRENT FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: PCT/US00/26013  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 60/155,709  
PRIOR FILING DATE: 1999-09-24  
NUMBER OF SEQ ID NOS: 217  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 145  
LENGTH: 487  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-800-729-145

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Best Local Similarity 78.9%; Pred. No. 4.7e-45;  
Matches 101; Conservative 10; Mismatches 8; Indels 9; Gaps 1;  
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Db 80 YNPSLKSRLTSLVDTSKNQFSLRSLSSVTAADTAVYYCAKDHTRATRDGYQLEYRFPDYWGQ 139  
Qy 112 GTLVTVSS 119  
Db 140 GILVTVSS 147  
RESULT 8  
US-09-049-672A-4  
Sequence 4, Application US/09049672A  
Patent No. 6135941  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Lal, Preeti  
APPLICANT: Tang, Y. Tom  
APPLICANT: Yue, Henry  
APPLICANT: Au-Young, Janice  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Baughn, Mariah R.  
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq For Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049,672A  
FILING DATE: HEREWITH  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cerrone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0497 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 473 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: PANCUT01  
CLONE: 1513264  
US-09-049-672A-4

Query Match 82.3%; Score 523.5; DB 3; Length 473;  
Best Local Similarity 82.3%; Pred. No. 3.6e-44;  
Matches 102; Conservative 5; Mismatches 12; Indels 5; Gaps 1;  
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGGYMSWIRQHPGKGLWIGYIYSSGSTY 60  
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGGINSGGYMSWIRQHPGKGLWIGYIYSSGSTY 79  
Qy 61 YNPSLKSRLTSLVDTSKNQFSLKLSMTAATAVYYCARDRETAGFDYWGQGLTV 115  
Db 80 YNPSLKSRLTSLVDTSKNQFSLKLSMTAATAVYYCARDRETAGFDYWGQGLTV 139  
Qy 116 TVSS 119

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Db      140 TVSS 143
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RESULT 9
US-09-025-769B-25
; Sequence 25, Application US/09025769B
; Patent No. 630064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-25
; Query Match 80.7%; Score 513.5; DB 3; Length 118;
; Best Local Similarity 85.0%; Pred. No. 6.8e-44;
; Matches 102; Conservative 6; Mismatches 9; Indels 3; Gaps 2;
Qy      1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPKGLGWIGYIYSGSTY 60
Db      1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPKGLGWIGYIYSGSTN 58
Qy      61 YNPSLKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRETAG-PDYWGQGTFLTVSS 119
Db      59 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGGGGVFDYWGQGTFLTVSS 118

RESULT 10
US-09-490-070A-25
; Sequence 25, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25
; Query Match 80.7%; Score 513.5; DB 4; Length 118;
; Best Local Similarity 85.0%; Pred. No. 6.8e-44;
; Matches 102; Conservative 6; Mismatches 9; Indels 3; Gaps 2;
Qy      1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPKGLGWIGYIYSGSTY 60
Db      1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPKGLGWIGYIYSGSTN 58
Qy      61 YNPSLKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRETAG-PDYWGQGTFLTVSS 119
Db      59 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGGGGVFDYWGQGTFLTVSS 118

RESULT 11
US-09-490-153-25
; Sequence 25, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-153-25

Query Match      80.7%; Score 513.5; DB 4; Length 118;
Best Local Similarity 85.0%; Pred. No. 6.8e-44;
Matches 102; Conservative 6; Mismatches 9; Indels 3; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCCYNSWIRQHPGKGLEWIGYIYSSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINS--YYNSWIRQPPGKGLEWIGEIYHSGSTN 58
QY 61 YNPFLSKSRITLSVDTSKNQFSLKNSMTAADTAVYVCARDRETAG-FDYWGQGTTLTVSS 119
DB 59 YNPFLSKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARGGGGVFDYWGQGTTLTVSS 118

RESULT 12
US-09-490-324-25
Sequence 25, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25

Query Match      80.7%; Score 513.5; DB 4; Length 118;
Best Local Similarity 85.0%; Pred. No. 6.8e-44;
Matches 102; Conservative 6; Mismatches 9; Indels 3; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCCYNSWIRQHPGKGLEWIGYIYSSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINS--YYNSWIRQPPGKGLEWIGEIYHSGSTN 58
QY 61 YNPFLSKSRITLSVDTSKNQFSLKNSMTAADTAVYVCARDRETAG-FDYWGQGTTLTVSS 119
DB 59 YNPFLSKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARGGGGVFDYWGQGTTLTVSS 118

RESULT 13
US-09-472-087-7
Sequence 7, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, ELLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFI
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 7
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-7

Query Match      79.6%; Score 506.5; DB 4; Length 172;
Best Local Similarity 84.2%; Pred. No. 5.3e-43;
Matches 96; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 7 SGPGLVKPSQTLSTCTVSGGSINSGCCYNSWIRQHPGKGLEWIGYIYSSGSTYYPNPSLK 66
DB 1 SGPGLVKPSQTLSTCTVSGGSINS--YYNSWIRQPPGKGLEWIGEIYHSGSTN 60
QY 67 SRTLLSVDTSKNQFSLKNSMTAADTAVYVCARDRETAG-FDYWGQGTTLTVSS 119
DB 61 SRTVTSVDTSKNQFSLKLSVTAADTAVYVCARDSDGYIGIDWGQGTTLTVSS 114

RESULT 14
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US-09-472-087-86  
; Sequence 86, Application US/09472087  
; Patent No. 6682736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEVEU, MARK J.  
; APPLICANT: MUELLER, ELLEN E.  
; APPLICANT: HANKE, JEFFREY H.  
; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEOFFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-PFI  
; CURRENT APPLICATION NUMBER: US/09/472,087  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/113,647  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 86  
; LENGTH: 172  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-472-087-86

Query Match 79.6%; Score 506.5; DB 4; Length 172;  
Best Local Similarity 84.2%; Pred. No: 5.3e-43;  
Matches 96; Conservative 7; Mismatches 10; Indels 1; Gaps 1;  
  
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Db 1 SGPLVKPSQTLSTCTVSGGINSGCCYWSWIRQHPGKLEWIGYIYIGNTYNNPSLK 60  
  
QY 67 SRITLSVDTSKNQFSLKLSMTAADTAVYYCARDR-ETAGFDYWGQGLTVTVSS 119  
Db 61 SRVTISVDTSKNQFSLKLSVTAADTAVYYCARDSDGYDGIDVWGQGLTVTVSS 114

RESULT 15  
US-09-720-493-2  
; Sequence 2, Application US/09720493  
; Patent No. 6827925  
; GENERAL INFORMATION:  
; APPLICANT: Cambridge Antibody Technology Limited  
; APPLICANT: Williams, Andrew J  
; APPLICANT: Tempest, Philip R  
; APPLICANT: Holtet, Thor L  
; APPLICANT: Main, Sarah H  
; APPLICANT: Jackson, Helen  
; APPLICANT: Daramola, Olalekan  
; TITLE OF INVENTION: Improvements relating to antibodies  
; FILE REFERENCE: AHB/CP5775333  
; CURRENT APPLICATION NUMBER: US/09/720,493  
; CURRENT FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: GB 9814383.7  
; PRIOR FILING DATE: 1998-07-02  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-720-493-2

Query Match 79.1%; Score 503; DB 4; Length 117;  
Best Local Similarity 83.2%; Pred. No: 7.5e-43;  
Matches 99; Conservative 8; Mismatches 10; Indels 2; Gaps 2;  
  
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Db 1 QVOLQESGPGLVKPSQTLSTCTVSGGINSGCCYWSWIRQHPGKLEWIGYIYSSGSTY 59  
  
QY 61 YNPSLKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119

Db 60 YNPSLKSRITLSVDTSKNQFSLKLSVTAADTAVYYCARDGK-WSKFDYWGQGLTVTVSS 117

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Job time : 19.4912 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2005, 11:40:37 ; Search time 66.1111 Seconds  
(without alignments)  
- 753.137 Million cell updates/sec

Title: US-10-660-357A-25  
 Perfect score: 636  
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 Scoring table: BLOSUM62  
 Gapop 10.0 , Gabext 0.5

Searched: 1867879 seqs, 418409474 residues  
Total number of hits satisfying chosen parameters: 1867879

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                  Maximum Match 10%
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Published Applications AA:\*\*

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11: /cgn2\_6/ptodata/1/pubppaa/US09C PUBCOMB.pcp

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16: /cgn2\_6/ptodata/1/pubppaa/US10D PUBCOMB.pcp

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18: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW PUB.pcp:

19: /cgn2\_6/ptodata/1/pubppaa/US11A PUBCOMB.pcp

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22: /cgn2\_6/ptodata/1/pubppaa/US60 PUBCOMB.pcp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query $\#$			ID	Description
	Score	Match	Length		
1	636	100.0	119	US-10-330-613-25	Sequence 25, Appl
2	636	100.0	119	US-10-330-530-25	Sequence 25, Appl
3	636	100.0	119	US-10-660-357-25	Sequence 25, Appl
4	561	88.2	117	US-10-330-613-13	Sequence 13, Appl
5	561	88.2	117	US-10-330-530-13	Sequence 13, Appl
6	561	88.2	117	US-10-660-357-13	Sequence 13, Appl
7	560.5	88.1	125	US-10-805-177-53	Sequence 53, Appl
8	556.5	87.5	122	US-10-984-960A-20	Sequence 20, Appl
9	554.5	87.2	136	US-11-131-648-15	Sequence 15, Appl
10	554.5	87.2	136	US-11-131-648-39	Sequence 39, Appl
11	553.5	87.0	118	US-10-309-762-138	Sequence 138, Appl

12	552	86.8	123	15	US-10-309-762-10	Sequence 10, Appl
13	551	86.6	119	15	US-10-309-762-140	Sequence 140, App
14	551	86.6	121	17	US-10-706-689-8	Sequence 8, Appl
15	551	86.6	121	18	US-10-988-360-8	Sequence 8, Appl
16	549	86.3	123	15	US-10-309-762-18	Sequence 18, Appl
17	549	86.3	123	15	US-10-309-762-19	Sequence 19, Appl
18	547.5	86.1	121	15	US-10-308-817-137	Sequence 137, App
19	547.5	86.1	121	15	US-10-453-698-137	Sequence 137, App
20	547.5	86.1	122	18	US-10-984-960A-56	Sequence 56, Appl
21	547	86.0	119	15	US-10-309-762-131	Sequence 131, App
22	547	86.0	446	17	US-10-644-277-62	Sequence 62, Appl
23	546.5	85.9	120	15	US-10-309-762-13	Sequence 13, Appl
24	546.5	85.9	120	15	US-10-309-762-134	Sequence 144, App
25	545.5	85.8	252	10	US-09-880-748-1994	Sequence 1994, Ap
26	545.5	85.8	252	15	US-10-293-418-1994	Sequence 1994, Ap
27	545	85.7	119	17	US-10-483-994-7	Sequence 7, Appl
28	545	85.7	119	17	US-10-483-993-7	Sequence 7, Appl
29	545	85.7	119	18	US-10-497-516-7	Sequence 7, Appl
30	545	85.7	127	15	US-10-309-762-14	Sequence 14, Appl
31	544.5	85.6	124	15	US-10-309-762-75	Sequence 75, Appl
32	544.5	85.6	143	15	US-10-309-762-96	Sequence 96, Appl
33	544	85.5	144	17	US-10-893-576-35	Sequence 35, Appl
34	543.5	85.5	120	17	US-10-706-689-40	Sequence 40, Appl
35	543.5	85.5	120	18	US-10-988-360-40	Sequence 40, Appl
36	542	85.2	117	14	US-10-330-613-5	Sequence 5, Appl
37	542	85.2	117	14	US-10-330-530-5	Sequence 5, Appl
38	542	85.2	117	16	US-10-660-357-5	Sequence 5, Appl
39	542	85.2	123	15	US-10-309-762-9	Sequence 9, Appl
40	542	85.2	480	17	US-10-910-901-6	Sequence 6, Appl
41	541.5	85.1	122	15	US-10-309-762-147	Sequence 147, App
42	541	85.1	125	15	US-10-309-762-11	Sequence 11, Appl
43	540	84.9	121	15	US-10-309-762-152	Sequence 152, App
44	540	84.9	125	15	US-10-309-762-8	Sequence 8, Appl
45	540	84.9	125	15	US-10-309-762-16	Sequence 16, Appl

## ALIGNMENTS

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RESULT 1
US-10-330-613-25
; Sequence 25, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudae, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ARGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-25

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## RESULT 2

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US-10-330-530-25
; Sequence 25, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-25

Query Match      100.0%; Score 636; DB 14; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.9e-48;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGCYWSWIROHPGKGLEWIGYIYSSGSTY 60

QY 61 YNPSLKSRITLSVDTSKNQFSLKLSNMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119
DB 61 YNPSLKSRITLSVDTSKNQFSLKLSNMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119

RESULT 3
US-10-660-357-25
; Sequence 25, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-25

Query Match      100.0%; Score 636; DB 16; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.9e-48;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGCYWSWIROHPGKGLEWIGYIYSSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGCYWSWIROHPGKGLEWIGYIYSSGSTY 60

QY 61 YNPSLKSRITLSVDTSKNQFSLKLSNMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119
DB 61 YNPSLKSRITLSVDTSKNQFSLKLSNMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119

RESULT 4
US-10-330-613-13
; Sequence 13, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-13

Query Match      88.2%; Score 561; DB 14; Length 117;
Best Local Similarity 88.2%; Pred. No. 7.5e-42;
Matches 105; Conservative 9; Mismatches 3; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGCYWSWIROHPGKGLEWIGYIYSSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGCYWSWIROHPGKGLEWIGYIYSSGSTY 60

QY 61 YNPSLKSRITLSVDTSKNQFSLKLSNMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119
DB 61 YNPSLKSRITLSVDTSKNQFSLKLSNMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119

RESULT 5
US-10-330-530-13
; Sequence 13, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-13

Query Match      88.2%; Score 561; DB 14; Length 117;
Best Local Similarity 88.2%; Pred. No. 7.5e-42;
Matches 105; Conservative 9; Mismatches 3; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGCYWSWIROHPGKGLEWIGYIYSSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGCYWSWIROHPGKGLEWIGYIYSSGSTY 60

QY 61 YNPSLKSRITLSVDTSKNQFSLKLSNMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119
DB 61 YNPSLKSRITLSVDTSKNQFSLKLSNMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119

RESULT 6
US-10-660-357-13
; Sequence 13, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
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```
Query Match      87.2%; Score 554.5; DB 20; Length 136;
Best Local Similarity 84.8%; Pred. No. 3.2e-41;
Matches 106; Conservative 6; Mismatches 6; Indels 7; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGGCYWMSWIRQHPGKGLEWIGYIYSSGSTY 60
DB 12 QVQLQESGPGLVKPSQTLSTCTVSGGINSGGCYWMSWIRQHPGKGLEWIGYIYSSGSTY 71

QY 61 YNPSLKSRITLSVDTSKNQFSLKNSMTAADTAVYYCARDRET-----AGFDYWGQGT 113
DB 72 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARDRIITWVRGGIPSGMDVWGQGT 131

QY 114 LVTVS 118
DB 132 TVTVS 136

RESULT 10
US-11-131-648-39
; Sequence 39, Application US/11131648
; Publication No. US20050221400A1
; GENERAL INFORMATION:
; APPLICANT: Gudus, Jean
; APPLICANT: Jakobovits, Aya
; APPLICANT: Xiao-Chi, Jia
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Shao, Hui
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT BIND TO PSCA PROTEINS
; FILE REFERENCE: 51158-20088.20
; CURRENT APPLICATION NUMBER: US/11/131,648
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/616,381
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: 60/617,881
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/621,310
; PRIOR FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: 60/633,077
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: 10/857,484
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/475,064
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-131-648-39

Query Match      87.2%; Score 554.5; DB 20; Length 136;
Best Local Similarity 84.8%; Pred. No. 3.2e-41;
Matches 106; Conservative 6; Mismatches 6; Indels 7; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGGCYWMSWIRQHPGKGLEWIGYIYSSGSTY 60
DB 12 QVQLQESGPGLVKPSQTLSTCTVSGGINSGGCYWMSWIRQHPGKGLEWIGYIYSSGSTY 71

QY 61 YNPSLKSRITLSVDTSKNQFSLKNSMTAADTAVYYCARDRET-----AGFDYWGQGT 113
DB 72 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARDRIITWVRGGIPSGMDVWGQGT 131

QY 114 LVTVS 118
DB 132 TVTVS 136

RESULT 11
US-11-131-648-39
```

```
US-10-309-762-138
; Sequence 138, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudus, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-138

Query Match      87.0%; Score 553.5; DB 15; Length 118;
Best Local Similarity 89.1%; Pred. No. 3.5e-41;
Matches 106; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGGCYWMSWIRQHPGKGLEWIGYIYSSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGGCYWMSWIRQHPGKGLEWIGYIYSSGSTY 60

QY 61 YNPSLKSRITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGFDYWGQGT 119
DB 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAR--YVSGSDYWGQGT 118

RESULT 12
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudus, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-10

Query Match      86.8%; Score 552; DB 15; Length 123;
Best Local Similarity 86.2%; Pred. No. 4.9e-41;
Matches 106; Conservative 6; Mismatches 7; Indels 4; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGGCYWMSWIRQHPGKGLEWIGYIYSSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGGCYWMSWIRQHPGKGLEWIGYIYSSGSTY 60

QY 61 YNPSLKSRITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAG----FDYWGQGT 116
DB 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARAGKYVSGSLDYWGQGT 120

QY 117 VSS 119
```

Db 121 VSS 123  
RESULT 13  
US-10-309-762-140  
; Sequence 140, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
; FILE REFERENCE: ABGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309,762  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/337275  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 140  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-140  
Query Match 86.6%; Score 551; DB 15; Length 119;  
Best Local Similarity 87.4%; Pred. No. 5.8e-41;  
Matches 104; Conservative 5; Mismatches 10; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSGSTY 60  
QY 61 YNPSLKSRITLSVDTSKNQFSLKLSNSMTAADTAVYYCARDRETAG--FDYWGQGLTVTVSS 119  
Db 61 YNPSLKSRITISVDTSKNQFSLKLSNSMTAADTAVYYCARDRETAG--FDYWGQGLTVTVSS 119  
RESULT 14  
US-10-706-689-8  
; Sequence 8, Application US/10706689  
; Publication No. US20050100965A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghayur, Tariq  
; APPLICANT: Labkovsky, Boris  
; APPLICANT: Voss, Jeffrey  
; APPLICANT: Green, Larry  
; APPLICANT: Babcock, John  
; APPLICANT: Jia, Xiao-chi  
; APPLICANT: Wieler, James  
; APPLICANT: Kang, Paul  
; APPLICANT: Hegberg, Brad  
; TITLE OF INVENTION: IL-18 Binding Proteins  
; FILE REFERENCE: BBC-085  
; CURRENT APPLICATION NUMBER: US/10/706,689  
; CURRENT FILING DATE: 2003-11-12  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 8  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-706-689-8  
Query Match 86.6%; Score 551; DB 17; Length 121;  
Best Local Similarity 86.0%; Pred. No. 5.9e-41;  
Matches 104; Conservative 9; Mismatches 6; Indels 2; Gaps 1;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSGSTY 60  
Db 1 ZVQLQESGPGLVTPSPQTLSTCTVSGGSINSGGHYWTWIRQHPGKGLEWIGYIYSGSTY 60  
QY 61 YNPSLKSRITLSVDTSKNQFSLKLSNSMTAADTAVYYCARDRETAG--FDYWGQGLTVTVSS 118  
Db 61 YNPSLKSRITISVDTSKNQFSLKLSNSMTAADTAVYYCARDRETAG--FDYWGQGLTVTVSS 120  
RESULT 15  
US-10-988-360-8  
; Sequence 8, Application US/10988360  
; Publication No. US20050147610A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghayur, Tariq  
; APPLICANT: Labkovsky, Boris  
; APPLICANT: Voss, Jeffrey  
; APPLICANT: Green, Larry  
; APPLICANT: Babcock, John  
; APPLICANT: Jia, Xiao-chi  
; APPLICANT: Wieler, James  
; APPLICANT: Kang, Paul  
; APPLICANT: Hegberg, Brad  
; TITLE OF INVENTION: IL-18 Binding Proteins  
; FILE REFERENCE: BBC-085US  
; CURRENT APPLICATION NUMBER: US/10/988,360  
; CURRENT FILING DATE: 2004-11-12  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 8  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-988-360-8  
Query Match 86.6%; Score 551; DB 18; Length 121;  
Best Local Similarity 86.0%; Pred. No. 5.9e-41;  
Matches 104; Conservative 9; Mismatches 6; Indels 2; Gaps 1;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSGSTY 60  
Db 1 ZVQLQESGPGLVTPSPQTLSTCTVSGGSINSGGHYWTWIRQHPGKGLEWIGYIYSGSTY 60  
QY 61 YNPSLKSRITLSVDTSKNQFSLKLSNSMTAADTAVYYCARDRETAG--FDYWGQGLTVTVSS 118  
Db 61 YNPSLKSRITISVDTSKNQFSLKLSNSMTAADTAVYYCARDRETAG--FDYWGQGLTVTVSS 120  
Search completed: November 9, 2005, 12:43:01  
Job time : 66.1111 secs

Db 121 VSS 123  
RESULT 13  
US-10-309-762-140  
; Sequence 140, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
; FILE REFERENCE: ABGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309,762  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/337275  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 140  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-140  
Query Match 86.6%; Score 551; DB 15; Length 119;  
Best Local Similarity 87.4%; Pred. No. 5.8e-41;  
Matches 104; Conservative 5; Mismatches 10; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSGSTY 60  
QY 61 YNPSLKSRITLSVDTSKNQFSLKLSNSMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119  
Db 61 YNPSLKSRITISVDTSKNQFSLKLSNSMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119  
RESULT 14  
US-10-706-689-8  
; Sequence 8, Application US/10706689  
; Publication No. US20050100965A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghayur, Tariq  
; APPLICANT: Labkovsky, Boris  
; APPLICANT: Voss, Jeffrey  
; APPLICANT: Green, Larry  
; APPLICANT: Babcock, John  
; APPLICANT: Jia, Xiao-chi  
; APPLICANT: Wieler, James  
; APPLICANT: Kang, Paul  
; APPLICANT: Hegberg, Brad  
; TITLE OF INVENTION: IL-18 Binding Proteins  
; FILE REFERENCE: BBC-085  
; CURRENT APPLICATION NUMBER: US/10/706,689  
; CURRENT FILING DATE: 2003-11-12  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 8  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-706-689-8  
Query Match 86.6%; Score 551; DB 17; Length 121;  
Best Local Similarity 86.0%; Pred. No. 5.9e-41;  
Matches 104; Conservative 9; Mismatches 6; Indels 2; Gaps 1;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSGSTY 60  
Db 1 ZVQLQESGPGLVTPSPQTLSTCTVSGGSINSGGHYWTWIRQHPGKGLEWIGYIYSGSTY 60

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OM protein - protein search, using sw model

Run on: November 9, 2005, 12:25:58 ; Search time 12.8246 Seconds  
(without alignments)  
892.802 Million cell updates/sec

Title: US-10-660-357A-25

Perfect score: 636  
Sequence: 1 QVQLQSGPGLVKPSQTL...DRETAGFDYWGQGLTVTVSS 119

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517.5	81.4	130	2 S30534	Ig heavy chain V r
2	515	81.0	147	2 S13519	Ig heavy chain V r
3	513	80.7	140	2 I37782	Ig variable region
4	500	78.6	130	2 S31690	Ig heavy chain V r
5	499.5	78.5	122	2 S69912	Ig V-D-J region (N
6	498	78.3	135	2 S78051	Ig heavy chain pre
7	496	78.0	128	2 S31514	Ig heavy chain - h
8	494	77.7	99	2 S26801	Ig heavy chain V r
9	493	77.5	116	2 S37456	Ig mu chain - huma
10	493	77.5	121	2 S44113	Ig heavy chain V r
11	490.5	77.1	137	2 S31676	Ig heavy chain V r
12	487	76.6	146	2 S09711	Ig heavy chain V r
13	486.5	76.5	139	2 S31586	Ig heavy chain V r
14	484	76.1	123	2 S30530	Ig heavy chain V r
15	483.5	76.0	118	2 S20780	Ig heavy chain V r
16	483.5	76.0	129	2 S44114	Ig heavy chain V r
17	479	75.3	146	2 S09710	Ig heavy chain V r
18	479	75.3	155	2 S31511	Ig heavy chain - h
19	477	75.0	99	2 S26803	Ig heavy chain V r
20	477	75.0	155	2 S31512	Ig heavy chain - h
21	473.5	74.4	145	2 S78055	Ig heavy chain pre
22	472	74.2	99	2 S26802	Ig heavy chain V r
23	465	73.1	118	2 A26340	Ig heavy chain pre
24	461.5	72.6	110	2 S44110	Ig heavy chain V-D
25	461	72.5	140	2 A49045	Ig heavy chain V r
26	460	72.3	127	2 S19668	Ig heavy chain V r
27	460	72.3	139	2 S31696	Ig heavy chain V r
28	459	72.2	99	2 S26807	Ig heavy chain V r
29	459	72.2	109	2 PH1673	Ig heavy chain V r

30	458.5	72.1	117	2 E34964	Ig heavy chain pre
31	458.5	72.1	118	2 S24443	Ig heavy chain V r
32	456.5	71.8	140	2 S78052	Ig heavy chain pre
33	454	71.4	99	2 S26899	Ig heavy chain V r
34	453.5	71.3	137	2 S31585	Ig heavy chain V r
35	453	71.2	99	2 S12418	Ig heavy chain V r
36	453	71.2	135	2 S31604	Ig heavy chain V r
37	453	71.2	140	2 A24770	Ig heavy chain V r
38	451	70.9	105	2 S44125	hypothetical hybri
39	451	70.9	132	2 A38911	Ig lambda chain V
40	449	70.6	97	2 S26906	Ig heavy chain V r
41	448	70.4	97	2 PL0118	Ig heavy chain V r
42	448	70.4	116	2 B26340	Ig heavy chain V-I
43	447	70.3	97	2 S12416	Ig heavy chain pre
44	447	70.3	99	2 S12412	Ig heavy chain V r
45	447	70.3	134	2 S54906	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S30534  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Aug-1996  
C;Accession: S30534  
R;Marette, X.  
submitted to the EMBL Data Library, October 1992  
A;Reference number: S30520  
A;Accession: S30534  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-130 <VAR>  
A;Cross-references: EMBL:Z18320  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 517.5; DB 2; Length 130;  
Best Local Similarity 77.7%; Pred. No. 1.9e-39;  
Matches 101; Conservative 8; Mismatches 10; Indels 11; Gaps 1;  
  
QY 1 QVQLQSGPGLVKPSQTLSTCTVSGSINSGCYWSWIROHPKGLGIEWIYSSGSTV 60  
DB 1 QVQLQSGPGLVKPSQTLSTCTVSGSISSGSYWISWIROPAGKLEWIGRIYTSGSTN 60  
  
QY 61 YNPSLKSRITLSVDTSKNQFSLKNSMTAADTAVYYCARDR-----ETAGFDYW 109  
DB 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARDKGGFWSGYYTNSRAAPDIW 120  
  
QY 110 GQGTLYTVSS 119  
DB 121 GQGTWYTVSS 130

RESULT 2

S13519  
Ig heavy chain V region precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S13519  
R;Nortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.  
Nucleic Acids Res. 19, 673, 1991  
A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked  
A;Reference number: S13519; MUID:91187691; PMID:2011536  
A;Accession: S13519  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-147 <MOR>  
A;Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin

F;41-125/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 515; DB 2; Length 147;  
Best Local Similarity 82.6%; Pred. No. 3.6e-39;  
Matches 100; Conservative 7; Mismatches 12; Indels 2; Gaps 1;  
  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWMSWIRQHPGKLEWIGYIYSGSTY 60  
Db QQLQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWMSWIRQHPGKLEWIGYIYSGSTY 86  
QY 61 YNPSLKSRITLSVDTSKNQFSLKNSMTAADTAVYVCARDRETAG--FDYWGQGLTVTVS 118  
Db YNPSLKSRITLSVDTSKNQFSLKNSMTAADTAVYVCARDRETAG--FDYWGQGLTVTVS 146  
QY 119 S 119  
Db 147 S 147

RESULT 3  
I37782  
Ig variable region (VDJ) (clone T23-9) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
C:Accession: I37782; S25476  
R;Demaision, C.; Chastagner, P.; Theze, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A:Title: Somatic diversification in the heavy chain variable region genes expressed by B  
A:Reference number: A36876; MUID:94119917; PMID:8290556  
A:Accession: I37782  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140 <RES>  
A:Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F;46-128/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 513; DB 2; Length 140;  
Best Local Similarity 82.1%; Pred. No. 5.2e-39;  
Matches 101; Conservative 8; Mismatches 8; Indels 6; Gaps 2;  
  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWMSWIRQHPGKLEWIGYIYSGSTY 60  
Db QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWMSWIRQHPGKLEWIGYIYSGSTN 77  
QY 61 YNPSLKSRITLSVDTSKNQFSLKNSMTAADTAVYVCARDRETAG---FDYWGQGLTVT 116  
Db YNPSLKSRITLSVDTSKNQFSLKNSMTAADTAVYVCARDRETAG---FDYWGQGLTVT 137  
QY 117 VSS 119  
Db 138 VSS 140

RESULT 4  
S31690  
Ig heavy chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31690  
R;Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A:Reference number: S31585  
A:Accession: S31690  
A:Molecule type: mRNA  
A:Residues: 1-130 <CUI>  
A:Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;20-102/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 500; DB 2; Length 130;  
Best Local Similarity 78.7%; Pred. No. 7e-38;  
Matches 100; Conservative 6; Mismatches 11; Indels 10; Gaps 2;  
  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWMSWIRQHPGKLEWIGYIYSGSTY 60  
Db QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWMSWIRQHPGKLEWIGYIYSGSTN 63  
QY 61 YNPSLKSRITLSVDTSKNQFSLKNSMTAADTAVYVCARDRETA-----GFDYWGQGL 112  
Db YNPSLKSRITLSVDTSKNQFSLKNSMTAADTAVYVCARDRETA-----GFDYWGQGL 123  
QY 113 TLVTVSS 119  
Db 124 TLVTVSS 130

RESULT 5  
S69912  
Ig V-D-J region (ND) - human  
C:Species: Homo sapiens (man)  
C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
C:Accession: S69912  
R;Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.  
Leukemia 8, 1285-1289, 1994  
A:Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multi-  
A:Reference number: S69909; MUID:94335315; PMID:8057663  
A:Accession: S69912  
A>Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-122 <SAH>  
A:Cross-references: EMBL:Z33398; NID:g871347; PIDN:CAA83849.1; PID:g987460  
A>Note: the sequence of residues 108-122 and the corresponding nucleic acid sequence at-  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 78.5%; Score 499.5; DB 2; Length 122;  
Best Local Similarity 78.7%; Pred. No. 7.3e-38;  
Matches 96; Conservative 12; Mismatches 11; Indels 3; Gaps 1;  
  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWMSWIRQHPGKLEWIGYIYSGSTY 60  
Db RVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWMSWIRQHPGKLEWIGYIYSGSSY 60  
QY 61 YNPSLKSRITLSVDTSKNQFSLKNSMTAADTAVYVCARD---RETAGPDYWGQGLTVTV 117  
Db YNPSLKSRITLSVDTSKNQFSLKNSMTAADTAVYVCARD---RETAGPDYWGQGLTVTV 120  
QY 118 SS 119  
Db 121 SS 122

RESULT 6  
S78051  
Ig heavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C:Accession: S78051; S23716  
R;Harindranath, N.  
submitted to the EMBL Data Library, August 1990  
A:Reference number: S78051  
A:Accession: S78051  
A:Molecule type: mRNA  
A:Residues: 1-135 <HAR>  
A:Cross-references: EMBL:X54437; NID:g37814; PIDN:CAA38306.1; PID:g930117  
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Nockin,  
inc. Immunol. 3, 865-875, 1991  
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and  
patient.  
A:Reference number: S23716; MUID:92031262; PMID:1718404  
A:Accession: S23716  
A:Molecule type: mRNA



A;Residues: 13-111 <HAW>  
A;Cross-references: EMBL:X54437  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;1-13/Domain: signal sequence (fragment) #status predicted <SIG>  
F;14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>  
F;27-111/Domain: immunoglobulin homology <IMM>

Query Match 78.3%; Score 498; DB 2; Length 135;  
Best Local Similarity 78.0%; Pred. No. 1.1e-37;  
Matches 96; Conservative 9; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGCCYWSWIRQHPGKGLEWIGYIYSSGSTY 60  
Db 13 QQLQESGPGLVKPSQTLSTCTVSGGINSRSHYWGIRQPPGKGLEWIGSIYSGNTY 72  
|||  
QY 61 YNPFLSKRITLSVDTSKNQFSLKNSMTAADTAVYYCAR----DRETAGDYWGQGLT 116  
|||  
Db 73 FNSFLSKRVITISVDTSKNQFSLKSSVTAADTAVYYCARLGPDDYTLDGMDVWGQGLT 132  
|||

QY 117 VSS 119  
Db 133 VSS 135  
|||

RESULT 7  
S31514  
Ig heavy chain - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S31514  
R;Chastagner, P.; Dematison, C.; Theze, J.; Zouali, M.  
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto  
submitted to the EMBL Data Library, December 1992  
A;Reference number: S31509  
A;Accession: S31514  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-128 <CHA>  
A;Cross-references: EMBL:X69862; NID:g33086; PIDN:CAA49496.1; PID:g33087  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;22-106/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 496; DB 2; Length 128;  
Best Local Similarity 79.3%; Pred. No. 1.6e-37;  
Matches 96; Conservative 8; Mismatches 15; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGCCYWSWIRQHPGKGLEWIGYIYSSGSTY 60  
Db 8 QVQLQESGPGLVKPSQTLSTCTVSGGINSRSHYWGIRQHPGMALEWIAHYIYPSGSTY 67  
|||  
QY 61 YNPFLSKRITLSVDTSKNQFSLKNSMTAADTAVYYCARDRET--AGFDYWGQGLT 118  
|||  
Db 68 YNPFLSKRVITISVDTSENQFSLRSTSVTPADTAVYYCARIGNFYGFDPWGQGLT 127  
|||

QY 119 S 119  
Db 128 S 128  
|||

RESULT 8  
S26801  
Ig heavy chain V region (DP-65) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 25-Oct-1996 #text\_change 20-Jun-2000  
C;Accession: S26801; S26900  
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.  
Eur. J. Immunol. 22, 1075-1082, 1992  
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.  
A;Reference number: S26800; MUID:92201299; PMID:1348029  
A;Accession: S26801  
A;Status: preliminary

A;Molecule type: DNA  
A;Residues: 1-99 <WEN>  
A;Cross-references: EMBL:Z14237; NID:g37706; PIDN:CAA78606.1; PID:gl335372  
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of  
F;14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>  
F;27-111/Domain: immunoglobulin homology <IMM>

Query Match 77.7%; Score 494; DB 2; Length 99;  
Best Local Similarity 92.9%; Pred. No. 1.8e-37;  
Matches 92; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGCCYWSWIRQHPGKGLEWIGYIYSSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSRSHYWGIRQHPGKGLEWIGYIYSSGSTY 60  
|||  
QY 61 YNPFLSKRITLSVDTSKNQFSLKNSMTAADTAVYYCAR 99  
|||  
Db 61 YNPFLSKRVITISVDTSKNQFSLKSSVTAADTAVYYCAR 99  
|||

RESULT 9  
S37456  
Ig mu chain - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S37456  
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.  
submitted to the EMBL Data Library, September 1993  
A;Reference number: S37453  
A;Accession: S37456  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-116 <MCI>  
A;Cross-references: EMBL:X75024; NID:g404313; PIDN:CAA52932.1; PID:g758095  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;8-90/Domain: immunoglobulin homology <IMM>

Query Match 77.5%; Score 493; DB 2; Length 116;  
Best Local Similarity 81.0%; Pred. No. 2.6e-37;  
Matches 94; Conservative 8; Mismatches 8; Indels 6; Gaps 1;

QY 10 GLVKPSQTLSTCTVSGGINSGCCYWSWIRQHPGKGLEWIGYIYSSGSTYNPSPKSR 69  
|||  
Db 1 GLVKPSQTLSTCTVSGGINSRSHYWGIRQHPGKGLEWIGYIYSSGSTYNPSPKSRV 60  
|||  
QY 70 TLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGF-----DYWGQGLT 119  
|||  
Db 61 TISVDTSKNQFSLKSSVTAADTAVYYCARGSYSGYIYNDVWGKGT 116  
|||

RESULT 10  
S44113  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C;Accession: S44113  
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable  
A;Reference number: S44105  
A;Accession: S44113  
A;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-121 <HAW>

A:Cross-references: EMBL:Z31389; NID:g472967; PIDN:CAA83264.1; PID:g940524

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 77.5%; Score 493; DB 2; Length 121;  
Best Local Similarity 79.3%; Pred. No. 2.8e-37;  
Matches 96; Conservative 7; Mismatches 16; Indels 2; Gaps 1;

QY 1 OVQLOESGPGLVKPSOTLSLTCTVSGGSINSGCYWSWIRQHPGKLEWIGYIYSSGSTY 60

Db 1 OVQLOESGPGLVKPSOTLSLTCTVSGGSINSGCYWSWIRQHPGKLEWIGYIYSSGSTY 60

QY 61 YNPPLSKSRITLSVDTSKNQFSLKLSMTAADTAVYYCAR--DRETAGFDYWGQGLTVTVS 118

Db 61 YNPPLSKSRITLSVDTSKNQFSLKLSMTAADTAVYYCAR--DRETAGFDYWGQGLTVTVS 120

QY 119 S 119

Db 121 S 121

#### RESULT 11

S31676

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S31676

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A:Reference number: S31585

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Accession: S31676

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-137 <CUI>

A:Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 490.5; DB 2; Length 137;  
Best Local Similarity 81.7%; Pred. No. 5.3e-37;  
Matches 98; Conservative 7; Mismatches 12; Indels 3; Gaps 2;

QY 1 OVQLOESGPGLVKPSOTLSLTCTVSGGSINSGCYWSWIRQHPGKLEWIGYIYSSGSTY 60

Db 20 OVQLOESGPGLVKPSOTLSLTCTVSGGSINSGCYWSWIRQHPGKLEWIGYIYSSGSTN 77

QY 61 YNPPLSKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRETA-GFDYWGQGLTVTVS 119

Db 78 YNPPLSKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRETA-GFDYWGQGLTVTVS 137

#### RESULT 12

S09711

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C>Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996

C:Accession: S09711

R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.

Biochem. J. 268, 135-140, 1990

A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of

A:Reference number: S09710; MUID:90262535; PMID:2111699

A:Accession: S09711

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-146 <HUG>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-118/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 487; DB 2; Length 146;

Best Local Similarity 74.0%; Pred. No. 1.2e-36;

Matches 94; Conservative 11; Mismatches 14; Indels 8; Gaps 1;

QY 1 OVQLOESGPGLVKPSOTLSLTCTVSGGSINSGCYWSWIRQHPGKLEWIGYIYSSGSTY 60

Db 20 OVQLOESGPGLVKPSOTLSLTCTVSGGSINSGCYWSWIRQHPGKLEWIGYIYSSGSTN 79

QY 61 YNPPLSKSRITLSVDTSKNQFSLKLSMTAADTAVYYCAR-----DRETAGFDYWGQ 112

Db 80 YNPPLSKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARVSRISQSYMYMDVWGK 139

QY 113 TLTVSS 119

Db 140 TLTVSS 146

#### RESULT 13

S31586

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S31586

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A:Reference number: S31585

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Accession: S31586

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-139 <CUI>

A:Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 486.5; DB 2; Length 139;  
Best Local Similarity 79.5%; Pred. No. 1.2e-36;  
Matches 97; Conservative 8; Mismatches 12; Indels 5; Gaps 2;

QY 1 OVQLOESGPGLVKPSOTLSLTCTVSGGSINSGCYWSWIRQHPGKLEWIGYIYSSGSTY 60

Db 20 OVQLOESGPGLVKPSOTLSLTCTVSGGSINSGCYWSWIRQHPGKLEWIGYIYSSGSTN 77

QY 61 YNPPLSKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDR---ETAGFDYWGQGLTVTV 117

Db 78 YNPPLSKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDR---ETAGFDYWGQGLTVTV 137

QY 118 SS 119

Db 138 SS 139

#### RESULT 14

S30530

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C>Date: 03-Mar-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996

C:Accession: S30530

R:Mariette, X.

submitted to the EMBL Data Library, October 1992

A:Reference number: S30520

A:Accession: S30530

A:Molecule type: mRNA

A:Residues: 1-123 <MAR>

A:Cross-references: EMBL:Z18316

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.1%; Score 484; DB 2; Length 123;

Best Local Similarity 77.4%; Pred. No. 1.8e-36;  
Matches 96; Conservative 10; Mismatches 12; Indels 6; Gaps 2;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGCCYWSIRQHPGKGLEWIGYIYSSGSTY 60  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGCCYWSIRQHPGKGLEWIGYIYSSGSTY 59  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 61 YNPSLKSRLTSLVDTSKNQFSLKLNMTAADTAVYYCARDRETAG-----FDYWGQGTLLV 115  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 60 YNPSLKSRLTSLVDTSKNQFSLKLNMTAADTAVYYCARDRETAG-----FDYWGQGTLLV 119  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 116 TVSS 119  
|||||  
Db 120 TVSS 123  
|||||

## RESULT 15

S20780  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C;Accession: S20780  
R;Mortari, F.; Wang, J.; Schroeder, H.W.  
submitted to the EMBL Data Library, April 1992  
A;Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.  
A;Reference number: S20764  
A;Accession: S20780  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-118 <MOR>  
A;Cross-references: EMBL:Z11958; NID:G33893; PID:CAA78015.1; PID:G33894  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 483.5; DB 2; Length 118;  
Best Local Similarity 79.2%; Pred. No. 1.9e-36;  
Matches 95; Conservative 10; Mismatches 12; Indels 3; Gaps 2;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGCCYWSIRQHPGKGLEWIGYIYSSGSTY 60  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGCCYWSIRQHPGKGLEWIGYIYSSGSTY 58  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 61 YNPSLKSRLTSLVDTSKNQFSLKLNMTAADTAVYYCARDRETAGFDYWGQGTLLVTVSS 119  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 59 YNPSLKSRLTSLVDTSKNQFSLKLNMTAADTAVYYCARDRETAGFDYWGQGTLLVTVSS 118  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Search completed: November 9, 2005, 13:08:04  
Job time : 13.8246 secs

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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:46:52 ; Search time 61.4386 Seconds  
(without alignments)  
991.843 Million cell updates/sec

Title: US-10-660-357A-25

Perfect score: 636

Sequence: 1 QVQLQESGPGLVKPSQTL...DRETAGFDYWGQGLTVTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	522	82.1	476	2 Q6GMX1	Q6gm1 homo sapien
2	507.5	79.8	465	2 Q6GMX6	Q6gm6 homo sapien
3	503.5	79.2	478	2 Q72379	Q72379 homo sapien
4	490.5	77.1	477	2 Q6GMX7	Q6gm7 homo sapien
5	489.5	77.0	620	2 Q96EY0	Q96ey0 homo sapien
6	486	76.4	119	2 Q9UL73	Q9ul73 homo sapien
7	476.5	74.9	150	2 Q95973	Q95973 homo sapien
8	475.5	74.8	496	2 Q96KX8	Q96kx8 homo sapien
9	466.5	73.3	576	2 Q6P418	Q6p418 homo sapien
10	461	72.5	492	2 Q72374	Q72374 homo sapien
11	457.5	71.9	130	2 Q81ZD7	Q81zd7 homo sapien
12	455	71.5	139	2 Q86SX2	Q86sx2 homo sapien
13	444	69.8	129	1 HV2F_HUMAN	P01824 homo sapien
14	432.5	68.0	122	2 Q9UL75	Q9ul75 homo sapien
15	429	67.5	478	2 Q6NVH3	Q6nyh3 homo sapien
16	425	66.8	595	2 Q8WUX4	Q8wux4 homo sapien
17	425	66.8	597	2 Q6GMX5	Q6gm5 homo sapien
18	425	66.8	597	2 Q9BU10	Q9bul0 homo sapien
19	425	66.8	625	2 Q96AA6	Q96aa6 homo sapien
20	419	65.9	597	2 Q9BQB8	Q9bb8 homo sapien
21	417.5	65.6	146	1 HV2I_HUMAN	P06331 homo sapien
22	414.5	65.2	473	2 Q8TC63	Q8tc63 homo sapien
23	409	64.3	479	2 Q99M22	Q99m22 mus musculus
24	407.5	64.1	136	2 Q6LBQ5	Q6lbq5 mus musculus
25	407	64.0	137	1 HV46_MOUSE	Q65211 mus musculus
26	407	64.0	262	2 Q65211	Q65211 mus musculus
27	406	63.8	113	1 HV47_MOUSE	P01823 mus musculus
28	405	63.7	117	1 HV2C_HUMAN	P01825 mus musculus
29	387	60.8	476	2 Q6MZX7	Q6mzx7 homo sapien
30	385	60.5	116	2 Q723Y6	Q723y6 homo sapien
31	369.5	58.1	482	2 Q91X92	Q91x92 mus musculus

#### RESULT 1

ID	Q6GMX1	PRELIMINARY;	PRT;	476 AA.
AC	Q6GMX1;			
DT	05-JUL-2004 (TrEMBLrel. 27, Created)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
ON	NCBI_TaxID=9606;			
RX	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Splicein;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,			
RA	Blakesley R.W., Touchman J.W., Shevchenko Y., Bouffard G.G.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Splicein;			
RA	Strausberg R.;			
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC073773; AAH73773.1; -.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG.CI.			
DR	InterPro; IPR003006; IG.MHC.			
DR	InterPro; IPR003596; IG.V.			
DR	Pfam; PF07654; C1-set; 3.			
DR	Pfam; PF00047; IG; 4.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00409; IG; 1.			
DR	SMART; SM00406; IG; 1.			
DR	SMART; PS00835; IG LIKE; 4.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.			

#### ALIGNMENTS

32	369	58.0	117	1 HV62_MOUSE	P18533 mus musculus
33	366.5	57.6	116	1 HV60_MOUSE	P18531 mus musculus
34	365	57.4	144	1 HV43_MOUSE	P01819 mus musculus
35	361.5	56.8	116	1 HV61_MOUSE	P18532 mus musculus
36	361.5	56.8	121	2 Q99NG4	Q99ng4 mus musculus
37	357	56.1	121	2 Q9UL96	Q9ul96 homo sapien
38	353.5	55.6	118	2 Q811U5	Q811u5 mus musculus
39	344.5	54.2	135	1 HV02_XENLA	P20957 xenopus lae
40	339.5	53.4	118	2 Q9UL72	Q9ul72 homo sapien
41	331	52.0	119	1 HV2C_HUMAN	P01816 homo sapien
42	331	52.0	466	2 Q6IN78	Q6in78 homo sapien
43	326	51.3	470	2 Q6PUA4	Q6pu44 homo sapien
44	325	51.1	118	2 Q9UL74	Q9ul74 homo sapien
45	323	50.8	125	1 HV2D_HUMAN	P01817 homo sapien

```
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match      82.1%; Score 522; DB 2; Length 476;
Best Local Similarity 80.3%; Pred. No. 1.1e-45;
Matches 102; Conservative 9; Mismatches 8; Indels 8; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCCYWSWIRQHPGKGLEWIGYIYSGSTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISGGDYWYWSWIRQHPGKGLEWIGYIYSGSTY 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 YNPSLKSRITLSDTSKNQFSLKNSMTAADTAATVAVYCARD-----RETA--CFDYWGOG 112
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 YNPSLKSRVTSIDTSKNQFSLKNSVTAADTAATVAVYCARDVWGVSFRSWAIDGFNIWGOG 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 113 TLTVTSS 119
   |||||
Db 140 TMTVTSS 146
   |||||

RESULT 2
Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Primary B-Cells;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]

SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00407; Ig; 4.
DR SMART; SM00409; IG1; 3.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.

KW Hypothetical protein.
SQ SEQUENCE 478 AA; 51620 MW; 4AFCBS41F3217CAI CRC64;

Query Match      79.2%; Score 503.5; DB 2; Length 478;
Best Local Similarity 79.2%; Pred. No. 8.9e-44;
Matches 95; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCCYWSWIRQHPGKGLEWIGYIYSGSTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 19 QVQLQESGPGLVKPSQTLSTCTVSGGSIGSGDYFWSWIRQHPGKLEWYIYSGSTY 78
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 YNPSLKSRITLSDTSKNQFSLKNSMTAADTAATVAVYCARDRET-AGFDYWGOGTLTVTSS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 79 YNPESLSRLSIDTSKNQFSLKNSLTAAADTAATVAVYCARDVGLGTAFDIWGQGTVTVTSS 138
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
Q6GMX7 PRELIMINARY; PRT; 477 AA.
AC Q6GMX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

RP	SEQUENCE FROM N.A.
RQ	TISSUE=Primary B-Cells;
RX	MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klauster R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Alcega S.F., Zeeberg H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Hopkins R.F., Jordan K., Farmer A.A., Rubin G.M., Hong L.,
RA	Diatchenko L., Marsina K., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Stapleton M., Soares M.B., Tonello M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA	Bosak S.A., McEwan K.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Vallatou D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahney J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RL	and mouse cDNA sequences";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[2]
RC	SEQUENCE FROM N.A.
RC	TISSUE=Primary B-Cells;
RC	Strausberg R.;
RL	Submitted (JUL-2001) to the ENBL/GenBank/DDBJ databases.
DR	ENBL; BC011857; AAH11857.2; -
DR	PfR; S15590; S15590.
DR	HSP; P01820; IG7J.
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig-cl.
DR	InterPro; IPR003006; Ig-MHC.
DR	InterPro; IPR003596; Ig v.
DR	Pfam; PF07654; Cl-set; 4.
DR	SMART; SMO0409; IG; 2.
DR	SMART; SMO0407; IGcl; 4.
DR	SMART; SMO0406; IGv; 1.
DR	PROSITE; PS00835; IG LIKE; 5.
DR	PROSITE; PS00290; IG MHC; UNKNOWN 3.
SQ	SEQUENCE 620 AA; 68125 MW; 950A1AA46E8FF27B CRC64;
Query Match 77.0%; Score 489.5; DB 2; Length 620;	
Best Local Similarity 80.3%; Pred. No. 3.4e-42;	
Matches 98; Conservative 8; Mismatches 11; Indels 5; Gaps 2	
QY	1 QVQLQESGPGLVKPSTLSLTCTVSGSINSGCCWISIRHPGKLEWIGIYSSGSTY 60
Db	27 QVQLQESGPGLVKPSETLSLTCTVSGSISS--YYWSIRQPAGKLEWIGRIYTSNSTN 84
:     :     :     :     :     :     :     :     :     :	
QY	61 YNPFLSKSRITLSVDTSKNQPSLKLNSMTAADTAVYYCAR---DRETAGFDYWGQGTLTV 117
Db	85 YNPFLSKSRVTMSVDTSKNQPSLKLSSVTAADTAVYYCASQPWELPTVLGYFGWGQGLTV 144
:     :     :     :     :     :     :     :     :	
QY	118 SS 119
Db	145 SS 146
RESULT 6	
Q9UL73	ID Q9UL73 PRELIMINARY; PRT; 119 AA.
AC	Q9UL73;
DT	01-MAY-2000 (TrEMBLrel. 13, Created)
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Caranthropi; Homidae; Homo

```

OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035041; AAD56277.1; -.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EA0BE CRC64;

Query Match 76.4%; Score 486; DB 2; Length 119;
Best Local Similarity 81.0%; Pred. No. 1.2e-42;
Matches 98; Conservative 5; Mismatches 14; Indels 4; Gaps 2;

QY 1 OVQLOESGGLVKPSTLCTCTVSGGSINSGCCYWSWIROHPKGLWIGIYSSGSTY 60
DB 1 OVQLOESGGLVKPSETLSCTVSGGSISSTYYWGWIRPPKGLWIGIYSSGSTY 58
QY 61 YNPGLSKSRITLSVDTSKNOFSLKNSMTAADTAVVYCARDRETAG--PDYWGQGLTVTVS 118
DB 59 YTPSLKSRVTISVDRSKNOFSLKLTSLTAADTAVVFCARLSNWNWGPYFDYWGQGLTVTVS 118
QY 119 S 119
DB 119 S 119

RESULT 7
O95973 PRELIMINARY; PRT; 150 AA.
AC O95973;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE V4 heavy chain variable region precursor (Fragment).
DE Name=IGM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103795; AAC79084.1; -.
DR PIR; S31673; S31673.
DR HSSP; S78056; S78056.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 >150 V4 heavy chain variable region.
FT NON_TER 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04939AA7C9 CRC64;

Query Match 74.9%; Score 476.5; DB 2; Length 150;
Best Local Similarity 75.6%; Pred. No. 1.6e-41;
Matches 90; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

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QY 1 OVQLOESGGLVKPSTLCTCTVSGGSINSGCCYWSWIROHPKGLWIGIYSSGSTY 60
DB 20 QLOQESGGLVKPSETLSCTVSGGSISSTYYWGWIRPPKGLWIGIYSSGSTY 79
QY 61 YNPGLSKSRITLSVDTSKNOFSLKNSMTAADTAVVYCARDRETAGFDYWGQGLTVTVSS 119
DB 80 YNPGLSKSRVTISVDTSKNOFSLKNSMTAADTAVVYCAR-LGNGAFDFWGHGTMVTVSS 137

RESULT 8
O96KX8 PRELIMINARY; PRT; 496 AA.
AC O96KX8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC27165 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klautner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hoieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., roshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2];
RP SEQUENCE FROM N.A.
RC TISSUE=lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016369; AAHL6369.1; -.
DR HSSP; P01876; IOWO.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 74.8%; Score 475.5; DB 2; Length 496;
Best Local Similarity 74.2%; Pred. No. 7.6e-41;
Matches 92; Conservative 8; Mismatches 19; Indels 5; Gaps 1;

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Qy 116 TVSS 119
Db 140 TVSS 143
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RESULT 9
Q6P418 PRELIMINARY; PRT; 576 AA.
AC Q6P418;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGH domain protein.
GN Name=IGH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Frange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -
DR HSP; P01820; 1A7N.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 576 AA; 63363 MW; FB97C949D720F1E CRC64;

Query Match 73.3%; Score 466.5; DB 2; Length 576;
Best Local Similarity 77.7%; Pred. No. 7.9e-40;
Matches 94; Conservative 7; Mismatches 17; Indels 3; Gaps 2;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYKSWIRQHPKGLGWIGYISGSGTY 60
Db 27 QVQLQESGPGLVKPSQTLSTCTVSGGSINSSN-WWSVWRQPPKGLGWIGYISGSGTN 85
|||||
|||||

Qy 61 YNPSLKSRLTSLVDTSKNPFSLKNSMTAADTAVYICAR--DRETAGFDYWGQGLTVTS 118
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RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035039; AAD56275.1; -.
DR PIR; D36006; D36006.
DR PIR; PH1674; PH1674.
DR PIR; PLO117; PLO117.
DR PIR; PLO160; PLO160.
DR PIR; PS0089; PS0089.
DR PIR; PS0090; PS0090.
DR PIR; PS0091; PS0091.
DR PIR; S12433; S12433.
DR PIR; S24700; S24700.
DR HSP; P01820; I07J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13719 MW; 56CB0612586A6529 CRC64;

Query Match 68.0%; Score 432.5; DB 2; Length 122;
Best Local Similarity 68.9%; Pred. No. 4.7e-37;
Matches 84; Conservative 12; Mismatches 23; Indels 3; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGGCYMSWIRQHPGKGLEWIGYIYSSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTCAISGDSVSSNSAANNWIRQSPSRGLEWIGRYYSKWY 60
QY 61 --YNPSLKSRITLSVDTSKNQFSLKNSMTAATAVYYCARDRETAG-FDYWGQGLTVTV 117
DB 61 NDYRVSVKSRITINPTDSKQFSLQNSVTPEDTAVYYCARDLELLQPDYWGQGLTVTV 120
QY 118 SS 119
DB 121 SS 122

RESULT 15
Q6NYH3 PRELIMINARY; PRT; 478 AA.
AC Q6NYH3
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
```

```
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL EMBL; BC066594; AAH66594.1; -.
DR HSP; P01820; I07N.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IGV; 4.
DR SMART; SM00407; IGV; 3.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein_
SQ SEQUENCE 478 AA; 51856 MW; 5F8B98F60F077256 CRC64;

Query Match 67.5%; Score 429; DB 2; Length 478;
Best Local Similarity 69.4%; Pred. No. 5e-36;
Matches 84; Conservative 16; Mismatches 17; Indels 4; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGGCYMSWIRQHPGKGLEWIGYIYSSGSTY 60
DB 20 QVDLQESGPGLVKPSQTLSTCTCSVSGDSTAS--YYWSWIRKSPQGGMEWIGYIPHSQTL 77
QY 61 YNPISLKRITLSVDTSKNQFSLKNSMTAATAVYYCAR--DRETAGFDYWGQGLTVTVS 118
DB 78 YNPISLKRITLSVDTSKNQFSLKNSMTAATAVYYCAR--DRETAGFDYWGQGLTVTVS 137
QY 119 S 119
DB 138 S 138

Search completed: November 9, 2005, 13:05:50
Job time : 62.4386 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2005, 11:43:32 ; Search time 73.985 Seconds  
(without alignments)  
627.306 Million cell updates/sec

Title: US-10-660-357A-29

Perfect score: 629

Sequence: 1 QVQLVESGGGVQPGKSLRL.....FGVVIDYGMVMDVQGGTTVT 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	629	100.0	120	7	Adc99800 Anti-huma
2	629	100.0	120	7	AdD05404 Anti-MUC1
3	629	100.0	120	7	Adf09842 Human ant
4	580.5	92.3	123	8	AdS84372 Human ant
5	580.5	92.3	123	8	Adr68514 Anti-EPO-
6	577.5	91.8	123	8	AdS84396 Human ant
7	577.5	91.8	123	8	Adr68538 Anti-EPO-
8	576.5	91.7	123	8	AdS84376 Human ant
9	576.5	91.7	123	8	AdS84368 Human ant
10	576.5	91.7	123	8	Adr68518 Anti-EPO-
11	576.5	91.7	123	8	Adr68510 Anti-EPO-
12	576	91.6	118	5	AaM51167 Human DP-
13	571.5	90.9	144	6	Aae37209 Human AB-
14	571	90.8	122	8	Adp22128 Human ant
15	571	90.8	126	7	Adk18593 Anti-huma
16	571	90.8	126	7	Adk18785 Anti-huma
17	571	90.8	126	7	Adk18858 Anti-huma
18	571	90.8	126	8	AdL25404 Human mAb
19	569.5	90.5	121	7	AdP03979 Murine-ex
20	569.5	90.5	121	7	AdP03962 Murine-ex
21	569	90.5	126	7	AdP03963 Murine-ex
22	567.5	90.2	451	3	Aay93734 The heavy
23	567.5	90.2	451	6	Aae35889 Human 11.
24	565.5	89.9	125	8	Adp22316 Human ant
25	565	89.8	121	8	Adp47227 Human pho

ALIGNMENTS

RESULT 1

ADC99800

ID ADC99800 standard; protein; 120 AA.

XX AC ADC99800;

XX DT 01-JAN-2004 (first entry)

XX DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 29.

XX KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.

XX OS Homo sapiens.

XX PN WO2003057838-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041581.

XX PR 28-DEC-2001; 2001US-0346299P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J;

XX DR WPI; 2003-587113/55.

XX N-PSDB; ADC99802.

XX PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
or condition associated with expression of MUC18 in a patient, e.g.  
tumors, cancers, and other malignancies.

XX PS Claim 1; SEQ ID NO 29; 78pp; English.

XX CC The invention relates to a novel isolated monoclonal antibody comprising  
a heavy or light chain amino acid or a heavy or light chain variable  
domain where the antibody binds to MUC18. The monoclonal antibody of the  
invention demonstrates cytostatic activity and may be useful for treating  
a disease or condition associated with the expression of MUC18 on the  
cell surface such as tumours, specifically melanoma, oesophageal,  
pancreatic or colorectal tumours, carcinomas, particularly cervical  
carcinomas and cervical intraepithelial neoplasia and cancers including  
colorectal, breast or lung cancer, as well as other malignancies. The  
current sequence is that of the anti-human MUC18 monoclonal antibody

CC	heavy chain protein of the invention.	Best Local Similarity 100.0%; Pred. No. 3.3e-47; Mismatches 0; Indels 0; Gaps 0;
XX	Sequence 120 AA;	Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SQ	Query Match	Score 629; DB 7; Length 120;
	Best Local Similarity 100.0%; Pred. No. 3.3e-47; Mismatches 0; Indels 0; Gaps 0;	
	Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWAVISYDGSNKYY 60	
Db	1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWAVISYDGSNKYY 60	
QY	61 ADSVKGRFTISRDNKNTLYLQMNSLRADTAIVYCARSI FGWIDYGMVWGQGTITVTV 120	
Db	61 ADSVKGRFTISRDNKNTLYLQMNSLRADTAIVYCARSI FGWIDYGMVWGQGTITVTV 120	
RESULT 2		
ADD05404	ID ADD05404 standard; protein; 120 AA.	
XX	AC ADD05404;	
XX	DT 01-JAN-2004 (first entry)	
XX	DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 29.	
XX	KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;	
XX	KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.	
OS	Homo sapiens.	
XX	WO2003057006-A2.	
XX	17-JUL-2003.	
XX	26-DEC-2002; 2002WO-US041582.	
XX	28-DEC-2001; 2001US-0346460P.	
XX	(ABGE-) ABGENIX INC.	
PI	Gudas J, Bar-Eli M;	
XX	WPI; 2003-577496/54.	
DR	N-PSDB; ADD05406.	
XX	Use of monoclonal antibodies against MUC18 antigen, for diagnosing and	
PT	treating tumors, inhibiting tumor growth, inhibiting cell invasion	
PT	associated with melanoma, or increasing survival of an animal having a	
PT	metastatic tumor.	
XX	Claim 1; SEQ ID NO 29; 87pp; English.	
XX	The invention relates to a novel monoclonal antibody used for inhibiting	
CC	tumour growth in an animal. The tumour inhibition process comprises	
CC	selecting an animal in need of treatment for a tumour, providing a	
CC	monoclonal antibody comprising a heavy chain amino acid, where the	
CC	antibody consists of any one of 10 fully defined sequences of 117-123	
CC	amino acids given in the specification, and where the monoclonal antibody	
CC	binds MUC18, and contacting the tumour with the antibody resulting in	
CC	inhibited proliferation of the cells. The monoclonal antibody has	
CC	cytostatic and can be used in the production of a vaccine. The monoclonal	
CC	antibodies against the MUC18 antigen are useful for diagnosing and	
CC	treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or	
CC	tumour metastasis), inhibiting cell invasion associated with melanoma, or	
CC	increasing survival of an animal having a metastatic tumour. This	
CC	sequence represents an anti-MUC18 antibody heavy chain, variable region,	
CC	protein of the invention.	
XX	Sequence 120 AA;	
SQ	Query Match	Score 629; DB 7; Length 120;
	Best Local Similarity 100.0%; Pred. No. 3.3e-47; Mismatches 0; Indels 0; Gaps 0;	
	Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWAVISYDGSNKYY 60	
Db	1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWAVISYDGSNKYY 60	
QY	61 ADSVKGRFTISRDNKNTLYLQMNSLRADTAIVYCARSI FGWIDYGMVWGQGTITVTV 120	
Db	61 ADSVKGRFTISRDNKNTLYLQMNSLRADTAIVYCARSI FGWIDYGMVWGQGTITVTV 120	
RESULT 3		
ADF09842	ID ADF09842 standard; protein; 120 AA.	
XX	AC ADF09842;	
XX	DT 12-FEB-2004 (first entry)	
XX	DE Human anti-MUC18 monoclonal antibody heavy chain #8.	
XX	KW cell proliferation inhibition; MUC18 tumour antigen;	
XX	anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;	
XX	carcinoma; cancer; malignancy; heavy chain; human.	
OS	Homo sapiens.	
XX	WO2003057837-A2.	
XX	17-JUL-2003.	
XX	26-DEC-2002; 2002WO-US041580.	
XX	28-DEC-2001; 2001US-0346414P.	
XX	(ABGE-) ABGENIX INC.	
XX	Gudas J;	
XX	WPI; 2003-598367/56.	
DR	N-PSDB; ADF09844.	
XX	Inhibiting cell proliferation associated with expression of MUC18 tumor	
PT	antigen, involves incubating and inhibiting cell by administering anti-	
PT	MUC18 monoclonal antibody.	
XX	Claim 1; SEQ ID NO 29; 83pp; English.	
XX	The invention comprises a method for inhibiting cell proliferation	
CC	associated with expression of MUC18 tumour antigen. The method involves	
CC	administering anti-MUC18 monoclonal antibody. The method of the invention	
CC	is useful for inhibiting cell (e.g. melanoma or tumour cell)	
CC	proliferation associated with the expression of MUC18 tumour antigen, the	
CC	method is preferably useful for inhibiting tumour metastasis. The method	
CC	is useful for inhibiting cell proliferation in patients with tumours,	
CC	carcinomas, cancer and other malignancies. The present amino acid	
CC	sequence represents a heavy chain from an MUC18 tumour antigen-specific	
CC	monoclonal antibody.	
XX	Sequence 120 AA;	
SQ	Query Match	Score 629; DB 7; Length 120;
	Best Local Similarity 100.0%; Pred. No. 3.3e-47; Mismatches 0; Indels 0; Gaps 0;	
	Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWAVISYDGSNKYY 60	
Db	1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWAVISYDGSNKYY 60	
QY	61 ADSVKGRFTISRDNKNTLYLQMNSLRADTAIVYCARSI FGWIDYGMVWGQGTITVTV 120	
Db	61 ADSVKGRFTISRDNKNTLYLQMNSLRADTAIVYCARSI FGWIDYGMVWGQGTITVTV 120	

## RESULT 4

ADS84372 standard; protein; 123 AA.

XX ADS84372;

DT 18-NOV-2004 (first entry)

XX Human anti-EPO-R antibody heavy chain variable region SEQ ID NO:11.

XX human; erythropoietin receptor; EPO receptor;  
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;  
 KW antianemic; neuroprotective; vulnary; gene therapy; aplasia; anaemia;  
 KW wound healing; neural cell damage protection;  
 KW neural tissue damage protection; brain injury; spinal cord injury;  
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.

XX Homo sapiens.

XX WO2004035603-A2.

XX 29-APR-2004.

XX 14-OCT-2003; 2003WO-US032243.

XX 14-OCT-2002; 2002US-00269711.

XX 10-OCT-2003; 2003US-00684109.

XX (ABBO ) ABBOTT LAB.

XX Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;

XX WPI; 2004-348433/32.

XX N-PSDB; ADS84371.

XX New antibodies that bind to or activate an endogenous human  
 PT erythropoietin receptor, useful for diagnosing, preventing or treating  
 PT disorders associated with dysfunctional erythropoietin receptor, e.g.  
 PT anemia.

XX Claim 9; SEQ ID NO 11; 192pp; English.

XX The present invention describes an antibody or its fragment that binds to  
 CC or activates an endogenous activity of a human erythropoietin (EPO)  
 CC receptor in a mammal, but does not interact with a peptide having a  
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
 CC methods of modulating or activating an endogenous activity of a human EPO  
 CC receptor in a mammal, comprising administering to the mammal a  
 CC therapeutic amount of the above antibody or its fragment to modulate or  
 CC activate the receptor; (2) a method of treating a mammal suffering from  
 CC aplasia, comprising administering to the mammal a therapeutic amount of  
 CC the above antibody or its fragment to modulate or activate the receptor;  
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
 CC an isolated and purified polynucleotide sequence, and their fragments,  
 CC complements and degenerate codon equivalents; and (5) an isolated and  
 CC purified amino acid sequence, and their fragments. The EPO receptor  
 CC binding antibody has antianemic, neuroprotective and vulnary  
 CC activities, and can be used in gene therapy. The compositions and methods  
 CC from the present invention can be used for modulating an endogenous  
 CC activity of a human EPO receptor or for treating mammals suffering from  
 CC aplasia or anaemia. They may also be used for identifying mammals having  
 CC a dysfunctional EPO receptor. The composition may also be used in  
 CC promoting wound healing or in protecting against neural cell and/or  
 CC tissue damage resulting from brain/spinal cord injury, stroke and the  
 CC like. The present sequence represents a human anti-EPO-R antibody heavy  
 CC chain variable region, which is given in the exemplification of the  
 CC present invention.

XX Sequence 123 AA;

CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in  
 CC

Query Match 92.3%; Score 580.5; DB 8; Length 123;  
 Best Local Similarity 93.4%; Pred. No. 5.7e-43;  
 Matches 113; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60  
 DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARSIFFG-VVTDYGHVQGGTTVT 119  
 DB 61 ADSVKGRFTISRDNKNTLYLQWNSLRVEDTAIVYCARHGGRVYVDYGMVQGGTTVT 120

QY 120 V 120

DB 121 V 121

## RESULT 5

ADR68514

XX ID ADR68514 standard; protein; 123 AA.

XX AC ADR68514;

XX 02-DEC-2004 (first entry)

XX Anti-EPO-R-antibody heavy chain variable region seqid 11.

XX antianemic; respiratory; vulnary; gene therapy; vaccine;  
 KW erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;  
 KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;  
 KW wound healing; neural cell damage; tissue damage; brain injury;  
 KW spinal cord injury; stroke; anti-EPO-R-antibody; heavy chain;  
 KW variable region.

XX Homo sapiens.

XX US2004175379-A1.

XX 09-SEP-2004.

XX 10-OCT-2003; 2003US-00684109.

XX 14-OCT-2002; 2002US-0418031P.

XX (DEVV/) DEVRIES P J.

XX (OSTR/) OSTROW D H.

XX (REIL/) REILLY E B.

XX (GREE/) GREEN L L.

XX (WIEL/) WIELER J.

XX Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;

XX WPI; 2004-661369/64.

XX N-PSDB; ADR68513.

XX New antibody or its antibody fragment that activates an endogenous  
 PT activity or is capable of binding to a human erythropoietin receptor in a  
 PT mammal, useful for treating a mammal suffering aplasia or anemia.

XX Claim 9; SEQ ID NO 11; 156pp; English.

XX The invention describes an antibody or its fragment that activates an  
 CC endogenous activity or capable of binding to a human erythropoietin  
 CC receptor in a mammal, or that comprises at least one heavy or light chain  
 CC variable region having a sequence comprising 116 or 107 amino acids (SEQ  
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not  
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also  
 CC given in the specification. Also described are: a method of activating or  
 CC modulating an endogenous activity of a human erythropoietin receptor in a  
 CC mammal; a pharmaceutical composition comprising a therapeutic amount of  
 CC an antibody or antibody fragment above and a pharmaceutical excipient;  
 CC isolated and purified polynucleotide sequence selected from 28 sequences  
 CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in

CC the specification, and their fragments, complements, and degenerate codon  
 CC equivalents; and an isolated and purified amino acid sequence selected  
 CC from 39 sequences comprising 27-52 amino acids (odd SEQ ID NOs between  
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or  
 CC their fragments. The antibody or its antibody fragment that activates or  
 CC modulates the activity of the receptor is useful in a method of treating  
 CC a mammal suffering aplasia or anaemia. The antibodies are also useful for  
 CC treating disorders characterised by decreased or subnormal levels of  
 CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue  
 CC hypoxia and/or diseases characterised by inadequate blood circulation or  
 CC reduced blood flow. They are also useful for promoting wound healing or  
 CC for protecting against neural cell and/or tissue damage, resulting from  
 CC brain/spinal cord injury, stroke and the like. The antibodies are also  
 CC useful for identifying or diagnosing mammals having dysfunctional  
 CC erythropoietin receptor. This is the amino acid sequence of an anti-EPO-R  
 CC -antibody heavy chain variable region.

XX Sequence 123 AA;

Query Match 92.3%; Score 580.5; DB 8; Length 123;  
 Best Local Similarity 93.4%; Pred. No. 5.7e-43;  
 Matches 113; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWAVISYDGSNKYY 60  
 DB 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYGMHWVRQAPGKLEWAVISYDGSNKYY 60  
 QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRVEDTAVYICARSIFG-VVIDYGMVWGOGTTVT 119  
 DB 61 ADSVKGRFTISRDNKNTLYLQMNSLRVEDTAVYICARDHGGRVYVDYGMVWGOGTTVT 120  
 QY 120 V 120  
 DB 121 V 121

RESULT 6  
 ADS84396

ID ADS84396 standard; protein; 123 AA.

AC ADS84396;

DT 18-NOV-2004 (first entry)

DE Human anti-EPO-R antibody heavy chain variable region SEQ ID NO:35.

XX human; erythropoietin receptor; EPO receptor;  
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;  
 KW antianaemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia;  
 KW wound healing; neural cell damage protection;  
 KW neural tissue damage protection; brain injury; spinal cord injury;  
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.

XX Homo sapiens.

XX WO2004035603-A2.

XX 29-APR-2004.

XX 14-OCT-2003; 2003WO-US032243.

XX 14-OCT-2002; 2002US-00269711.

PR 10-OCT-2003; 2003US-00684109.

XX (ABBO ) ABBOTT LAB.

XX Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;

XX WPI; 2004-348433/32.

DR N-P8DB; ADS84395.

XX New antibodies that bind to or activate an endogenous human  
 PT erythropoietin receptor, useful for diagnosing, preventing or treating

PT disorders associated with dysfunctional erythropoietin receptor, e.g.  
 PT anemia.

XX Claim 9; SEQ ID NO 35; 192pp; English.

CC The present invention describes an antibody or its fragment that binds to  
 CC or activates an endogenous activity of a human erythropoietin (EPO)  
 CC receptor in a mammal, but does not interact with a peptide having a  
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
 CC methods of modulating or activating an endogenous activity of a human EPO  
 CC receptor in a mammal, comprising administering to the mammal a  
 CC therapeutic amount of the above antibody or its fragment to modulate or  
 CC activate the receptor; (2) a method of treating a mammal suffering from  
 CC aplasia, comprising administering to the mammal a therapeutic amount of  
 CC the above antibody or its fragment to modulate or activate the receptor;  
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
 CC an isolated and purified polynucleotide sequence, and their fragments;  
 CC complements and degenerate codon equivalents; and (5) an isolated and  
 CC purified amino acid sequence, and their fragments. The EPO receptor  
 CC binding antibody has antianaemic, neuroprotective and vulnerary  
 CC activities, and can be used in gene therapy. The compositions and methods  
 CC from the present invention can be used for modulating an endogenous  
 CC activity of a human EPO receptor or for treating mammals suffering from  
 CC aplasia or anaemia. They may also be used for identifying mammals having  
 CC a dysfunctional EPO receptor. The composition may also be used in  
 CC promoting wound healing or in protecting against neural cell and/or  
 CC tissue damage resulting from brain/spinal cord injury, stroke and the  
 CC like. The present sequence represents a human anti-EPO-R antibody heavy  
 CC chain variable region, which is given in the exemplification of the  
 CC present invention.

XX Sequence 123 AA;

Query Match 91.8%; Score 577.5; DB 8; Length 123;  
 Best Local Similarity 92.6%; Pred. No. 1e-42;  
 Matches 112; Conservative 1; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWAVISYDGSNKYY 60  
 DB 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYGMHWVRQAPGKLEWAVISYDGSNKYY 60  
 QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRVEDTAVYICARSIFG-VVIDYGMVWGOGTTVT 119  
 DB 61 ADSVKGRFTISRDNKNTLYLQMNSLRVEDTAVYICAKDHGRVYVDYGMVWGOGTTVT 120  
 QY 120 V 120  
 DB 121 V 121

RESULT 7

ADR68538

ID ADR68538 standard; protein; 123 AA.

XX ADR68538;

XX 02-DEC-2004 (first entry)

XX Anti-EPO-R-antibody heavy chain variable region seqid 35.

XX antianaemic; respiratory; vulnerary; gene therapy; vaccine;  
 KW erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;  
 KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;  
 KW wound healing; neural cell damage; tissue damage; brain injury;  
 KW spinal cord injury; stroke; anti-EPO-R-antibody; heavy chain;  
 KW variable region.

XX Homo sapiens.

XX US2004175379-A1.

XX 09-SEP-2004.



XX PF 10-OCT-2003; 2003US-00684109.  
 XX PR 14-OCT-2002; 2002US-0418031P.  
 XX PA (DEVRI/) DEVRIES P J.  
 XX PA (OSTR/) OSTROW D H.  
 XX PA (REIL/) REILLY E B.  
 XX PA (GREE/) GREEN L L.  
 XX PA (WIEL/) WIELER J.  
 XX PI Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;  
 XX DR WPI; 2004-661369/64.  
 XX DR N-PSDB; ADR68537.  
 XX PT New antibody or its antibody fragment that activates an endogenous  
 XX PT activity or is capable of binding to a human erythropoietin receptor in a  
 XX PT mammal, useful for treating a mammal suffering aplasia or anemia.  
 XX PS Claim 9; SEQ ID NO 35; 156pp; English.  
 XX CC The invention describes an antibody or its fragment that activates an  
 XX CC endogenous activity or capable of binding to a human erythropoietin  
 XX CC receptor in a mammal, or that comprises at least one heavy or light chain  
 XX CC variable region having a sequence comprising 116 or 107 amino acids (SEQ  
 XX CC ID NO: 3 or 5) given in the specification or its fragment, but does not  
 XX CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also  
 XX CC given in the specification. Also described are: a method of activating or  
 XX CC modulating an endogenous activity of a human erythropoietin receptor in a  
 XX CC mammal; a pharmaceutical composition comprising a therapeutic amount of  
 XX CC an antibody or antibody fragment above and a pharmaceutical excipient; an  
 XX CC isolated and purified polynucleotide sequence selected from 28 sequences  
 XX CC comprising 322-370 bp (even SEQ ID NOs between SEQ ID NO: 2-56) given in  
 XX CC the specification, and their fragments, complements, and degenerate codon  
 XX CC equivalents; and an isolated and purified amino acid sequence selected  
 XX CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOs between  
 XX CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or  
 XX CC their fragments. The antibody or its antibody fragment that activates or  
 XX CC modulates the activity of the receptor is useful in a method of treating  
 XX CC a mammal suffering aplasia or anemia. The antibodies are also useful for  
 XX CC treating disorders characterised by decreased or subnormal levels of  
 XX CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue  
 XX CC hypoxia and/or diseases characterised by inadequate blood circulation or  
 XX CC reduced blood flow. They are also useful for promoting wound healing or  
 XX CC for protecting against neural cell and/or tissue damage, resulting from  
 XX CC brain/spinal cord injury, stroke and the like. The antibodies are also  
 XX CC useful for identifying or diagnosing mammals having dysfunctional  
 XX CC erythropoietin receptor. This is the amino acid sequence of an anti-EPO-R  
 XX CC -antibody heavy chain variable region.  
 XX SQ Sequence 123 AA;  
 Query Match 91.8%; Score 577.5; DB 8; Length 123;  
 Best Local Similarity 92.6%; Pred. No. 1e-42;  
 Matches 112; Conservative 1; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 QVQLVSGGCVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
 Db 1 QVQLVSGGCVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
 QY 61 ADSVKGRFTISRDNKNTLLQWNSLRVEDTAVVYICARSIFG-VVIDYGMVDVWGQGTVT 119  
 Db 61 ADSVKGRFTISRDNKNTLLQWNSLRVEDTAVVYICAKDHGGRVVDYGMVDVWGQGTVT 120  
 QY 120 V 120  
 Db 121 V 121  
 RESULT 8  
 ADS84376  
 ID ADS84376 standard; protein; 123 AA.

XX ADS84376;  
 XX AC 18-NOV-2004 (first entry)  
 XX DT Human anti-EPO-R antibody heavy chain variable region SEQ ID NO:15.  
 XX DE human; erythropoietin receptor; EPO receptor;  
 XX KW erythropoietin receptor binding antibody; EPO receptor binding antibody;  
 KW antianaemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia;  
 KW wound healing; neural cell damage protection;  
 KW neural tissue damage protection; brain injury; spinal cord injury;  
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.  
 XX OS Homo sapiens.  
 XX PN WO2004035603-A2.  
 XX XX 29-APR-2004.  
 XX PF 14-OCT-2003; 2003WO-US032243.  
 XX PR 14-OCT-2002; 2002US-00269711.  
 XX PR 10-OCT-2003; 2003US-00684109.  
 XX PA (ABBO ) ABBOTT LAB.  
 XX PI Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;  
 XX DR WPI; 2004-348433/32.  
 XX DR N-PSDB; ADS84375.  
 XX PT New antibodies that bind to or activate an endogenous human  
 XX PT erythropoietin receptor, useful for diagnosing, preventing or treating  
 XX PT disorders associated with dysfunctional erythropoietin receptor, e.g.  
 XX PT anemia.  
 XX PS Claim 9; SEQ ID NO 15; 192pp; English.  
 XX CC The present invention describes an antibody or its fragment that binds to  
 XX CC or activates an endogenous activity of a human erythropoietin (EPO)  
 XX CC receptor in a mammal, but does not interact with a peptide having a  
 XX CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
 XX CC methods of modulating or activating an endogenous activity of a human EPO  
 XX CC receptor in a mammal comprising administering to the mammal a  
 XX CC therapeutic amount of the above antibody or its fragment to modulate or  
 XX CC activate the receptor; (2) a method of treating a mammal suffering from  
 XX CC aplasia, comprising administering to the mammal a therapeutic amount of  
 XX CC the above antibody or its fragment to modulate or activate the receptor;  
 XX CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
 XX CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
 XX CC an isolated and purified polynucleotide sequence, and their fragments,  
 XX CC complements and degenerate codon equivalents; and (5) an isolated and  
 XX CC purified amino acid sequence, and their fragments. The EPO receptor  
 XX CC binding antibody has antianaemic, neuroprotective and vulnerary  
 XX CC activities, and can be used in gene therapy. The compositions and methods  
 XX CC from the present invention can be used for modulating an endogenous  
 XX CC activity of a human EPO receptor or for treating mammals suffering from  
 XX CC aplasia or anaemia. They may also be used for identifying mammals having  
 XX CC a dysfunctional EPO receptor. The composition may also be used in  
 XX CC promoting wound healing or in protecting against neural cell and/or  
 XX CC tissue damage resulting from brain/spinal cord injury, stroke and the  
 XX CC like. The present sequence represents a human anti-EPO-R antibody heavy  
 XX CC chain variable region, which is given in the exemplification of the  
 XX CC present invention.  
 XX SQ Sequence 123 AA;  
 Query Match 91.7%; Score 576.5; DB 8; Length 123;  
 Best Local Similarity 92.6%; Pred. No. 1.3e-42;  
 Matches 112; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
 QY 1 QVQLVSGGCVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60

Db 1 QVQLVESGGGVQPGKSLRSLSCAASGFTSSYGHWVRQAPGKLEWVWVVISYDGSNKYY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCARSIFG-VVIDYGMVWVGQTTVT 119  
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYYCARDHGGRYVVDYGMVWVGQTTVT 120  
QY 120 V 120  
Db 121 V 121

RESULT 9  
ADS84368  
ID ADS84368 standard; protein; 123 AA.  
XX AC ADS84368;  
XX DT 18-NOV-2004 (first entry)  
XX DE Human anti-EPO-R antibody heavy chain variable region SEQ ID NO:7.  
XX KW human; erythropoietin receptor; EPO receptor;  
KW erythropoietin receptor binding antibody; EPO receptor binding antibody;  
KW antianaemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia;  
KW wound healing; neural cell damage protection;  
KW neural tissue damage protection; brain injury; spinal cord injury;  
KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.  
XX OS Homo sapiens.  
XX PN WO2004035603-A2.  
XX PD 29-APR-2004.  
XX PF 14-OCT-2003; 2003WO-US032243.  
XX PR 14-OCT-2002; 2002US-00269711.  
XX PR 10-OCT-2003; 2003US-00684109.  
XX PA (ABBO ) ABBOTT LAB.  
XX PI Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;  
XX WPI; 2004-348433/32.  
XX DR N-PSDB; ADS84367.  
XX PT New antibodies that bind to or activate an endogenous human  
PT erythropoietin receptor, useful for diagnosing, preventing or treating  
PT disorders associated with dysfunctional erythropoietin receptor, e.g.  
PT anemia.  
XX PS Claim 6; SEQ ID NO 7; 192pp; English.  
XX CC The present invention describes an antibody or its fragment that binds to  
CC or activates an endogenous activity of a human erythropoietin (EPO)  
CC receptor in a mammal, but does not interact with a peptide having a  
CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
CC methods of modulating or activating an endogenous activity of a human EPO  
CC receptor in a mammal, comprising administering to the mammal a  
CC therapeutic amount of the above antibody or its fragment to modulate or  
CC activate the receptor; (2) a method of treating a mammal suffering from  
CC aplasia, comprising administering to the mammal a therapeutic amount of  
CC the above antibody or its fragment to modulate or activate the receptor;  
CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
CC an isolated and purified polynucleotide sequence, and their fragments,  
CC complements and degenerate codon equivalents; and (5) an isolated and  
CC purified amino acid sequence, and their fragments. The EPO receptor  
CC binding antibody has antianaemic, neuroprotective and vulnerary  
CC activities, and can be used in gene therapy. The compositions and methods  
CC from the present invention can be used for modulating an endogenous  
CC activity of a human EPO receptor or for treating mammals suffering from

CC aplasia or anaemia. They may also be used for identifying mammals having  
CC a dysfunctional EPO receptor. The composition may also be used in  
CC promoting wound healing or in protecting against neural cell and/or  
CC tissue damage resulting from brain/spinal cord injury, stroke and the  
CC like. The present sequence represents a human anti-EPO-R antibody heavy  
CC chain variable region, which is given in the exemplification of the  
CC present invention.  
XX SQ Sequence 123 AA;  
XX Query Match 91.7%; Score 576.5; DB 8; Length 123;  
XX Best Local Similarity 92.6%; Pred. No. 1.3e-42;  
XX Matches 112; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
QY 1 QVQLVESGGGVQPGKSLRSLSCAASGFTSSYAMHWVRQAPGKLEWVWVVISYDGSNKYY 60  
Db 1 QVQLVESGGGVQPGKSLRSLSCVSGFTSSYGMHWVRQAPGKLEWVWVVISYDGSNKYY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCARSIFG-VVIDYGMVWVGQTTVT 119  
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYYCARDHGGRYVVDYGMVWVGQTTVT 120  
QY 120 V 120  
Db 121 V 121

RESULT 10  
ADR68518  
ID ADR68518 standard; protein; 123 AA.  
XX AC ADR68518;  
XX DT 02-DEC-2004 (first entry)  
XX DE Anti-EPO-R-antibody heavy chain variable region seqid 15.  
XX KW antianaemic; respiratory; vulnerary; gene therapy; vaccine;  
KW erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;  
KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;  
KW wound healing; neural cell damage; tissue damage; brain injury;  
KW spinal cord injury; stroke; anti-EPO-R-antibody; heavy chain;  
KW variable region.  
XX OS Homo sapiens.  
XX PN US2004175379-A1.  
XX PD 09-SEP-2004.  
XX PF 10-OCT-2003; 2003US-00684109.  
XX PR 14-OCT-2002; 2002US-0418031P.  
XX PA (DEVV/) DEVRIES P J.  
XX PA (OSTR/) OSTROW D H.  
XX PA (REIL/) REILLY E B.  
XX PA (GREE/) GREEN L L.  
XX PA (WIEL/) WIELER J.  
XX PI Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;  
XX WPI; 2004-661369/64.  
XX DR N-PSDB; ADR68517.  
XX PT New antibody or its antibody fragment that activates an endogenous  
PT activity or is capable of binding to a human erythropoietin receptor in a  
PT mammal, useful for treating a mammal suffering aplasia or anemia.  
XX Claim 9; SEQ ID NO 15; 156pp; English.  
XX CC The invention describes an antibody or its fragment that activates an  
CC endogenous activity or capable of binding to a human erythropoietin

receptor in a mammal, or that comprises at least one heavy or light chain variable region having a sequence comprising 116 or 107 amino acids (SEQ ID NO: 3 or 5) given in the specification or its fragment, but does not interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also given in the specification. Also described are: a method of activating or modulating an endogenous activity of a human erythropoietin receptor in a mammal; a pharmaceutical composition comprising a therapeutic amount of an antibody or antibody fragment above and a pharmaceutical excipient; an isolated and purified polynucleotide sequence selected from 28 sequences comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in the specification, and their fragments, complements, and degenerate codon equivalents; and an isolated and purified amino acid sequence selected from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or their fragments. The antibody or its antibody fragment that activates or modulates the activity of the receptor is useful in a method of treating a mammal suffering from aplasia or anaemia. The antibodies are also useful for treating disorders characterised by decreased or subnormal levels of oxygen in the blood or tissue such as hypoxaemia or chronic tissue hypoxia and/or diseases characterised by inadequate blood circulation or reduced blood flow. They are also useful for promoting wound healing or for protecting against neural cell and/or tissue damage, resulting from brain/spinal cord injury, stroke and the like. The antibodies are also useful for identifying or diagnosing mammals having dysfunctional erythropoietin receptor. This is the amino acid sequence of an anti-EPO-R antibody heavy chain variable region.

Sequence 123 AA;

Query Match 91.7%; Score 576.5; DB 8; Length 123;  
Best Local Similarity 92.6%; Pred. No. 1.3e-42;  
Matches 112; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYYCARSIFFG-VVIDYGMVWGQGTIVT 119  
DB 61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYYCARSIFFG-VVIDYGMVWGQGTIVT 120  
QY 120 V 120  
DB 121 V 121

# RESULT 11

AD68510  
ID ADR68510 standard; protein; 123 AA.

AC ADR68510;

XX 02-DEC-2004 (first entry)

DE Anti-EPO-R-antibody heavy chain variable region seqid 7.

XX antianemic; respiratory; vulnery; gene therapy; vaccine;  
KW erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;  
KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;  
KW wound healing; neural cell damage; tissue damage; brain injury;  
KW spinal cord injury; stroke; anti-EPO-R-antibody; heavy chain;  
KW variable region.

OS Homo sapiens.

XX US2004175379-A1.

XX 09-SEP-2004.

XX 10-OCT-2003; 2003US-00684109.

XX 14-OCT-2002; 2002US-0418031P.

XX

PA

(DEVV/) DEVRIES P J.

PA

(OSTR/) OSTROW D H.

PA

(REIL/) REILLY E B.

PA

(GREE/) GREEN L L.

PA

(WIEL/) WIELER J.

PI

Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;

XX

WPI: 2004-661369/64.

DR

N-PSDB; ADR68509.

XX

New antibody or its antibody fragment that activates an endogenous activity or is capable of binding to a human erythropoietin receptor in a mammal, useful for treating a mammal suffering from aplasia or anaemia.

Claim 6; SEQ ID NO 7; 156pp; English.

The invention describes an antibody or its fragment that activates an endogenous activity or capable of binding to a human erythropoietin receptor in a mammal, or that comprises at least one heavy or light chain variable region having a sequence comprising 116 or 107 amino acids (SEQ ID NO: 3 or 5) given in the specification or its fragment, but does not interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also given in the specification. Also described are: a method of activating or modulating an endogenous activity of a human erythropoietin receptor in a mammal; a pharmaceutical composition comprising a therapeutic amount of an antibody or antibody fragment above and a pharmaceutical excipient; an isolated and purified polynucleotide sequence selected from 28 sequences comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in the specification, and their fragments, complements, and degenerate codon equivalents; and an isolated and purified amino acid sequence selected from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or their fragments. The antibody or its antibody fragment that activates or modulates the activity of the receptor is useful in a method of treating a mammal suffering from aplasia or anaemia. The antibodies are also useful for treating disorders characterised by decreased or subnormal levels of oxygen in the blood or tissue such as hypoxaemia or chronic tissue hypoxia and/or diseases characterised by inadequate blood circulation or reduced blood flow. They are also useful for promoting wound healing or for protecting against neural cell and/or tissue damage, resulting from brain/spinal cord injury, stroke and the like. The antibodies are also useful for identifying or diagnosing mammals having dysfunctional erythropoietin receptor. This is the amino acid sequence of an anti-EPO-R antibody heavy chain variable region.

Sequence 123 AA;

Query Match 91.7%; Score 576.5; DB 8; Length 123;  
Best Local Similarity 92.6%; Pred. No. 1.3e-42;  
Matches 112; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYYCARSIFFG-VVIDYGMVWGQGTIVT 119  
DB 61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYYCARSIFFG-VVIDYGMVWGQGTIVT 120  
QY 120 V 120  
DB 121 V 121

# RESULT 12

AAM51167

ID AAM51167 standard; protein; 118 AA.

XX AAM51167;

XX 10-JUN-2002 (first entry)

XX

DE Human DP-46 heavy chain variable region.

XX Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;

KW complementarity determining region; antirheumatic; antiarthritis;

KW anticancer; antiasthmatic; antiallergic; antiinflammatory; antischlicking;

KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;

KW antianginal; cardiant; antibacterial; virucide; fungicide; antileprotic;

KW protozoacide; cyostatic; neuroprotective; antiparkinsonian; nootropic;

KW human; diagnosis; therapy; DP-46.

XX Homo sapiens.

XX Key Location/Qualifiers

FT 1..30

FT /label= FR1

FT 31..35

FT /label= CDR1

FT 36..49

FT /label= FR2

FT 50..66

FT /label= CDR2

FT 67..98

FT /label= FR3

FT 99..107

FT /label= CDR3

FT 108..118

FT /label= J6

XX WO200212502-A2.

XX 14-FEB-2002.

XX 07-AUG-2001; 2001WO-US024785.

XX 07-AUG-2000; 2000US-0223360P.

XX 29-SEP-2000; 2000US-0236826P.

XX 01-AUG-2001; 2001US-00920137.

XX (CENZ ) CENTOCOR INC.

XX Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;

XX WPI; 2002-217194/27.

XX N-PSDB; ABL53507.

XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for

XX treating sickle cell anemia, diabetes, atherosclerosis, restenosis,

XX angina pectoris, myocardial infarction, leprosy.

XX Example 3; Fig 4; 131pp; English.

PS The present sequence is that of a human DP-46 heavy chain variable region

XX encoded by a human germline DP-46 gene in a transgenic mouse used in

XX human monoclonal antibody (mAb) construction. A GENTV fusion was

XX performed using spleen cells from a hybrid mouse containing human

XX variable and constant region antibody transgenes that was immunised with

XX recombinant human tumour necrosis factor (TNF) alpha. Human mAbs were

XX obtained that bound immobilised human TNF alpha with apparently high

XX avidity. These mAbs had a totally human IgG1, kappa isotype. Their heavy

XX chain variable region deduced amino acid sequences (see AAMS1168-72)

XX showed high similarity to the DP-46 sequence. The invention provides

XX isolated human, primate, rodent, mammalian, chimeric, humanised and/or

XX complementarity determining region (CDR)-grafted anti-TNF antibodies,

XX immunoglobulins, and cleavage products and variants, as well as anti-TNF

XX antibody compositions, encoding or complementary nucleic acids, vectors,

XX host cells, compositions, formulations, devices, transgenic animals,

XX transgenic plants, and methods of making and using them. The anti-TNF

XX antibody comprises at least a portion of an immunoglobulin molecule,

XX especially the heavy chain and/or light chain variable regions given in

XX the present sequence and in AAMS1165, or either all of the CDRs of the

XX heavy chain (see AAMS1158-60) or all of the CDRs of the light chain (see

XX AAMS1161-63). The antibodies may inhibit TNF-induced cell adhesion

XX molecules, inhibit TNF binding to receptor, or provide Arthritic Index

CC improvement in a mouse model. They are useful for diagnosing or treating

CC a TNF related condition in a cell, tissue, organ or animal (claimed) such

CC as rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis,

CC Crohn's pathology, sickle cell anaemia, diabetes, a cardiovascular

CC disease such as arteriosclerosis, atherosclerosis, restenosis, angina

CC pectoris or myocardial infarction, an infectious disease in a cell such

CC as bacterial, viral, and fungal infections, pneumonia, leprosy and

CC malaria, a malignant disease such as leukaemia, chronic myelocytic

CC leukaemia, Burkitt's lymphoma and multiple myeloma, or a neurological

CC disease such as multiple sclerosis, Parkinson's disease, spinal ataxia,

CC Alzheimer's disease and Creutzfeldt-Jakob disease

XX Sequence 118 AA;

QY 1 QVQLVESGGGVOPGRSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60

DB 1 QVQLVESGGGVOPGRSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAVYVCARSIFGVVVDYGMVWGQTTVTV 120

DB 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAVYVCARYYY----YVGMVWGQTTVTV 116

RESULT 13

AAE37209

1D AAE37209 standard; protein; 144 AA.

XX AAE37209;

AC AAE37209;

XX 07-AUG-2003 (first entry)

XX Human AB-PG1-XG1-077 PSMA antibody heavy chain variable region (VH).

XX Human; Prostate specific membrane antigen; carcinoma; sarcoma; cancer;

XX PSMA; melanoma; therapy; N-acetylated alpha-linked acidic dipeptidase;

XX folate hydrolase; dipeptidyl dipeptidase IV; gamma-glutamyl hydrolase;

XX NAALADase; antibody; heavy chain variable region; VH.

XX Homo sapiens.

XX WO2003034903-A2.

XX 01-MAY-2003.

XX 23-OCT-2002; 2002WO-US033944.

XX 23-OCT-2001; 2001US-0335215P.

XX 07-MAR-2002; 2002US-0362747P.

XX 20-SEP-2002; 2002US-0412618P.

XX (PSMA-) PSMA DEV CO LLC.

XX Maddon PJ, Donovan GP, Olson WC, Schuelke N, Gardner J, Ma D;

XX WPI; 2003-403281/38.

XX N-PSDB; AAE56224.

XX Novel isolated antibody which binds to epitope on prostate specific

XX membrane antigen, and competitively inhibits binding of second antibody

XX to its target epitope on the antigen, useful for treating prostate

XX cancer.

XX Claim 26; Page 236; 238pp; English.

XX The invention relates to an antibody or its antigen-binding fragment

XX which specifically binds to epitope on prostate specific membrane antigen

XX (PSMA), and competitively inhibits the specific binding of a second

XX antibody to its target epitope on PSMA. The invention is useful for

XX diagnosing, treating or preventing PSMA-mediated disease such as prostate

CC cancer or non-prostate cancer bladder chosen from cancer including  
 CC transitional cell carcinoma, pancreatic cancer including pancreatic duct  
 CC carcinoma, lung cancer including non-small cell lung carcinoma, kidney  
 CC cancer including conventional renal cell carcinoma, sarcoma including  
 CC soft tissue sarcoma, breast cancer including breast carcinoma, brain  
 CC cancer including glioblastoma multiforme, neuroendocrine carcinoma, colon  
 CC cancer including colonic carcinoma, testicular cancer including  
 CC testicular embryonal carcinoma, or melanoma including malignant melanoma.  
 CC The invention is useful also for inhibiting or enhancing folate hydrolase  
 CC activity of a folate hydrolase polypeptide, N-acetylated alpha-linked  
 CC acidic dipeptidase (NAALADase) activity of a NAALADase polypeptide,  
 CC dipeptidyl dipeptidase IV activity of a dipeptidyl dipeptidase IV  
 CC polypeptide, gamma-glutamyl hydrolase activity of a gamma-glutamyl  
 CC hydrolase polypeptide. The present sequence is human PSMA antibody heavy  
 CC chain variable region (VH)  
 XX  
 XX Sequence 144 AA;

Query Match 90.9%; Score 571.5; DB 6; Length 144;  
 Best Local Similarity 90.2%; Pred. No. 4.1e-42;  
 Matches 111; Conservative 2; Mismatches 7; Indels 3; Gaps 1;  
 Qy 1 QVQLVESGGGVQPGRSRLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60  
 Db 20 QVQLVESGGGVQPGRSRLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 79  
 Qy 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARSLVGLYNYNYGMVWGQGT 117  
 Db 80 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARSLVGLYNYNYGMVWGQGT 139  
 Qy 118 VTV 120  
 Db 140 VTV 142

RESULT 14  
 ADP22128  
 ID ADP22128 standard; protein; 122 AA.

XX  
 AC ADP22128;  
 DT 09-SEP-2004 (first entry)

DE Human anti-TNFA antibody heavy chain variable region SEQ ID NO:34.

XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;  
 KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;  
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;  
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
 KW neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;  
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
 KW prostate cancer; immuno-mediated inflammatory disease;  
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
 KW septic shock; cachexia; anorexia; multiple sclerosis.

OS Homo sapiens.

XX WO2004050683-A2.

XX 17-JUN-2004.

XX 02-DEC-2003; 2003WO-US038281.

XX 02-DEC-2002; 2002US-0430729P.

XX (ABGE-) ABGENIX INC.

XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
 PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;  
 PI Manchulenchon K, Faggioni R, Senaldi G, Qiaojuan JS;

XX WPI; 2004-480601/45.  
 DR N-PSDB; ADP22127.  
 XX  
 PT New recombinant human monoclonal antibody that specifically binds to  
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.  
 XX  
 PS Example 10; SEQ ID NO 34; 213pp; English.

XX The present invention describes a human monoclonal antibody (I) that  
 CC specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDRI) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDRI having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNFA in a patient sample, comprising contacting with  
 CC (I), and detecting the level of binding between the antibody and TNFA in  
 CC the sample; (2) a composition comprising the antibody or its functional  
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFA induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNFA induced apoptosis by administering the human monoclonal antibody of  
 CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,  
 CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-  
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,  
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 CC as a TNFA antagonist. The antibody (I) is useful in the preparation of  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNFA  
 CC antibody heavy chain variable region, which is used in the  
 CC exemplification of the present invention.

XX Sequence 122 AA;

Query Match 90.8%; Score 571; DB 8; Length 122;  
 Best Local Similarity 92.5%; Pred. No. 3.8e-42;  
 Matches 111; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVQPGRSRLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60  
 Db 1 QVQLVESGGGVQPGRSRLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60  
 Qy 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARSLVGLYNYNYGMVWGQGT 120  
 Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARSLVGLYNYNYGMVWGQGT 120

RESULT 15

ADK18593

ID ADK18593 standard; protein; 126 AA.

XX

AC ADK18593;

DT 06-MAY-2004 (first entry)

DE Anti-human PDGF-D antibody heavy chain protein sequence.

XX antiinflammatory; immunomodulator; cytostatic; gene therapy.

XX Homo sapiens.

OS

XX WO2003057857-A2.

XX

PD 17-JUL-2003.  
XX  
PF 06-JAN-2003; 2003WO-US000398.  
XX  
PR 07-JAN-2002; 2002US-00041860.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
PI Bezabeh B;  
XX  
DR WPI; 2003-587119/55.  
XX  
XX New human monoclonal antibody that binds to platelet-derived growth  
PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
PT diseases, such as inflammation, autoimmunity and cancer.  
XX  
PS Disclosure; SEQ ID NO 17; 255pp; English.  
XX  
CC The invention relates to a human monoclonal antibody that binds to  
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
CC treating chronic and recurrent human diseases, such as inflammation,  
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
CC useful for modulating collagen formation, and for staging various  
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
CC generated using an active protein fragment of the gene product from the  
CC clone 30664188.0.99 arising in the conditioned medium obtained when  
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
CC sequence corresponds to a protein used in the invention.  
XX  
SQ Sequence 126 AA;  
  
Query Match 90.8%; Score 571; DB 7; Length 126;  
Best Local Similarity 89.5%; Pred. No. 3.9e-42;  
Matches 111; Conservative 1; Mismatches 8; Indels 4; Gaps 1;  
  
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSKYY 60  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAIVSYDGSKYY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYICARS----IFGVWIDYGMVWGQT 116  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYICARDQGYRYAGYYDYGMVWGQT 120  
  
QY 117 TTVV 120  
Db ||||  
121 TTVV 124

Search completed: November 9, 2005, 12:55:30  
Job time : 74.985 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55 ; Search time 18.6466 Seconds  
(without alignments)  
480.403 Million cell updates/sec

Title: US-10-660-357A-29

Perfect score: 629

Sequence: 1 QVQLVESGGGVQPGKSLRL.....FGVVIDYGMVWGQTTTV 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	567.5	90.2	451	4	US-09-472-087-70
2	559	88.9	123	3	US-08-983-607-38
3	550	87.4	248	4	US-09-315-926A-80
4	549.5	87.4	123	4	US-09-424-840B-6
5	546.5	86.9	120	1	US-07-942-245-35
6	544.5	86.6	119	1	US-08-331-398A-46
7	544.5	86.6	119	2	US-08-331-397B-46
8	544.5	86.6	119	3	US-08-759-804A-46
9	544.5	86.6	119	3	US-09-227-693-46
10	542.5	86.2	123	4	US-09-560-198A-2
11	538	85.5	124	4	US-09-424-840B-16
12	530	84.3	126	3	US-09-240-274-26
13	529	84.1	310	3	US-09-079-029-11
14	527.5	83.9	115	4	US-09-726-219A-167
15	526.5	83.7	123	4	US-09-560-198A-4
16	526.5	83.7	225	4	US-09-456-090A-60
17	526.5	83.7	225	4	US-09-456-090A-92
18	526.5	83.7	225	4	US-09-456-090A-108
19	526.5	83.7	225	4	US-09-453-234-60
20	526.5	83.7	225	4	US-09-453-234-92
21	526.5	83.7	225	4	US-09-453-234-108
22	526	83.6	126	3	US-09-240-274-152
23	524.5	83.4	123	4	US-09-560-198A-10
24	524.5	83.4	167	4	US-09-472-087-80
25	524	83.3	126	3	US-09-240-274-153
26	522	83.0	126	3	US-09-240-274-25
27	522	83.0	174	4	US-09-472-087-12

28	521.5	82.9	225	4	US-09-456-090A-102	Sequence 102, App
29	521.5	82.9	225	4	US-09-453-234-102	Sequence 102, App
30	520.5	82.8	117	3	US-09-025-769B-24	Sequence 24, Appl
31	520.5	82.8	117	4	US-09-490-070A-24	Sequence 24, Appl
32	520.5	82.8	117	4	US-09-490-153-24	Sequence 24, Appl
33	520.5	82.8	117	4	US-09-456-090A-106	Sequence 106, App
34	520.5	82.8	225	4	US-09-453-234-106	Sequence 106, App
35	520.5	82.8	225	4	US-09-472-087-4	Sequence 4, Appli
36	520	82.7	463	4	US-09-472-087-68	Sequence 68, Appl
37	519.5	82.6	116	1	US-08-211-202-141	Sequence 141, App
38	519.5	82.6	225	4	US-09-456-090A-110	Sequence 110, App
39	519.5	82.6	225	4	US-09-453-234-110	Sequence 110, App
40	519.5	82.6	225	4	US-08-862-124-17	Sequence 17, Appl
41	519.5	82.6	304	3	US-08-862-124-14	Sequence 14, Appl
42	519.5	82.6	304	3	US-09-240-274-24	Sequence 24, Appl
43	518.5	82.4	125	3	US-09-456-090A-56	Sequence 56, Appl
44	518.5	82.4	225	4	US-09-453-234-56	Sequence 56, Appl
45	518.5	82.4	225	4		

ALIGNMENTS

RESULT 1

US-09-472-087-70  
; Sequence 70, Application US/09472087  
; Patent No. 6682736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEVEU, MARK J.  
; APPLICANT: MUELLER, EILLEN E.  
; APPLICANT: HANKE, JEFFREY H.  
; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEORFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-PFI  
; CURRENT APPLICATION NUMBER: US/09/472,087  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/113,647  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 70  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-472-087-70

Query Match	90.2%	Score 567.5;	DB 4;	Length 451;
Best Local Similarity	90.2%	Pred. No. 6.7e+49;		
Matches 111;	Conservative 1;	Mismatches 8;	Indels 3;	Gaps 1;
Qy	1	QVQLVESGGGVQPGKSLRLSCAASGFTSSVAMHWVRQAPGKLEWVAIVSYDGSNKYY	60	
Db	1	QVQLVESGGGVQPGKSLRLSCAASGFTSSVAMHWVRQAPGKLEWVAIVSYDGSNKYY	60	
Qy	61	ADSVKGRFTISRDNSKNTLYLQNSLRABDTAVYYCARSIFGVVI---DYGMVWGQTTT	117	
Db	61	ADSVKGRFTISRDNSKNTLYLQNSLRABDTAVYYCARSIFGVVI---DYGMVWGQTTT	117	
Qy	118	VTV 120		
Db	121	VTV 123		

RESULT 2

US-08-983-607-38  
; Sequence 38, Application US/08983607  
; Patent No. 6140470  
; GENERAL INFORMATION:  
; APPLICANT: Alan Garen  
; APPLICANT: Xiaohong Cai

;; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-  
;; TITLE OF INVENTION: boddies  
;; NUMBER OF SEQUENCES: 51  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Department of Molecular Biophysics  
;; ADDRESSEE: and Biochemistry, Yale University  
;; STREET: 266 Whitney Avenue  
;; CITY: New Haven  
;; STATE: Connecticut  
;; COUNTRY: United States of America  
;; ZIP: 06520-8114  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" 1.44 Mb diskette  
;; COMPUTER: IBM PC  
;; OPERATING SYSTEM: MS DOS  
;; SOFTWARE: Word Processing  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/983,607  
;; FILING DATE: April 27, 1998  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/IB96/01032  
;; FILING DATE: June 28, 1996  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mary M. Krinsky  
;; REGISTRATION NUMBER: 32423  
;; REFERENCE/DOCKET NUMBER: OCR-679  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 203-773-9544  
;; TELEFAX: 203-773-1183  
;; INFORMATION FOR SEQ ID NO: 38:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 123 residues  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE:  
;; DESCRIPTION: polypeptide  
;; ORIGINAL SOURCE:  
;; ORGANISM: Homo sapiens (melanoma patient  
;; ORGANISM: immunized with autologous tumor cells)  
;; INDIVIDUAL ISOLATE: peripheral blood lympho-  
;; INDIVIDUAL ISOLATE: Cycles  
;; IMMEDIATE SOURCE:  
;; LIBRARY: DM414 scFv antibodies obtained from  
;; LIBRARY: fuses fusion phage construct  
;; CLONE: V575  
;; FEATURE:  
;; NAME/KEY: heavy chain  
;; US-08-983-607-38

Query Match 88.9%; Score 559; DB 3; Length 123;  
Best Local Similarity 91.0%; Pred. No. 1.le-48;  
Matches 111; Conservative 1; Mismatches 8; Indels 2; Gaps 2;  
  
Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
  
Qy 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARSI--FGVVIDYGMVWGQTTV 118  
Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARSI--FGVVIDYGMVWGQTTV 120  
  
Qy 119 TV 120  
Db 121 TV 122

RESULT 3  
US-09-315-926A-80  
; Sequence 80, Application US/09315926A  
; Patent No. 6498027

;; GENERAL INFORMATION:  
;; APPLICANT: Es van, Helmut  
;; APPLICANT: Havenga, Menzo  
;; APPLICANT: Verlingen, Stefan  
;; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER  
;; FILE REFERENCE: 2183-4080US  
;; CURRENT APPLICATION NUMBER: US/09/315,926A  
;; CURRENT FILING DATE: 1999-05-20  
;; PRIOR APPLICATION NUMBER: EP 99201593.3  
;; PRIOR FILING DATE: 1999-05-20  
;; PRIOR APPLICATION NUMBER: EP 98201693.3  
;; PRIOR FILING DATE: 1998-05-20  
;; NUMBER OF SEQ ID NOS: 81  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 80  
;; LENGTH: 248  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; OTHER INFORMATION: Description of Artificial Sequence: phase  
;; NAME/KEY: PEPTIDE  
;; LOCATION: (1)..(248)  
;; OTHER INFORMATION: /note="hCAT1 amino acid sequence"  
;; US-09-315-926A-80

Query Match 87.4%; Score 550; DB 4; Length 248;  
Best Local Similarity 90.0%; Pred. No. 1.9e-47;  
Matches 108; Conservative 1; Mismatches 9; Indels 2; Gaps 1;  
  
Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
Db 23 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 82  
  
Qy 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARSI--FGVVIDYGMVWGQTTV 120  
Db 83 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARSI--TVTKSRFDYWGQTLTV 140

RESULT 4  
US-09-424-840B-6  
; Sequence 6, Application US/09424840B  
; Patent No. 6790938  
;; GENERAL INFORMATION:  
;; APPLICANT: Berchtold, Peter  
;; APPLICANT: Escher, Robert F. A.  
;; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES  
;; FILE REFERENCE: 100564-09049  
;; CURRENT APPLICATION NUMBER: US/09/424,840B  
;; CURRENT FILING DATE: 1999-12-03  
;; PRIOR APPLICATION NUMBER: DE 19820663.1  
;; PRIOR FILING DATE: 1998-05-08  
;; PRIOR APPLICATION NUMBER: DE 19755227.7  
;; PRIOR FILING DATE: 1997-12-12  
;; PRIOR APPLICATION NUMBER: DE 19723904.8  
;; PRIOR FILING DATE: 1997-06-06  
;; NUMBER OF SEQ ID NOS: 128  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 6  
;; LENGTH: 123  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; US-09-424-840B-6

Query Match 87.4%; Score 549.5; DB 4; Length 123;  
Best Local Similarity 88.5%; Pred. No. 9.9e-48;  
Matches 108; Conservative 7; Mismatches 4; Indels 3; Gaps 2;  
  
Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
  
Qy 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARSI--FGVVIDYGMVWGQTTV 118



||||| 61 ADSVKGRFAISRDNKNTLYLQMSLRADTAFTVYCARALGSWG-GWDHYMDVWGKGTTV 119  
||| 119 TV 120  
|| 120 TV 121

APPLICANT: Fitzgerald, David  
APPLICANT: Brinkmann, Ulrich  
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Street Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,398A  
FILING DATE: 28-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-126110US  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1-119  
OTHER INFORMATION: /note= "Human fetal immunoglobulin  
OTHER INFORMATION: 56P1/CL Variable Heavy chain (V-H)"  
US-08-331-398A-46

Query Match 86.6%; Score 546.5; DB 1; Length 120;  
Best Local Similarity 89.2%; Pred. No. 3e-47;  
Matches 107; Conservative 1; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVQLVSGGVPQGRSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAISYDGSNKYY 60  
|||  
DB 1 QVQLVSGGVPQGRSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAISYDGSNKYY 60  
|||  
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAFTVYCARSI FGVIYDYGMDVWGQGTITV 120  
|||  
DB 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAFTVYCARSI FGVIYDYGMDVWGQGTITV 117  
|||

RESULT 7  
US-08-331-397B-46  
; Sequence 46, Application US/08331397B  
; Patent No. 5981726  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Benhar, Itai  
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-  
; SPECIFIC ANTIBODY FRAGMENTS, FUSION PROTEINS, AND USES  
; THEREOF  
; NUMBER OF SEQUENCES: 68

## RESULT 7

US-08-331-397B-46  
; Sequence 46, Application US/08331397B  
; Patent No. 5981726  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Benhar, Itai  
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-  
; SPECIFIC ANTIBODY FRAGMENTS, FUSION PROTEINS, AND USES  
; THEREOF  
; NUMBER OF SEQUENCES: 68

US-07-942-245-35  
; Sequence 35, Application US/07942245  
; Patent No. 5639641  
; GENERAL INFORMATION:  
; APPLICANT: PEDERSEN, Jan T.  
; APPLICANT: SEARLE, Stephen M.J.  
; APPLICANT: REES, Anthony R.  
; APPLICANT: ROGUSKA, Michael A.  
; APPLICANT: GUILD, Braydon C.  
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT  
; ANTIBODIES  
; NUMBER OF SEQUENCES: 522  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: United States  
; ZIP: 20037-3202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: HP 9000/700 Workstation  
; OPERATING SYSTEM: UNIX  
; SOFTWARE: In house  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/942,245  
; FILING DATE: 09-SEP-1992  
; CLASSIFICATION: 530  
; TELEPHONE: (202) 293-7060  
; TELEFAX: (202) 293-7860  
; TELEX: 6491103  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-942-245-35

Query Match 86.9%; Score 546.5; DB 1; Length 120;  
Best Local Similarity 88.6%; Pred. No. 1.9e-47;  
Matches 109; Conservative 1; Mismatches 6; Indels 7; Gaps 2;

QY 1 QVQLVSGGVPQGRSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAISYDGSNKYY 60  
|||  
DB 1 QVQLVSGGVPQGRSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAISYDGSNKYY 60  
|||  
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAFTVYCARSI FGVIYDYGMDVWGQGTITV 117  
|||  
DB 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAFTVYCARSI FGVIYDYGMDVWGQGTITV 116  
|||

RESULT 6  
US-08-331-398A-46  
; Sequence 46, Application US/08331398A  
; Patent No. 5608039  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Willingham, Mark

```

CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin
OTHER INFORMATION: 56Pl'CL Variable Heavy chain (V-H) "
US-08-331-397B-46
Query Match 86.6%; Score 544.5; DB 2; Length 119;
Best Local Similarity 89.2%; Pred. No. 3e-47;
Matches 107; Conservative 1; Mismatches 9; Indels 3; Gaps 1;
Qy 1 QVQLVSGGQVQPGKSLRLSCAASGFTFSSYAMHWVRQAPGKLEWAVISYDGSNKYY 60
|||
Db 1 QVELVSGGVQPGKSLRLSCAASGFTFSSYAMHWVRQAPGKLEWAVISYDGSNKYY 60
|||
Qy 61 ADSVKGRFTISRDNSKNTLYLQNSLRADDTAVYCARSIFGWIDYGMVWGQGTITV 120
|||
Db 61 ADSVKGRFTISRDNSKNTLYLQNSLRADDTAVYCARSIFGWIDYGMVWGQGTITV 117
|||
RESULT 8
US-08-759-804A-46
Sequence 46, Application US/08759804A
Patent No. 5990296
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pal, Lee
TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
and Uses Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin
OTHER INFORMATION: 56Pl'CL Variable Heavy chain (V-H) "
US-08-331-397B-46
Query Match 86.6%; Score 544.5; DB 2; Length 119;
Best Local Similarity 89.2%; Pred. No. 3e-47;
Matches 107; Conservative 1; Mismatches 9; Indels 3; Gaps 1;
Qy 1 QVQLVSGGQVQPGKSLRLSCAASGFTFSSYAMHWVRQAPGKLEWAVISYDGSNKYY 60
|||
Db 1 QVELVSGGVQPGKSLRLSCAASGFTFSSYAMHWVRQAPGKLEWAVISYDGSNKYY 60
|||
Qy 61 ADSVKGRFTISRDNSKNTLYLQNSLRADDTAVYCARSIFGWIDYGMVWGQGTITV 120
|||
Db 61 ADSVKGRFTISRDNSKNTLYLQNSLRADDTAVYCARSIFGWIDYGMVWGQGTITV 117
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RESULT 9
US-09-227-693-46
Sequence 46, Application US/09227693
Patent No. 6287562
GENERAL INFORMATION:
APPLICANT: PASTAN, Ira
APPLICANT: BENHAR, Itai
APPLICANT: PADLAN, Eduardo A.
APPLICANT: JUNG, Sun-Hee
APPLICANT: LEE, Byungkook
TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California

```

COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/227,693  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/331,396  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 15280-126-1-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..119  
OTHER INFORMATION: /note= "Human fetal immunoglobulin  
US-09-227-693-46

Query Match 86.6%; Score 544.5; DB 3; Length 119;  
Best Local Similarity 89.2%; Pred. No. 3e-47;  
Matches 107; Conservative 1; Mismatches 9; Indels 3; Gaps 1;  
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
QY 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCARSIFGVVVIDY----GMDVWGQTTVTV 120  
DB 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCARR---SARTYYFDYWGQGLTVTV 117

RESULT 10  
US-09-560-198A-2  
Sequence 2, Application US/09560198A  
Patent No. 6492497  
GENERAL INFORMATION:  
APPLICANT: Thompson, Julia E  
APPLICANT: Lennard, Simon N  
APPLICANT: Wilton, Alison J  
APPLICANT: Braddock, Peta SH  
APPLICANT: Du Fou, Sarah L  
APPLICANT: McCafferty, John G  
APPLICANT: Conroy, Louise A  
APPLICANT: Tempest, Philip R  
TITLE OF INVENTION: Specific binding members for TGFbeta1  
FILE REFERENCE: 28111/35620A  
CURRENT APPLICATION NUMBER: US/09/560,198A  
CURRENT FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/131,983  
PRIOR FILING DATE: 1999-04-30  
NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 123  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-560-198A-2

Query Match 86.2%; Score 542.5; DB 4; Length 123;  
Best Local Similarity 87.0%; Pred. No. 5e-47;  
Matches 107; Conservative 5; Mismatches 6; Indels 5; Gaps 2;  
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
QY 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCARSIFGVVVIDY----GMDVWGQTTT 117  
DB 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCART--GEYSGYDTSGVELWGQTTT 118  
QY 118 TVTV 120  
DB 119 TVTV 121

RESULT 11  
US-09-424-840B-16  
Sequence 16, Application US/09424840B  
Patent No. 6790938  
GENERAL INFORMATION:  
APPLICANT: Berchtold, Peter  
APPLICANT: Escher, Robert F. A.  
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES  
FILE REFERENCE: 100564-09049  
CURRENT APPLICATION NUMBER: US/09/424,840B  
CURRENT FILING DATE: 1999-12-03  
PRIOR APPLICATION NUMBER: DE 19820663.1  
PRIOR FILING DATE: 1998-05-08  
PRIOR APPLICATION NUMBER: DE 19755227.7  
PRIOR FILING DATE: 1997-12-12  
PRIOR APPLICATION NUMBER: DE 19723904.8  
PRIOR FILING DATE: 1997-06-06  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 16  
LENGTH: 124  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-424-840B-16

Query Match 85.5%; Score 538; DB 4; Length 124;  
Best Local Similarity 85.5%; Pred. No. 1.4e-46;  
Matches 106; Conservative 4; Mismatches 8; Indels 6; Gaps 2;  
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
QY 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCARSIFGVVVIDY----GMDVWGQTT 116  
DB 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCAKD--GRSGSYARFDGMDVWGQTT 118  
QY 117 TVTV 120  
DB 119 TVTV 122

RESULT 12  
US-09-240-274-26  
Sequence 26, Application US/09240274  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

```
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D31
US-09-240-274-26

Query Match      84.3%; Score 530; DB 3; Length 126;
Best Local Similarity 81.2%; Pred. No. 9.1e-46;
Matches 104; Conservative 7; Mismatches 5; Indels 12; Gaps 2;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 1 EVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAIVSYDGSNKHY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVVYCAR-----SIFGWIDYGMVW 112
Db 61 SDSVKGRFTISRDNKNTLYLQMSLRRAEDTAVVYCARERNFRSGYSRY----YYGMDVW 116

QY 113 GGGTTTV 120
Db 117 GPGTTTV 124

RESULT 13
US-09-079-029-11
; Sequence 11, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: Amino Acid

; TITLE OF INVENTION: Linear
; US-09-079-029-11

Query Match      84.1%; Score 529; DB 3; Length 310;
Best Local Similarity 85.4%; Pred. No. 3.1e-45;
Matches 105; Conservative 2; Mismatches 6; Indels 10; Gaps 2;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 40 QVQLVQSGGGVQPGKSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAGIFYDGGNKYY 99

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVVYCARSIKGVVID---YGMDEVGSGTT 117
Db 100 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVVYCAR-----DRGYVMDVWGKGT 152

QY 118 VTV 120
Db 153 VTV 155

RESULT 14
US-09-726-219A-167
; Sequence 167, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clarkson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00013
; CURRENT APPLICATION NUMBER: US/09/726,219A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-219A-167

Query Match      83.9%; Score 527.5; DB 4; Length 115;
Best Local Similarity 88.0%; Pred. No. 1.5e-45;
Matches 103; Conservative 4; Mismatches 7; Indels 3; Gaps 2;
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Qy	1	QVQLVSGGUVQPGSRSLRLCAAGSFTSSVMHWRQAPCKGLEWAVSYDGSNKYY	60
Db	1	QVQLVSGGUVQPGSRSLRLCAAGSFTSSVMHWRQAPCKGLEWAVSYDGSNKYY	60
Qy	61	ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCARSIFGWIDYG-MDVWQGGT	116
Db	61	ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCAK--GYSSGMGYFYDWGGT	115

**RESULT 15**

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US-09-560-198A-4
; Sequence 4, Application US/09560198A
; Patent No. 6492497
; GENERAL INFORMATION:
; APPLICANT: Thompson, Julia E
; APPLICANT: Lennard, Simon N
; APPLICANT: Wilton, Alison J
; APPLICANT: Braddock, Peta SH
; APPLICANT: Du Fou, Sarah L
; APPLICANT: McCafferty, John G
; APPLICANT: Conroy, Louise A
; APPLICANT: Tempest, Phillip R
; TITLE OF INVENTION: Specific binding members for TGFbeta1
; FILE REFERENCE: 2811/35620A
; CURRENT APPLICATION NUMBER: US/09/560,198A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/131,983
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-198A-4

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Query Match 83.7%; Score 526.5; DB 4; Length 123;  
Best Local Similarity 86.2%; Pred. No. 2e-45;  
Matches 106; Conservative 2; Mismatches 10; Indels 5; Gaps 2;

1	QVLVESGGVVQGRSLRLSCAASGFTFSYAMHWVRQAPGKLEWAVISYDGSNKTY	60
:		:
:		:
:		:
:		:
:		:
1	EVQLVESGGVVQGRSLRLSCAASGFTFSYGMHWVRQAPGKELEWAVISYDGSIKTY	60
:		:
:		:
:		:
:		:
:		:
61	ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYICARSIFGVVLDYGM-----VMQGQTT	117
:		:
:		:
:		:
:		:
:		:
61	ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYICART--GRYSGVDTPQVSGQGTT	118
:		:
:		:
:		:
118	VTV 120	
:		
:		
119	VTV 121	
:		
:		
db		

Search completed: November 9, 2005, 11:46:41  
Job time : 19.6466 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:40:37 ; Search time 66.6667 Seconds  
(without alignments)  
753.137 Million cell updates/sec

Title: US-10-660-357A-29

Perfect score: 629

Sequence: 1 QVOLVSGGGVQPGRLSLRL.....FGVVIDYGMVWGQGTTVTV 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09D\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
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19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	629	100.0	120	14	US-10-330-613-29
2	629	100.0	120	14	US-10-330-530-29
3	629	100.0	120	16	US-10-660-357-29
4	580.5	92.3	123	15	US-10-269-711-11
5	580.5	92.3	123	15	US-10-269-711-23
6	580.5	92.3	123	15	US-10-269-711-27
7	580.5	92.3	123	15	US-10-269-711-31
8	580.5	92.3	123	15	US-10-269-711-35
9	580.5	92.3	123	16	US-10-684-109-11
10	578	91.9	124	15	US-10-292-088-106
11	577.5	91.8	123	15	US-10-269-711-43

12	577.5	91.8	123	16	US-10-684-109-35	Sequence 35, Appl
13	577	91.7	141	17	US-10-858-855-11	Sequence 11, Appl
14	576.5	91.7	123	15	US-10-269-711-7	Sequence 7, Appl
15	576.5	91.7	123	15	US-10-269-711-15	Sequence 15, Appl
16	576.5	91.7	123	16	US-10-684-109-7	Sequence 7, Appl
17	576.5	91.7	123	16	US-10-684-109-15	Sequence 15, Appl
18	574.5	91.3	122	20	US-11-031-485-116	Sequence 116, App
19	574.5	91.3	123	15	US-10-292-088-115	Sequence 115, App
20	572.5	91.0	123	15	US-10-292-088-117	Sequence 117, App
21	571.5	90.9	144	15	US-10-395-894-31	Sequence 31, Appl
22	571.5	90.9	144	16	US-10-695-667-31	Sequence 31, Appl
23	571.5	90.9	144	18	US-10-976-352-31	Sequence 31, Appl
24	571	90.8	122	17	US-10-727-155-34	Sequence 34, Appl
25	571	90.8	126	14	US-10-041-860-17	Sequence 17, Appl
26	571	90.8	126	14	US-10-041-860-209	Sequence 209, Appl
27	571	90.8	126	14	US-10-041-860-282	Sequence 282, App
28	571	90.8	126	16	US-10-665-383-14	Sequence 14, Appl
29	569.5	90.5	121	15	US-10-309-762-132	Sequence 132, App
30	569.5	90.5	121	15	US-10-309-762-149	Sequence 149, App
31	569	90.5	126	15	US-10-309-762-133	Sequence 133, App
32	568.5	90.4	123	15	US-10-292-088-116	Sequence 116, App
33	567.5	90.2	117	20	US-11-009-731-47	Sequence 47, Appl
34	567.5	90.2	451	14	US-10-153-382-17	Sequence 17, Appl
35	567.5	90.2	451	16	US-10-612-497-70	Sequence 70, Appl
36	567.5	90.2	451	16	US-10-776-649-70	Sequence 70, Appl
37	567.5	90.2	451	20	US-11-085-368-17	Sequence 17, Appl
38	566.5	90.1	125	15	US-10-292-088-107	Sequence 107, App
39	565.5	89.9	125	17	US-10-727-155-222	Sequence 222, App
40	565	89.8	121	17	US-10-726-332-142	Sequence 142, App
41	565	89.8	124	15	US-10-371-942-82	Sequence 82, Appl
42	564	89.7	117	20	US-11-031-485-115	Sequence 115, App
43	563.5	89.6	252	10	US-09-880-748-1731	Sequence 1731, Ap
44	563.5	89.6	252	15	US-10-293-418-1731	Sequence 1731, Ap
45	563	89.5	122	9	US-09-144-886-69	Sequence 69, Appl

#### ALIGNMENTS

RESULT 1  
US-10-330-613-29  
; Sequence 29, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; PRIOR FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-29

Query Match 100.0%; Score 629; DB 14; Length 120;  
Best Local Similarity 100.0%; Pred. No. 3.6e-53;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QVOLVSGGGVQPGRLSLRLSCAAGTFTSSAMHWVRQAPGKLEWVAIVSDGSKNY 60  
Db 1 QVOLVSGGGVQPGRLSLRLSCAAGTFTSSAMHWVRQAPGKLEWVAIVSDGSKNY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARSI FGVIIDYGMVWGQGTTVTV 120  
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARSI FGVIIDYGMVWGQGTTVTV 120

RESULT 2

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US-10-330-530-29
; Sequence 29, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-29

Query Match          100.0%; Score 629; DB 14; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.6e-53;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCARSI FGVVVDYGMVWGQGTITV 120
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCARSI FGVVVDYGMVWGQGTITV 120

RESULT 3
US-10-660-357-29
; Sequence 29, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-29

Query Match          100.0%; Score 629; DB 16; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.6e-53;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCARSI FGVVVDYGMVWGQGTITV 120
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCARSI FGVVVDYGMVWGQGTITV 120

RESULT 4
US-10-269-711-11
; Sequence 11, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Devries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 6989.US.O1
; CURRENT APPLICATION NUMBER: US/10/269,711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-711-11

Query Match          92.3%; Score 580.5; DB 15; Length 123;
Best Local Similarity 93.4%; Pred. No. 1.9e-48;
Matches 113; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCARSI FG-VVVDYGMVWGQGTITV 119
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCARSI FG-VVVDYGMVWGQGTITV 120

120 V 120
121 V 121

RESULT 5
US-10-269-711-23
; Sequence 23, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Devries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 6989.US.O1
; CURRENT APPLICATION NUMBER: US/10/269,711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-711-23

Query Match          92.3%; Score 580.5; DB 15; Length 123;
Best Local Similarity 93.4%; Pred. No. 1.9e-48;
Matches 113; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCARSI FG-VVVDYGMVWGQGTITV 119
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCARSI FG-VVVDYGMVWGQGTITV 120

120 V 120
121 V 121
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Db      121 V 121
RESULT 6
US-10-269-711-27
; Sequence 27, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: DeVries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 6989 US 01
; CURRENT APPLICATION NUMBER: US/10/269,711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-711-27

Query Match      92.3%; Score 580.5; DB 15; Length 123;
Best Local Similarity 93.4%; Pred. No. 1.9e-48;
Matches 113; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY      1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db      1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
QY      61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYYCARDHGGRYVYDYGMDVWGQGTTVT 119
Db      61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYYCARDHGGRYVYDYGMDVWGQGTTVT 120
QY      120 V 120
Db      121 V 121

RESULT 8
US-10-269-711-35
; Sequence 35, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: DeVries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 6989 US 01
; CURRENT APPLICATION NUMBER: US/10/269,711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-711-35

Query Match      92.3%; Score 580.5; DB 15; Length 123;
Best Local Similarity 93.4%; Pred. No. 1.9e-48;
Matches 113; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY      1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db      1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
QY      61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYYCARDHGGRYVYDYGMDVWGQGTTVT 119
Db      61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYYCARDHGGRYVYDYGMDVWGQGTTVT 120
QY      120 V 120
Db      121 V 121

RESULT 9
US-10-684-109-11
; Sequence 11, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Weiler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989 US 02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-711-31

Query Match      92.3%; Score 580.5; DB 15; Length 123;
Best Local Similarity 93.4%; Pred. No. 1.9e-48;
Matches 113; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY      1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db      1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
QY      61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYYCARDHGGRYVYDYGMDVWGQGTTVT 119
Db      61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYYCARDHGGRYVYDYGMDVWGQGTTVT 120
QY      120 V 120
Db      121 V 121

RESULT 7
US-10-269-711-31
; Sequence 31, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: DeVries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 6989 US 01
; CURRENT APPLICATION NUMBER: US/10/269,711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-711-31

Query Match      92.3%; Score 580.5; DB 15; Length 123;
Best Local Similarity 93.4%; Pred. No. 1.9e-48;
Matches 113; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY      1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db      1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
QY      61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYYCARDHGGRYVYDYGMDVWGQGTTVT 119
Db      61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYYCARDHGGRYVYDYGMDVWGQGTTVT 120
QY      120 V 120
Db      121 V 121
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```

; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-11

Query Match          92.3%; Score 580.5; DB 16; Length 123;
Best Local Similarity 93.4%; Pred. No. 1.9e-48;
Matches 113; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQWNSLRVEDTAVYICARSHFG-VVIDYGMVWGQGTTVT 119
Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRVEDTAVYICARDHGRYVVDYGMVWGQGTTVT 120

Qy 120 V 120
Db 121 V 121

RESULT 10
US-10-292-088-106
; Sequence 106, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 106
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-106

Query Match          91.9%; Score 578; DB 15; Length 124;
Best Local Similarity 91.8%; Pred. No. 3.3e-48;
Matches 112; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQWNSLRVEDTAVYICAR--SIFGVVIDYGMVWGQGTTV 118
Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRVEDTAVYICARGHQLLGYYVVDYGMVWGQGTTV 120

Qy 119 TV 120
Db 121 TV 122

RESULT 11
US-10-269-711-43
; Sequence 43, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: DeVries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James

```

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; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; TITLE REFERENCE: ANTIBODIES
; FILE REFERENCE: 6989.US.O1
; CURRENT APPLICATION NUMBER: US/10/269,711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-711-43

Query Match          91.8%; Score 577.5; DB 15; Length 123;
Best Local Similarity 92.6%; Pred. No. 3.6e-48;
Matches 112; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQWNSLRVEDTAVYICARSHFG-VVIDYGMVWGQGTTVT 119
Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRVEDTAVYICARDHGRYVVDYGMVWGQGTTVT 120

Qy 120 V 120
Db 121 V 121

RESULT 12
US-10-684-109-35
; Sequence 35, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Weiler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989.US.O2
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-35

Query Match          91.8%; Score 577.5; DB 16; Length 123;
Best Local Similarity 92.6%; Pred. No. 3.6e-48;
Matches 112; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQWNSLRVEDTAVYICARSHFG-VVIDYGMVWGQGTTVT 119
Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRVEDTAVYICARDHGRYVVDYGMVWGQGTTVT 120

Qy 120 V 120
Db 121 V 121

```

RESULT 13  
US-10-858-855-11  
; Sequence 11, Application US/10858855  
; Publication No. US20050118651A1  
; GENERAL INFORMATION:  
; APPLICANT: BASI, Gurik  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA  
; FILE REFERENCE: ELN-028  
; CURRENT APPLICATION NUMBER: US/10/858,855  
; PRIOR FILING DATE: 2004-06-01  
; PRIOR FILING DATE: 2003-05-30  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 141  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)...(19)  
US-10-858-855-11

Query Match 91.7%; Score 577; DB 17; Length 141;  
Best Local Similarity 93.3%; Pred. No. 4.7e-48;  
Matches 112; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
Db 20 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 79  
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCARSIFGVVVDYGMVWGQGTITV 120  
Db 80 ADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCARRHSSWYIGMDVWGQGTITV 139

RESULT 14  
US-10-269-711-7  
; Sequence 7, Application US/10269711  
; Publication No. US20040071694A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: DeVries, Peter J.  
; APPLICANT: Reilly, Edward B.  
; APPLICANT: Ostrow, Dave  
; APPLICANT: Weiler, James  
; APPLICANT: Green, Larry  
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING  
; FILE REFERENCE: 6989 US.O1  
; CURRENT APPLICATION NUMBER: US/10/269,711  
; CURRENT FILING DATE: 2002-10-14  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-269-711-7

Query Match 91.7%; Score 576.5; DB 15; Length 123;  
Best Local Similarity 92.6%; Pred. No. 4.6e-48;  
Matches 112; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
Db 1 QVQLVESGGGVQPGKSLRLSCVASGFTFSYGMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCARSIFG-VVIDYGMVWGQGTITV 119  
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYYCARDHGGRYVVDYGMVWGQGTITV 120

QY 120 V 120  
Db 121 V 121

RESULT 15  
US-10-269-711-15  
; Sequence 15, Application US/10269711  
; Publication No. US20040071694A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: DeVries, Peter J.  
; APPLICANT: Reilly, Edward B.  
; APPLICANT: Ostrow, Dave  
; APPLICANT: Weiler, James  
; APPLICANT: Green, Larry  
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING  
; FILE REFERENCE: 6989 US.O1  
; CURRENT APPLICATION NUMBER: US/10/269,711  
; CURRENT FILING DATE: 2002-10-14  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-269-711-15

Query Match 91.7%; Score 576.5; DB 15; Length 123;  
Best Local Similarity 92.6%; Pred. No. 4.6e-48;  
Matches 112; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCARSIFG-VVIDYGMVWGQGTITV 119  
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYYCARDHGGRYVVDYGMVWGQGTITV 120  
QY 120 V 120  
Db 121 V 121

Search completed: November 9, 2005, 12:43:02  
Job time : 67.6667 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2005, 12:25:58 ; Search time 12.9323 Seconds  
(without alignments)  
892.802 Million cell updates/sec

Title: US-10-660-357A-29  
Perfect score: 629  
Sequence: 1 QVQLVSGGGVQPGKSLRL.....FGVVIDYGMVWGQTTVT 120

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	577	91.7	122	E36005	Ig heavy chain V r
2	559	88.9	128	S48797	Ig heavy chain V r
3	553	87.9	120	S31112	Ig heavy chain - h
4	550.5	87.5	132	S31603	Ig heavy chain V r
5	549.5	87.4	134	S31679	Ig heavy chain V r
6	549	87.3	114	S46390	Ig heavy chain V r
7	546.5	86.9	121	G36005	Ig heavy chain V r
8	545.5	86.7	119	F36005	Ig heavy chain V r
9	543.5	86.4	123	S38493	Ig heavy chain - h
10	542	86.2	122	S31117	Ig heavy chain - h
11	540	85.9	118	S31116	Ig heavy chain - h
12	539.5	85.8	121	S19666	Ig heavy chain V r
13	537	85.4	114	S46392	Ig heavy chain V r
14	536.5	85.3	130	S31601	Ig heavy chain V r
15	535	85.1	137	S31701	Ig heavy chain V r
16	532	84.6	139	S31674	Ig heavy chain V r
17	529.5	84.2	130	PL0098	Ig heavy chain pre
18	524	83.3	140	S70442	Ig heavy chain pre
19	523.5	83.2	133	A49028	Ig heavy chain V-I
20	522	83.0	147	I37780	Ig variable region
21	521.5	82.9	135	S31598	Ig heavy chain V r
22	521	82.8	114	S46391	Ig heavy chain V r
23	520	82.7	133	S31510	Ig heavy chain - h
24	517	82.2	118	PH1660	Ig heavy chain V r
25	516.5	82.1	113	S38490	Ig heavy chain - h
26	516.5	82.1	160	S05271	Ig heavy chain pre
27	516	82.0	122	S31119	Ig heavy chain - h
28	515.5	82.0	109	PH1644	Ig heavy chain V-I
29	514	81.7	122	M3HUM	Ig heavy chain V-I

30	512.5	81.5	109	2	PH1646	Ig heavy chain V r
31	512	81.4	98	2	S29546	Ig heavy chain V r
32	510.5	81.2	111	2	PH1645	Ig heavy chain V r
33	509.5	81.0	111	2	PH1643	Ig heavy chain V r
34	505	80.3	98	2	FL0116	Ig heavy chain V-I
35	503	80.0	118	2	S31677	Ig heavy chain V r
36	503	80.0	151	2	A60943	Ig heavy chain pre
37	502	79.8	108	2	PH1642	Ig heavy chain V r
38	502	79.7	124	2	S20782	Ig heavy chain V r
39	501.5	79.7	117	2	S36270	Ig heavy chain V r
40	501	79.7	119	2	S31111	Ig heavy chain - h
41	499.5	79.4	123	2	S26794	Ig heavy chain V r
42	498	79.2	122	2	S69910	Ig V-D-J region (K
43	497	79.0	134	2	S31688	Ig heavy chain V r
44	496	78.9	118	2	PH1662	Ig heavy chain V r
45	494.5	78.6	125	2	S37455	Ig mu chain - huma

ALIGNMENTS

RESULT 1

E36005  
Ig heavy chain V region (M72) - human  
C/Species: Homo sapiens (man)  
C/Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 16-Dec-1998  
C/Accession: E36005  
R/Schroeder Jr., H.W.; Wang, J.Y.

Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene

A/Reference number: A36005; MUID:90349571; PMID:2117273

A/Accession: E36005

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-122 <SCH>

A/Cross-references: GB:M34030

C/Genetics:

A/Gene: GDB:IGH@; IGHDI1

A/Cross-references: GDB:118731; OMIM:146910

A/Map position: 14q32.33-14q32.33

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 91.7%; Score 577; DB 2; Length 122;  
Best Local Similarity 93.3%; Pred. No. 3.Se-45;  
Matches 112; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 QVQLVSGGGVQPGKSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVISYDGSNKYY 60

Db 1 QVQLVSGGGVQPGKSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYVCARSIFGVVIDYGMVWGQTTVT 120

Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYVCARDRSSWYGMVWGQTTVT 120

RESULT 2

S48797

Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence\_revision 13-Sep-1998 #text\_change 23-Jul-1999

C/Accession: S48797; S26893

R/Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.

submitted to the EMBL Data Library, October 1994

A/Description: Molecular characterization of natural human anti-Sm autoantibodies.

A/Reference number: S48797

A/Molecule type: mRNA

A/Residues: 1-128 <NAH>

A/Cross-references: EMBL:Z46379; NID:g587147; PIDN:CAA86512.1; PID:g1340168

R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992



```
Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60
:|||||:
Db 1 EVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60
|||||

Qy 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVVYCARSIFFGVVIDYGMVWGQGTITVTV 120
|||||
Db 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVVYCAR-----DWG-DYWGQGTITVTV 112

RESULT 7
G36005
Ig heavy chain V region (M74) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C;Accession: G36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: G36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <SCH>
A;Cross-references: UNIPROT:Q8WUK1; GB:M34031
C;Genetics:
A;Gene: GDB:IGH@; IGHDI1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.9%; Score 546.5; DB 2; Length 121;
Best Local Similarity 88.6%; Pred. No. 2e-42;
Matches 109; Conservative 1; Mismatches 6; Indels 7; Gaps 2;

Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60
|||||
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60
|||||

Qy 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVVYCARSIFFGVVIDYGMVWGQGTITVTV 117
|||||
Db 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVVYCAR-----RKDWGWLFDYWGQGTIL 116

Qy 118 VTV 120
|||
Db 117 VTV 119
|||

RESULT 8
F36005
Ig heavy chain V region (M49) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C;Accession: F36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: F36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
A;Cross-references: UNIPROT:Q8WUK1; GB:M34026
C;Genetics:
A;Gene: GDB:IGH@; IGHDI1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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Query Match 86.7%; Score 545.5; DB 2; Length 119;
Best Local Similarity 89.2%; Pred. No. 2.4e-42;
Matches 107; Conservative 1; Mismatches 9; Indels 3; Gaps 1;

Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60
|||||
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60
|||||

Qy 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVVYCARSIFFGVVIDYGMVWGQGTITVTV 120
|||||
Db 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVVYCARD---RKASDAFDIWGQGTITVTV 117

RESULT 9
S38493
Ig heavy chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38493
R;Marks, J.D.; Ouweland, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe,
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a
A;Reference number: S38488
A;Accession: S38493
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-123 <NAR>
A;Cross-references: EMBL:Z23036; NID:g414033; PIDN:CAA80571.1; PID:g414034
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.4%; Score 543.5; DB 2; Length 123;
Best Local Similarity 89.3%; Pred. No. 3.7e-42;
Matches 108; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60
|||||
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60
|||||

Qy 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVVYCARSIFFGVVIDYGMVWGQGTITVTV 119
|||||
Db 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVVYCARARSNWNYYYMDVWGKGTITV 120

Qy 120 V 120
|||
Db 121 V 121
|||

RESULT 10
S31117
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31117
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma,
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31117
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-122 <RAA>
A;Cross-references: EMBL:X62967
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 542; DB 2; Length 122;
Best Local Similarity 88.3%; Pred. No. 5.1e-42;
Matches 106; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
```

1	QVQLVESGGGVQVQPGSR	LRLSCAASGFTFSYAHHWVRQAPGKGLEWAV	ISVDGSKYY	60
Qy				
1	QVQLVESGGGVQVQPGSR	LRLSCAASGFTFSYAHHWVRQAPGKGLEWAV	ISVDGSKYY	60
Db				
61	ADSVKGRFTISRDNSKNTLYIQMNSLR	AEFTAVYICARSIFGVVIDYGM	DMVQGGT	120
Qy				
61	ADSVKGRFTISRDNSKNTLYIQMNSLR	AEFTAVYICARDFEAPPNWSHF	FWCGGLTAV	120
Db				

RESULT 11  
S31116  
IG heavy chain - human  
C/Species: Homo sapiens (man)  
C/Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
C/Accession: S31116  
R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman  
Eur. J. Immunol. 22, 247-251, 1992  
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple  
A/Reference number: S31104; MUID:92111633; PMID:1730252  
A/Accession: S31116  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-118 <PAA>  
A/Cross-references: UNIPROT:Q8WUK1; EMBL:X62966  
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match	85.9%;	Score 540;	DB 2;	Length 118;
Best Local Similarity	87.0%;	Pred. No. 7.4e-42;		
Matches 107;	Conservative 1;	Mismatches 5;	Indels 10;	Gaps 2
Qy	1	QVQLVESGGGVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKLEWAVISVDGSKYY	60	
Db	1	QVQLVESGGGVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKLEWAVISVDGSKYY	60	
Qy	61	AUSVKGRFTISRDNKNTLYLQMSLRADETAVYYCARISFGVVDYGV---	MDVWGQGT	117
Db	61	AUSVKGRFTISRDNKNTLYLQMSLRADETAVYYCA-----	TDGKAAPDIWGQGT	113
Qy	118	VTV	120	
Db	114	VTV	116	

Db 61 ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYCAKT--GYSSGNGYFDYMGQGT LVT 118

Qy 120 V 120

Db 119 V 119

```

RESULT 14
S31601
1g heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31601
R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate
A:Reference number: S31585
A:Accession: S31601
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <CUI>
A:Cross-references: EMBL:Z14192; NID:G31018; PIDN:CAA78561.1; PID:G31019
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
E:30-113/Domains: immunoglobulin homology <IMM>

```

RESULT 15



S31701  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31701  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31701  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-137 <CUI>  
A;Cross-references: EMBL:Z14177; NID:G31020; PIDN:CAA78546.1; PID:G31021  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 85.1%; Score 535; DB 2; Length 137;  
Best Local Similarity 86.7%; Pred. NO. 2.4e-41;  
Matches 104; Conservative 4; Mismatches 8; Indels 4; Gaps 1;  
  
Qy 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60  
Db |||||  
20 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 79  
Qy |||||  
61 ADSVKGRFTIIRDNSKNTLYLQMSLRAEDTAVYYCATPNW----NDAFDIWGGGTWTV 120  
Db |||||  
80 PDSVKGRFTIIRDNSKNTLYLQMSLRAEDTAVYYCATPNW----NDAFDIWGGGTWTV 135

Search completed: November 9, 2005, 13:08:04  
Job time : 12.9323 secs

THE PEOPLE'S REPUBLIC OF CHINA  
(1982-1983)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2005, 11:46:52 ; Search time 61.9549 Seconds  
(without alignments)  
991.843 Million cell updates/sec

Title: US-10-660-357A-29

Perfect score: 629

Sequence: 1 QVQLVSGGGEVQPGKSLRL.....FGVVDYGMVDVGMGGTGVTVV 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541	86.0	613	2 Q8WUK1	Q8wuk1 homo sapien
2	531.5	84.5	240	2 Q652C9	Q652c9 homo sapien
3	529.5	84.2	116	2 Q9UL93	Q9ul93 homo sapien
4	517.5	82.3	113	2 Q9UL90	Q9ul90 homo sapien
5	514	81.7	122	1 HV3G_HUMAN	P01768 homo sapien
6	499	79.3	573	2 Q8WUJ8	Q8wuJ8 homo sapien
7	495	78.7	122	2 Q9UL84	Q9ul84 homo sapien
8	494.5	78.6	472	2 Q6N089	Q6n089 homo sapien
9	493.5	78.5	478	2 Q6PI81	Q6pi81 homo sapien
10	493	78.4	122	1 HV3H_HUMAN	P01769 homo sapien
11	490.5	78.0	121	2 Q9UL71	Q9ul71 homo sapien
12	489	77.7	147	2 Q9Y509	Q9y509 homo sapien
13	482.5	76.7	121	1 HV3J_HUMAN	P01771 homo sapien
14	481	76.5	606	2 Q6GMV2	Q6gmv2 homo sapien
15	480.5	76.4	119	1 HV3I_HUMAN	P01770 homo sapien
16	476	75.7	126	1 HV3K_HUMAN	P01772 homo sapien
17	472.5	75.1	470	2 Q6PJA4	Q6pjA4 homo sapien
18	470	74.7	544	2 Q6PJ95	Q6pj95 homo sapien
19	467.5	74.3	464	2 Q6MZU6	Q6mzu6 homo sapien
20	466.5	74.2	597	2 Q96BB9	Q96bb9 homo sapien
21	465.5	74.0	519	2 Q6N092	Q6n092 homo sapien
22	463.5	73.7	493	2 Q6GNX2	Q6gnx2 homo sapien
23	463	73.6	118	2 Q9UL91	Q9ul91 homo sapien
24	460.5	73.2	482	2 Q7Z351	Q7z351 homo sapien
25	459	73.0	118	2 Q9UL72	Q9ul72 homo sapien
26	454	72.2	112	2 Q9HCC1	Q9hcc1 homo sapien
27	454	72.2	494	2 Q96K68	Q96k68 homo sapien
28	453	72.0	136	1 HV16_MOUSE	P01783 mus musculus
29	453	72.0	479	2 Q6MZV6	Q6mzv6 homo sapien
30	451.5	71.8	119	1 HV3L_HUMAN	P01773 homo sapien
31	450.5	71.6	499	2 Q8N5K4	Q8n5k4 homo sapien

#### RESULT 1

ID	Q8WUK1	PRELIMINARY;	PRT;	613 AA.
AC	Q8WUK1;			
DT	01-MAR-2002 (TrEMBLrel. 20, Created)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	IGHM protein.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RI	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Primary B-Cells;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Primary B-Cells;			
RA	Strausberg R.;			
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC020240; AAH0240.1; -.			
DR	PIR; F36005; F36005.			
DR	PIR; G36005; G36005.			
DR	PIR; PH1642; PH1642.			
DR	PIR; PH1643; PH1643.			
DR	PIR; PH1645; PH1645.			
DR	PIR; PH1646; PH1646.			
DR	PIR; PL0098; PL0098.			
DR	PIR; PL0120; PL0120.			
DR	PIR; S15590; S15590.			
DR	PIR; S31116; S31116.			
DR	PIR; S31119; S31119.			
DR	PIR; S70442; S70442.			

#### ALIGNMENTS

32	449	71.4	473	2 Q91205	Q91205 mus musculus
33	447.5	71.1	493	2 Q68CN4	Q68cn4 homo sapien
34	447	71.1	475	2 Q6MZQ6	Q6mzq6 homo sapien
35	446.5	71.0	493	2 Q8NCL6	Q8ncL6 homo sapien
36	445.5	70.8	485	2 Q6PDB8	Q6pDb8 mus musculus
37	445	70.7	473	2 Q6MZV7	Q6mzv7 homo sapien
38	444.5	70.7	466	2 Q6IN78	Q6in78 homo sapien
39	443	70.4	475	2 Q6GMW7	Q6gmw7 homo sapien
40	442	70.3	117	1 HV3C_HUMAN	P01764 homo sapien
41	440	70.0	116	1 HV3T_HUMAN	P01781 homo sapien
42	440	70.0	483	2 Q6MZK9	Q6mzK9 homo sapien
43	439	69.8	487	2 Q99K44	Q99k44 mus musculus
44	438	69.6	465	2 Q6P6C4	Q6p6C4 homo sapien
45	434	69.0	114	1 HV3B_HUMAN	P01763 homo sapien

```
DR HSSP; P01861; 1ADQ.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 613 AA; 67295 MW; 60C7F5950671E315 CRC64;

Query Match      86.0%; Score 541; DB 2; Length 613;
Best Local Similarity 84.8%; Pred. No. 5.7e-48;
Matches 106; Conservative 3; Mismatches 4; Indels 12; Gaps 2;

QY 1 QVQLVSGGVPQGRSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 20 QVQLVSGGVPQGRSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 79

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVVYCARSIFGVVIDYG-----MDVWGQG 115
Db 80 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVVYCAK-----DWSGEVETFDINGQG 132

QY 116 TVTVV 120
Db 133 TVTVV 137

RESULT 2
Q65ZC9 PRELIMINARY; PRT; 240 AA.
AC Q65ZC9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SQ SEQUENCE FROM N.A.
STRAIN=C1q/7;
RX Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 1_1
FT NON_TER 240 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match      84.5%; Score 531.5; DB 2; Length 240;
Best Local Similarity 85.2%; Pred. No. 1.9e-47;
Matches 104; Conservative 5; Mismatches 4; Indels 9; Gaps 2;

QY 1 QVQLVSGGVPQGRSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 1 QVQLVSGGVPQGRSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVVYCARSIFGVVIDYG--MDVWGQGTTV 118
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVVYCAR-----DWGSLDPWGKTLV 113

QY 119 TV 120
Db 114 TV 115
```

```
RESULT 3
Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SQ SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR PIR; PH1644; PH1644.
DR PIR; PL0120; PL0120.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1_1
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12434 MW; ODA0348154DD6061 CRC64;

Query Match      84.2%; Score 529.5; DB 2; Length 116;
Best Local Similarity 87.4%; Pred. No. 1.3e-47;
Matches 104; Conservative 2; Mismatches 8; Indels 5; Gaps 1;

QY 2 VOLVESGGGVQGRSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYYA 61
Db 1 VOLVESGGGVQGRSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYYA 60

QY 62 DSVKGRFTISRDNKNTLYLQNSLRAEDTAVVYCARSIFGVVIDYGMVWGQGTTVV 120
Db 61 DSVKGRFTISRDNKNTLYLQNSLRAEDTAVVYICAGG-----GGLGLGWGQGTTLTV 114

RESULT 4
Q9UL93 PRELIMINARY; PRT; 113 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SQ SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR PIR; S78486; S78486.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
```

[illegible]

```
ID OSUL84 PRELIMINARY; PRT; 122 AA.
AC Q9UL84;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035030; AAD56266.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 78.7%; Score 495; DB 2; Length 122;
Best Local Similarity 80.0%; Pred. No. 5.7e-44;
Matches 96; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVQPGKSLRLSCLASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVSGGCVQPGKSLRLSCLASGFTFSYMGHWVRQAPGKLEWVAISNDGSKFY 60

QY 61 ADSVKGRTISRDNKNTLYLQNSLRADTAIVYCARSIKFGV--VIDYGMVWGQGTIV 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRTIFRDNKNTLYLQNSLRADTAIVYCARSIKFGV--VIDYGMVWGQGTIV 120

RESULT 8
ID Q9N089 PRELIMINARY; PRT; 472 AA.
AC Q9N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686P15220.
GN Names=DKFZp686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAB45781.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.

QY 1 QVQLVSGGCVQPGKSLRLSCLASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVSGGCVQPGKSLRLSCLASGFTFSYMGHWVRQAPGKLEWVAISNDGSKFY 60

QY 61 ADSVKGRTISRDNKNTLYLQNSLRADTAIVYCARSIKFGV--VIDYGMVWGQGTIV 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRTIFRDNKNTLYLQNSLRADTAIVYCARSIKFGV--VIDYGMVWGQGTIV 120

RESULT 8
ID Q9N089 PRELIMINARY; PRT; 472 AA.
AC Q9N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686P15220.
GN Names=DKFZp686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAB45781.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
```

```
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 78.6%; Score 494.5; DB 2; Length 472;
Best Local Similarity 79.5%; Pred. No. 3.1e-43;
Matches 97; Conservative 9; Mismatches 13; Indels 3; Gaps 2;

QY 1 QVQLVSGGCVQPGKSLRLSCLASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVQLVSGGCVQPGKSLRLSCLASGFTFDDYAMHWVRQAPGKLEWVSGISWSSGIAY 79

QY 61 ADSVKGRTISRDNKNTLYLQNSLRADTAIVYCARSIKFGV--VIDYGMVWGQGTIV 118
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 ADSVKGRTISRDNKNTLYLQNSLRADTAIVYCAKEI-GAHNFYFYGYMDVWGQGTIV 138

QY 119 TV 120
Db 139 TV 140

RESULT 9
Q6PI81 PRELIMINARY; PRT; 478 AA.
ID Q6PI81;
AC Q6PI81;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feilgold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
```

```

RESULT 11
Q9UL71      PRELIMINARY;          PRT;       121 AA.
ID Q9UL71;
AC Q9UL71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2003 (TrEMBLrel. 13, Last sequence update)
DT 01-NOV-2000 (TrEMBLrel. 13, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis S.N., Bernsey S.M.,
   "Myosin D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -.
DR HSP; P01852; INFD.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV_1-.
DR PROSITE; PS50835; IC_LIKE; 1.
FT NON_TER            1
FT TER                121
SQ SEQUENCE           121 AA;  13154 MW;  2F045CCFA5D0736 CRC64;

Query Match              78.0%; Score 490.5; DB 2; Length 121;
Best Local Similarity    78.3%; Pred. No. 1.7e+13;
Matches 94; Conservative 9; Mismatches 46; Indels 1; Gaps 10

QY        1 QVQLVESGGGVQPGRSLRSLCAASGTFFSYAHWVRQAPKGLEWVAIVSYDGSKNKYY 60
Db         :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DY        1 EVQLVESGGGVQPFGSIRLFCAAGSTFFGYAHWVRQAPKGLEWSLVISDGSGTYY 60
QY        61 ADSVKRGPTTSRDNSKNTLYLNWSLRAEATAVVYICARSIFGVVDYGMDVGQGTTVTV 120
Db         |||||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DY        61 ADSVKRGPTTSRDNSKNLSYLQNWSLAEDATLYYCAGKKVTIYD-RFDIWQQGTMTVT 119


RESULT 12
Q9Y509      PRELIMINARY;          PRT;       147 AA.
ID Q9Y509;
AC Q9Y509;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH3 protein (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
   Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
   myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
DR EMBL; S80860; AAD14339.1; -.
DR HSP; P01842; IAOK.
DR GO; GO:0005867; C:integral to plasma membrane; NAS.
DR GO; GO:0016086; P:cellular defense response (sensu Vertebrata); NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IGV.
DR SMART; SM00406; IGV_1-
```

—



## RESULT 15

```

HV3I HUMAN
ID HV3I HUMAN STANDARD; PRT; 119 AA.
AC P01770;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region NIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic
RT peptides of the H-chain, alignment of the tryptic peptides and
RT discussion of the complete structure."
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein NIE). I: purification and
RT characterization of the protein, the L- and H-chains, the cyanogen
RT bromide cleavage products, and the disulfide bridges."
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC -I- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC protein.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A91668; GIKUNI.
DR HSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Direct protein sequencing; Immunoglobulin V region;
KW Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT DISULFID 22 96
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13242 MW; C96935A6E55E165B CRC64;
Query Match 76.4%; Score 480.5; DB 1; Length 119;
Best Local Similarity 77.0%; Pred. No. 1.8e-42;
Matches 94; Conservative 9; Mismatches 12; Indels 7; Gaps 2;
QY 1 QVQLVESGGGVQPGKSLRSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
DB 1 QVQLVQSGGSGVQPGKSLRSCAASGFTFSKRTIHWVRQAPGKLEWVAIVSYBGBKHYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCARSIFGVVIDYGMV--WGQGTTV 118
DB 61 ADSVNGRFTISRDNKNTLYLNNLSRPEDTAVVYCARSIFGVVIDYGMV--WGQGTTV 118
QY 119 TV 120
DB 116 TV 117

```

Search completed: November 9, 2005, 13:05:51  
Job time : 62.9549 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:43:32 ; Search time 72.1353 Seconds  
(without alignments)  
627.306 Million cell updates/sec

Title: US-10-660-357A-33

Perfect score: 626

Sequence: 1 QVQLESGFGLVKPSTLSL.....ARGGDGYRWGQTLTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 segs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	626	100.0	117	7	ADC99804 Anti-huma
2	626	100.0	117	7	ADD05408 Anti-MUC1
3	626	100.0	117	7	ADF09846 Human ant
4	604	96.5	117	7	ADC99776 Anti-huma
5	604	96.5	117	7	ADD05380 Anti-MUC1
6	604	96.5	117	7	ADF09818 Human ant
7	568	90.7	117	7	ADC99784 Anti-huma
8	568	90.7	117	7	ADD05388 Anti-MUC1
9	568	90.7	117	7	ADF09826 Human ant
10	552.5	88.3	118	7	ADC99368 Murine-ex
11	552	88.2	123	7	ADP03870 Murine-ex
12	549.5	87.8	120	7	ADP03974
13	549.5	87.8	120	7	ADP03873 Murine-ex
14	548	87.5	123	7	ADP03869 Murine-ex
15	542	86.6	120	4	AAB62775 Human HIV
16	541	86.4	119	7	ADP03970 Murine-ex
17	540.5	86.3	121	7	ADJ80377 Antibody
18	539	86.1	122	4	AAB62765 Human HIV
19	539	86.1	123	2	AAW78433 Antibody
20	539	86.1	123	5	ABW79796 Heavy cha
21	539	86.1	123	7	ADG88414 anti-Ob-R
22	537.5	85.9	110	7	ADP03934 Murine-ex
23	537.5	85.9	123	4	AAB62745 Human HIV
24	537.5	85.9	124	7	ADP03935 Murine-ex
25	536.5	85.7	122	7	ADP03977 Murine-ex

26	536	85.6	121	7	ADP03981 Murine-ex
27	536	85.6	129	5	AAU81276 Human trk
28	535	85.5	125	7	ADP03871 Murine-ex
29	534.5	85.4	246	3	AAV15126 Anti-muri
30	534	85.3	125	7	ADP03868 Murine-ex
31	534	85.3	125	7	ADP03876 Murine-ex
32	533.5	85.2	221	7	ADP03875 Murine-ex
33	533.5	85.2	221	7	ADJ32126 Human int
34	533	85.1	127	8	ADQ91396 Amino aci
35	532.5	85.1	110	8	ADP22366 Human ant
36	532.5	85.1	252	5	ABP45983 Human Bly
37	532.5	85.1	252	7	ADG96810 Single ch
38	532	85.0	123	7	ADP03872 Murine-ex
39	531	84.8	119	7	ADP03961 Murine-ex
40	531	84.8	121	7	ADP03982 Murine-ex
41	531	84.8	253	5	ABP45608 Human Bly
42	531	84.8	253	7	ADG96435 Single ch
43	530.5	84.7	120	7	ADP03969 Murine-ex
44	530	84.7	119	2	AAW27554 Human Ab
45	530	84.7	119	6	ABJ18676 Antibody

## ALIGNMENTS

### RESULT 1

ADC99804

ID ADC99804 standard; protein; 117 AA.

AC ADC99804;

DT 01-JAN-2004 (first entry)

DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 33.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.

XX Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

XX N-PSDB; ADC99806.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
or condition associated with expression of MUC18 in a patient, e.g.  
tumors, cancers, and other malignancies.

XX Claim 1; SEQ ID NO 33; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising  
a heavy or light chain amino acid or a heavy or light chain variable  
domain where the antibody binds to MUC18. The monoclonal antibody of the  
invention demonstrates cytostatic activity and may be useful for treating  
a disease or condition associated with the expression of MUC18 on the  
cell surface such as tumours, specifically melanoma, oesophageal,  
pancreatic or colorectal tumours, carcinomas, particularly cervical  
carcinomas and cervical intraepithelial neoplasia and cancers including  
colorectal, breast or lung cancer, as well as other malignancies. The  
current sequence is that of the anti-human MUC18 monoclonal antibody

CC heavy chain protein of the invention.

XX Sequence 117 AA;

Query Match 100.0%; Score 626; DB 7; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.8e-46; Mismatches 0; Indels 0; Gaps 0;

Matches 117; Conservative 0;

QY 1 QVLEQSGPGLVKPSETLSLTCTVSGSISSTGYHWSWIRQHPGRGLEWIGYIYSGSTY 60

Db 1 QVLEQSGPGLVKPSETLSLTCTVSGSISSTGYHWSWIRQHPGRGLEWIGYIYSGSTY 60

QY 61 HNPGLSKRITISVDTSKNQFSLKLSVTAADTAVYYCARGDGYRYWGQGLTVTVSS 117

Db 61 HNPGLSKRITISVDTSKNQFSLKLSVTAADTAVYYCARGDGYRYWGQGLTVTVSS 117

#### RESULT 2

ADP05408  
ID ADD05408 standard; protein; 117 AA.

XX AC ADD05408;

DT 01-JAN-2004 (first entry)

XX DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 33.  
XX KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
XX KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
XX OS Homo sapiens.

XX WO2003057006-A2.

XX 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041582.  
XX PR 28-DEC-2001; 2001US-0346460P.  
XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J, Bar-Eli M;

XX WP1; 2003-577496/54.

XX DR N-PSDB; ADD05410.

XX PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
XX PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
XX PT associated with melanoma, or increasing survival of an animal having a  
XX PT metastatic tumor.  
XX PS Claim 1; SEQ ID NO 33; 87pp; English.

XX CC The invention relates to a novel monoclonal antibody used for inhibiting  
XX CC tumour growth in an animal. The tumour inhibition process comprises  
XX CC selecting an animal in need of treatment for a tumour, providing a  
XX CC monoclonal antibody comprising a heavy chain amino acid, where the  
XX CC antibody consists of any one of 10 fully defined sequences of 117-123  
XX CC amino acids given in the specification, and where the monoclonal antibody  
XX CC binds MUC18, and contacting the tumour with the antibody resulting in  
XX CC inhibited proliferation of the cells. The monoclonal antibody has  
XX CC cytostatic and can be used in the production of a vaccine. The monoclonal  
XX CC antibodies against the MUC18 antigen are useful for diagnosing and  
XX CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or  
XX CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
XX CC increasing survival of an animal having a metastatic tumour. This  
XX CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
XX CC protein of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 626; DB 7; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.8e-46; Mismatches 0; Indels 0; Gaps 0;

Matches 117; Conservative 0;

QY 1 QVLEQSGPGLVKPSETLSLTCTVSGSISSTGYHWSWIRQHPGRGLEWIGYIYSGSTY 60

Db 1 QVLEQSGPGLVKPSETLSLTCTVSGSISSTGYHWSWIRQHPGRGLEWIGYIYSGSTY 60

QY 61 HNPGLSKRITISVDTSKNQFSLKLSVTAADTAVYYCARGDGYRYWGQGLTVTVSS 117

Db 61 HNPGLSKRITISVDTSKNQFSLKLSVTAADTAVYYCARGDGYRYWGQGLTVTVSS 117

#### RESULT 3

ADF09846  
ID ADF09846 standard; protein; 117 AA.

XX AC ADF09846;

DT 12-FEB-2004 (first entry)

XX DE Human anti-MUC18 monoclonal antibody heavy chain #9.  
XX KW cell proliferation inhibition; MUC18 tumour antigen;  
XX KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
XX KW carcinoma; cancer; malignancy; heavy chain; human.  
XX OS Homo sapiens.

XX WO2003057837-A2.

XX 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041580.

XX PR 28-DEC-2001; 2001US-0346414P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J;

XX WP1; 2003-598367/56.

XX DR N-PSDB; ADF09846.

XX PT Inhibiting cell proliferation associated with expression of MUC18 tumour  
XX PT antigen, involves incubating and inhibiting cell by administering anti-  
XX PT MUC18 monoclonal antibody.  
XX PS Claim 1; SEQ ID NO 33; 83pp; English.

XX CC The invention comprises a method for inhibiting cell proliferation  
XX CC associated with expression of MUC18 tumour antigen. The method involves  
XX CC administering anti-MUC18 monoclonal antibody. The method of the invention  
XX CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
XX CC proliferation associated with the expression of MUC18 tumour antigen, the  
XX CC method is preferably useful for inhibiting tumour metastasis. The method  
XX CC is useful for inhibiting cell proliferation in patients with tumours,  
XX CC carcinomas, cancer and other malignancies. The present amino acid  
XX CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
XX CC monoclonal antibody.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 626; DB 7; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.8e-46;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLEQSGPGLVKPSETLSLTCTVSGSISSTGYHWSWIRQHPGRGLEWIGYIYSGSTY 60

Db 1 QVLEQSGPGLVKPSETLSLTCTVSGSISSTGYHWSWIRQHPGRGLEWIGYIYSGSTY 60

QY 61 HNPGLSKRITISVDTSKNQFSLKLSVTAADTAVYYCARGDGYRYWGQGLTVTVSS 117

Db 61 HNPGLSKRITISVDTSKNQFSLKLSVTAADTAVYYCARGDGYRYWGQGLTVTVSS 117

DT	01-JAN-2004	(first entry)
XX		
DE	Anti-MUC18	antibody heavy chain variable region protein, SEQ ID No 5.
XX		
KW	monoclonal antibody;	tumour; MUC18; proliferation; cytostatic; vaccine;
KW	antigen;	tumour metastasis; melanoma; metastatic; human; heavy chain.
XX		
OS	Homo sapiens.	
XX		
FN	W02003057006-A2.	
XX		
PD	17-JUL-2003.	
XX		
PF	26-DEC-2002;	2002WO-US041592.
XX		
PR	28-DEC-2001;	2001US-0346460P.
XX		
PA	(ABGE-)	ABGENIX INC.
XX		
PI	Gudas J,	Bar-Eli M;
XX		
WPI	2003-577496/54.	
DR	N-PSDB;	ADD05382.
XX		
PT	Use of monoclonal antibodies	against MUC18 antigen, for diagnosing and
PT	treating tumors,	inhibiting tumor growth, inhibiting cell invasion
PT	associated with melanoma,	or increasing survival of an animal having a
PT	metastatic tumor.	
XX		
PS	Claim 1;	SEQ ID NO 5; 87pp; English.
XX		
CC	The invention relates to a novel monoclonal antibody used for inhibiting	
CC	tumour growth in an animal. The tumour inhibition process comprises	
CC	selecting an animal in need of treatment for a tumour, providing a	
CC	monoclonal antibody comprising a heavy chain amino acid, where the	
CC	antibody consists of any one of 10 fully defined sequences of 117-123	
CC	amino acids given in the specification, and where the monoclonal antibody	
CC	binds MUC18, and contacting the tumour with the antibody resulting in	
CC	inhibited proliferation of the cells. The monoclonal antibody has	
CC	cytostatic and can be used in the production of a vaccine. The monoclonal	
CC	antibodies against the MUC18 antigen are useful for diagnosing and	
CC	treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or	
CC	tumour metastasis), inhibiting cell invasion associated with melanoma, or	
CC	increasing survival of an animal having a metastatic tumour. This	
CC	sequence represents an anti-MUC18 antibody heavy chain, variable region,	
CC	protein of the invention.	
XX		
SQ	Sequence 117 AA;	
	Query Match	96.5%; Score 604; DB 7; Length 117;
	Best Local Similarity	94.0%; Pred. No. 1.4e-44;
	Matches 110; Conservative	7; Mismatches 0; Indels 0; Gaps 0
Qy	1	QVQLQSGPGLVKPSETLSLTCTVSGSGISGTVHWSWIRQHPGKLEWIGYIYSGSTY 60
Db	1	QVQLQSGPGLVKPSETLSLTCTVSGSGISGTVHWSWIRQHPGKLEWIGYIYSGSTY 60
Qy	61	HNPSLSKRITISVDTSKNQPSLSSVTADTAVYYCARGDGYRYWGQGLTIVTSS 117
Db	61	YNPSLSKRVTISVDTSKNQPSLSSVTADTAVYYCARGDGYRYWGQGLTIVTSS 117
RESULT 6		
ADFO9818		
ID	ADFO9818	standard; protein; 117 AA.
XX	AC	ADFO9818;
XX		
DT	12-FEB-2004	(first entry)
XX		
DE	Human anti-MUC18 monoclonal antibody heavy chain #2.	
XX		
KW	cell proliferation inhibition;	MUC18 tumour antigen;

KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
 KW carcinoma; cancer; malignancy; heavy chain; human.  
 XX Homo sapiens.  
 OS  
 XX WO2003057837-A2.  
 PN  
 XX  
 XX 17-JUL-2003.  
 PD  
 XX  
 XX 26-DEC-2002; 2002WO-US041580.  
 PF  
 XX  
 XX 28-DEC-2001; 2001US-0346414P.  
 PR  
 XX  
 XX (ABGE-) ABGENIX INC.  
 PA  
 XX  
 XX Gudas J;  
 PI  
 XX  
 XX WPI; 2003-598367/56.  
 DR  
 XX N-PSDB; ADF09820.  
 DR  
 XX  
 XX Inhibiting cell proliferation associated with expression of MUC18 tumor  
 PT antigen, involves incubating and inhibiting cell by administering anti-  
 PT MUC18 monoclonal antibody.  
 XX  
 XX  
 PS Claim 1; SEQ ID NO 5; 83pp; English.  
 CC The invention comprises a method for inhibiting cell proliferation  
 CC associated with expression of MUC18 tumour antigen. The method involves  
 CC administering anti-MUC18 monoclonal antibody. The method of the invention  
 CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
 CC proliferation associated with the expression of MUC18 tumour antigen, the  
 CC method is preferably useful for inhibiting tumour metastasis. The method  
 CC is useful for inhibiting cell proliferation in patients with tumours,  
 CC carcinomas, cancer and other malignancies. The present amino acid  
 CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
 CC monoclonal antibody.  
 XX  
 XX Sequence 117 AA;  
 SQ  
 Query Match 96.5%; Score 604; DB 7; Length 117;  
 Best Local Similarity 94.0%; Pred. No. 1.4e-44;  
 Matches 110; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISGGTYHWSWIRQHPGKLEWIGYIYSGSTY 60  
 Db 1 QVQLQESGPGLVKPSQTLSTLTCTVSGGSISGGTYHWSWIRQHPGKLEWIGYIYSGSTY 60  
 Qy 61 HNPFLKSRITISVDTSKNQPSLKLSSVTAADTAVVYCARGDGYRYWGQGLTVTVSS 117  
 Db 61 YNPFLKSRITISVDTSKNQPSLKLSSVTAADTAVVYCARGDGYRYWGQGLTVTVSS 117  
 RESULT 7  
 ADC99784  
 ID ADC99784 standard; protein; 117 AA.  
 AC  
 AC ADC99784;  
 XX  
 XX 01-JAN-2004 (first entry)  
 DT  
 XX  
 DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 13.  
 XX  
 KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
 KW cytosolic; melanoma; oesophageal; pancreatic; colorectal tumour;  
 KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
 KW lung cancer; human.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003057838-A2.  
 PN  
 XX 17-JUL-2003.  
 PD  
 XX

PF 26-DEC-2002; 2002WO-US041581.  
 XX  
 XX 28-DEC-2001; 2001US-0346299P.  
 PR  
 XX  
 XX (ABGE-) ABGENIX INC.  
 PA  
 XX  
 XX Gudas J;  
 PI  
 XX  
 XX WPI; 2003-587113/55.  
 DR  
 XX N-PSDB; ADC99786.  
 DR  
 XX  
 XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
 PT or condition associated with expression of MUC18 in a patient, e.g.  
 PT tumors, cancers, and other malignancies.  
 PT  
 XX  
 XX Claim 1; SEQ ID NO 13; 78pp; English.  
 PS  
 XX  
 XX The invention relates to a novel isolated monoclonal antibody comprising  
 CC a heavy or light chain amino acid or a heavy or light chain variable  
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
 CC invention demonstrates cytostatic activity and may be useful for treating  
 CC a disease or condition associated with the expression of MUC18 on the  
 CC cell surface such as tumours, specifically melanoma, oesophageal,  
 CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
 CC carcinomas and cervical intraepithelial neoplasia and cancers including  
 CC colorectal, breast or lung cancer, as well as other malignancies. The  
 CC current sequence is that of the anti-human MUC18 monoclonal antibody  
 CC heavy chain protein of the invention.  
 CC  
 XX Sequence 117 AA;  
 SQ  
 Query Match 90.7%; Score 568; DB 7; Length 117;  
 Best Local Similarity 88.9%; Pred. No. 1.8e-41;  
 Matches 104; Conservative 10; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISGGTYHWSWIRQHPGKLEWIGYIYSGSTY 60  
 Db 1 QVQLQESGPGLVKPSQTLSTLTCTVSGGSISGGTYHWSWIRQHPGKLEWIGYIYSGSTY 60  
 Qy 61 HNPFLKSRITISVDTSKNQPSLKLSSVTAADTAVVYCARGDGYRYWGQGLTVTVSS 117  
 Db 61 YNPFLKSRITISVDTSKNQPSLKLSSVTAADTAVVYCARGDGYRYWGQGLTVTVSS 117  
 RESULT 8  
 ADD05388  
 ID ADD05388 standard; protein; 117 AA.  
 XX  
 AC ADD05388;  
 XX  
 XX 01-JAN-2004 (first entry)  
 DT  
 XX  
 DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 13.  
 XX  
 KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
 KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003057006-A2.  
 PN  
 XX 17-JUL-2003.  
 PD  
 XX  
 XX 26-DEC-2002; 2002WO-US041582.  
 PF  
 XX  
 XX 28-DEC-2001; 2001US-0346460P.  
 PR  
 XX  
 XX (ABGE-) ABGENIX INC.  
 PA  
 XX  
 XX Gudas J, Bar-Eli M;  
 PI  
 XX  
 XX WPI; 2003-577496/54.  
 DR  
 XX N-PSDB; ADD05390.  
 DR

XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
PT associated with melanoma, or increasing survival of an animal having a  
PT metastatic tumor.

XX Claim 1; SEQ ID NO 13; 87pp; English.

PS The invention relates to a novel monoclonal antibody used for inhibiting  
CC tumor growth in an animal. The tumor inhibition process comprises  
CC selecting an animal in need of treatment for a tumor, providing a  
CC monoclonal antibody comprising a heavy chain amino acid, where the  
CC antibody consists of any one of 10 fully defined sequences of 117-123  
CC amino acids given in the specification, and where the monoclonal antibody  
CC binds MUC18, and contacting the tumor with the antibody resulting in  
CC inhibited proliferation of the cells. The monoclonal antibody has  
CC cytostatic and can be used in the production of a vaccine. The monoclonal  
CC antibodies against the MUC18 antigen are useful for diagnosing and  
CC treating tumors, inhibiting tumor growth (e.g. melanoma, lung tumor or  
CC tumor metastasis), inhibiting cell invasion associated with melanoma, or  
CC increasing survival of an animal having a metastatic tumor. This  
CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
CC protein of the invention.

XX Sequence 117 AA;

Query Match 90.7%; Score 568; DB 7; Length 117;  
Best Local Similarity 88.9%; Pred. No. 1.8e-41;  
Matches 104; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60  
Db 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60

Qy 61 HNPFLSKSRITISVDTSKNQFSLKLSVTAADTAVYVCARGDGYRYWGQGLTVTVSS 117  
Db 61 YNPSLSKSRVTISVDTSKNQFSLKLSVTAADTAVYVCAREGDGFDYWGQGLTVTVSS 117

RESULT 9  
ADF09826  
ID ADF09826 standard; protein; 117 AA.

AC ADF09826;

XX 12-FEB-2004 (first entry)

XX Human anti-MUC18 monoclonal antibody heavy chain #4.

XX cell proliferation inhibition; MUC18 tumour antigen;  
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
KW carcinoma; cancer; malignancy; heavy chain; human.

XX Homo sapiens.

XX WO2003057837-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041580.

XX 28-DEC-2001; 2001US-0346414P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-598367/56.  
XX N-PSDB; ADF09826.

XX Inhibiting cell proliferation associated with expression of MUC18 tumor  
PT antigen, involves incubating and inhibiting cell by administering anti-  
PT MUC18 monoclonal antibody.

XX Claim 1; SEQ ID NO 13; 83pp; English.

XX The invention comprises a method for inhibiting cell proliferation  
CC associated with expression of MUC18 tumour antigen. The method involves  
CC administering anti-MUC18 monoclonal antibody. The method of the invention  
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
CC proliferation associated with the expression of MUC18 tumour antigen, the  
CC method is preferably useful for inhibiting tumour metastasis. The method  
CC is useful for inhibiting cell proliferation in patients with tumours,  
CC carcinomas, cancer and other malignancies. The present amino acid  
CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
CC monoclonal antibody.

XX Sequence 117 AA;

Query Match 90.7%; Score 568; DB 7; Length 117;  
Best Local Similarity 88.9%; Pred. No. 1.8e-41;  
Matches 104; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60  
Db 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60

Qy 61 HNPFLSKSRITISVDTSKNQFSLKLSVTAADTAVYVCARGDGYRYWGQGLTVTVSS 117  
Db 61 YNPSLSKSRVTISVDTSKNQFSLKLSVTAADTAVYVCAREGDGFDYWGQGLTVTVSS 117

RESULT 10  
ADP03968  
ID ADP03968 standard; protein; 118 AA.

AC ADP03968;

XX 29-JUL-2004 (first entry)

XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138.

XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KW cytostatic; colorectal neoplasm; renal cell carcinoma;  
KW cervical intraepithelial squamous neoplasia;  
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX Unidentified.

XX WO2003048328-A2.

XX 12-JUN-2003.

XX 02-DEC-2002; 2002WO-US038550.

XX 03-DEC-2001; 2001US-0337275P.

XX (ABGE-) ABGENIX INC.

XX Gudas J, Foltz I, Handa M, Gallo M;

XX WPI; 2003-523295/49.

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX Example 2; SEQ ID NO 138; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mab)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cytostatic activity and may be useful for treating a tumour,

CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.

XX SQ Sequence 118 AA;

Query Match 88.1%; Score 552.5; DB 7; Length 118;

Best Local Similarity 89.0%; Pred. No. 4e-40;

Matches 105; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

QY 1 QVQLQSGPLVKPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 1 QVQLQSGPLVKPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 HNPSTLSKSRITISVDTSKNQFSLKSLSVTAADTAIVYCAR--GGDGYRWGGTLVTVSS 117

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 YNPSTLSKSRITISVDTSKNQFSLKSLSVTAADTAIVYCAR--GGDGYRWGGTLVTVSS 118

#### RESULT 11

ADP03870

ID ADP03870 standard; protein; 123 AA.

XX

AC ADP03870;

XX

DT 29-JUL-2004 (first entry)

XX

DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 10.

XX

KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;

KW cytotatic; colorectal neoplasm; renal cell carcinoma;

KW cervical intraepithelial squamous neoplasia;

KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;

KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX OS Unidentified.

XX

PN W02003048328-A2.

XX

PD 12-JUN-2003.

XX

PF 02-DEC-2002; 2002WO-US038550.

XX

PR 03-DEC-2001; 2001US-0337275P.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Gudas J, Foltz I, Handa M, Gallo M;

XX

DR WPI; 2003-523295/49.

XX

PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,

PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical

PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX

PS Claim 1; SEQ ID NO 10; 89pp; English.

XX

CC The invention relates to a novel isolated monoclonal antibody (mAb)

CC comprising a heavy chain polypeptide and light chain polypeptide having a

CC sequence chosen from one of 53 fully defined amino acid sequences given

CC in the specification, where the antibody specifically binds carbonic

CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention

CC demonstrates cytostatic activity and may be useful for treating a tumour,

CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,

CC cervical intraepithelial squamous and glandular neoplasia, oesophageal

CC tumour or breast cancer, possibly via gene therapy. The current sequence

CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH

CC (heavy chain variable domain) protein of the invention. The protein was

CC generated via the introduction of the human CA IX protein into a

CC transgenic mouse strain.

XX

SQ Sequence 123 AA;

XX

Query Match 88.2%; Score 552; DB 7; Length 123;

Best Local Similarity 85.4%; Pred. No. 4.6e-40;

Matches 105; Conservative 7; Mismatches 5; Indels 6; Gaps 1;

QY 1 QVQLQSGPLVKPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 1 QVQLQSGPLVKPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 HNPSTLSKSRITISVDTSKNQFSLKSLSVTAADTAIVYCARGGDY-----RWGGQTLVT 114

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 YNPSTLSKSRITISVDTSKNQFSLKSLSVTAADTAIVYCARAGKYGGSYLDYWGQTLVT 120

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 115 VSS 117

|||

Db 121 VSS 123

|||

#### RESULT 12

ADP03974

ID ADP03974 standard; protein; 120 AA.

XX

AC ADP03974;

XX

DT 29-JUL-2004 (first entry)

XX

DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.

XX

KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;

KW cytotatic; colorectal neoplasm; renal cell carcinoma;

KW cervical intraepithelial squamous neoplasia;

KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;

KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX OS Unidentified.

XX

PN W02003048328-A2.

XX

PD 12-JUN-2003.

XX

PF 02-DEC-2002; 2002WO-US038550.

XX

PR 03-DEC-2001; 2001US-0337275P.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Gudas J, Foltz I, Handa M, Gallo M;

XX

DR WPI; 2003-523295/49.

XX

PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,

PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical

PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX

PS Example 2; SEQ ID NO 144; 89pp; English.

XX

CC The invention relates to a novel isolated monoclonal antibody (mAb)

CC comprising a heavy chain polypeptide and light chain polypeptide having a

CC sequence chosen from one of 53 fully defined amino acid sequences given

CC in the specification, where the antibody specifically binds carbonic

CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention

CC demonstrates cytostatic activity and may be useful for treating a tumour,

CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,

CC cervical intraepithelial squamous and glandular neoplasia, oesophageal

CC tumour or breast cancer, possibly via gene therapy. The current sequence

CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH

CC (heavy chain variable domain) protein of the invention. The protein was

CC generated via the introduction of the human CA IX protein into a

CC transgenic mouse strain.

XX



SQ Sequence 120 AA;

Query Match 87.8%; Score 549.5; DB 7; Length 120;

Best Local Similarity 86.1%; Pred. No. 7.3e-40;

Matches 105; Conservative 8; Mismatches 2; Indels 7; Gaps 2;

Qy 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60

Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60

Qy 61 HNPFLSKSRITISVDTSKNQFSLKLSVTAADTAIVYICARGDGVY-----WGQGLTLTV 115

Db 61 YNPSLKSRTISVDTSKNQFSLKLSVTAADTAIVYICAR--DGYNYWYFDLWGRGTLTV 118

Qy 116 SS 117

Db 119 SS 120

RESULT 13

ADP03873

ID ADP03873 standard; protein; 120 AA.

XX

AC ADP03873;

XX

DT 29-JUL-2004 (first entry)

XX

DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.

XX

KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;

KW cytosatic; colorectal neoplasm; renal cell carcinoma;

KW cervical intraepithelial squamous neoplasia;

KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;

KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX

OS Unidentified.

XX

PN WO2003048328-A2.

XX

PD 12-JUN-2003.

XX

PF 02-DEC-2002; 2002WO-US038550.

XX

PR 03-DEC-2001; 2001US-0337275P.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Gudas J, Foltz I, Handa M, Gallo M;

XX

DR WPI; 2003-523295/49.

XX

PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.;

PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical

PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX

PS Claim 1; SEQ ID NO 13; 89pp; English.

XX

CC The invention relates to a novel isolated monoclonal antibody (mAb)

CC comprising a heavy chain polypeptide and light chain polypeptide having a

CC sequence chosen from one of 53 fully defined amino acid sequences given

CC in the specification, where the antibody specifically binds carbonic

CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention

CC demonstrates cytostatic activity and may be useful for treating a tumour,

CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,

CC cervical intraepithelial squamous and glandular neoplasia, oesophageal

CC tumour or breast cancer, possibly via gene therapy. The current sequence

CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH

CC (heavy chain variable domain) protein of the invention. The protein was

CC generated via the introduction of the human CA IX protein into a

CC transgenic mouse strain.

XX

SQ Sequence 120 AA;

Query Match 87.5%; Score 548; DB 7; Length 123;

Best Local Similarity 85.4%; Pred. No. 1e-39;

Query Match

Best Local Similarity

Matches 105; Conservative

Qy 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60

Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60

Qy 61 HNPFLSKSRITISVDTSKNQFSLKLSVTAADTAIVYICARGDGVY-----WGQGLTLTV 115

Db 61 YNPSLKSRTISVDTSKNQFSLKLSVTAADTAIVYICAR--DGYNYWYFDLWGRGTLTV 118

Qy 116 SS 117

Db 119 SS 120

RESULT 14

ADP03869

ID ADP03869 standard; protein; 123 AA.

XX

AC ADP03869;

XX

DT 29-JUL-2004 (first entry)

XX

DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 9.

XX

KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;

KW cytosatic; colorectal neoplasm; renal cell carcinoma;

KW cervical intraepithelial squamous neoplasia;

KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;

KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX

OS Unidentified.

XX

PN WO2003048328-A2.

XX

PD 12-JUN-2003.

XX

PF 02-DEC-2002; 2002WO-US038550.

XX

PR 03-DEC-2001; 2001US-0337275P.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Gudas J, Foltz I, Handa M, Gallo M;

XX

DR WPI; 2003-523295/49.

XX

PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.;

PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical

PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX

PS Claim 1; SEQ ID NO 9; 89pp; English.

XX

CC The invention relates to a novel isolated monoclonal antibody (mAb)

CC comprising a heavy chain polypeptide and light chain polypeptide having a

CC sequence chosen from one of 53 fully defined amino acid sequences given

CC in the specification, where the antibody specifically binds carbonic

CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention

CC demonstrates cytostatic activity and may be useful for treating a tumour,

CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,

CC cervical intraepithelial squamous and glandular neoplasia, oesophageal

CC tumour or breast cancer, possibly via gene therapy. The current sequence

CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH

CC (heavy chain variable domain) protein of the invention. The protein was

CC generated via the introduction of the human CA IX protein into a

CC transgenic mouse strain.

XX

SQ Sequence 123 AA;

Query Match

Best Local Similarity

Score 548; DB 7; Length 123;

Pred. No. 1e-39;

Job time : 73.1353 secs

Matches 105; Conservative 6; Mismatches 6; Indels 6; Gaps 1;

Qy 1 QVLEQSGPGLVXPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 QVLEQSGPGLVXPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 61 HNFSLKSRITISVDTSKNQFSLKLSVTAADTAVYVCARGDGY-----RYWGQGTLLVT 114  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 YNPSLSKSRVTISIDTSKNQFSLKLSVTAADTAVYVCARGDGY-----RYWGQGTLLVT 120  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 115 VSS 117  
:|||||  
Db 121 VSS 123  
:|||||

RESULT 15  
AAB62775  
ID AAB62775 standard; protein; 120 AA.  
XX  
AC AAB62775;  
XX  
DT 03-APR-2001 (first entry)  
XX  
DE Human HIV-1 monoclonal antibody SEQ ID NO: 74.  
XX  
KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;  
KW envelope glycoprotein; gp120; diagnosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200100678-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-US017327.  
XX  
PR 30-JUN-1999; 99US-0141701P.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Watkins BA, Reitz MS;  
XX  
DR WPI; 2001-112438/12.  
DR N-PSDB; AAF29076.  
XX  
PT Novel human monoclonal antibody immunoreactive with human  
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1  
PT in biological sample and providing passive immunotherapy to HIV-1  
PT infected mammal.  
XX  
PS Claim 1; Page 69; 81pp; English.  
XX  
CC The present invention provides the protein and coding sequences for the  
CC variable regions of human monoclonal antibodies which are immunoreactive  
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.  
CC These can be used in diagnosis and therapy of HIV-1 infection  
XX  
SQ Sequence 120 AA;

Query Match 86.6%; Score 542; DB 4; Length 120;  
Best Local Similarity 86.6%; Pred. No. 3.3e-39;  
Matches 103; Conservative 9; Mismatches 5; Indels 2; Gaps 1;

Qy 1 QVLEQSGPGLVXPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 2 EVQLESGPGLVXPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 61  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 61 HNFSLKSRITISVDTSKNQFSLKLSVTAADTAVYVCARG--GDGYRYWGQGTLLVTSS 117  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 62 YNPSLSKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARGVVVDWFDPMGQGTLLTVSS 120  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: November 9, 2005, 12:55:31

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55 ; Search time 18.1805 Seconds  
(without alignments)  
480.403 Million cell updates/sec

Title: US-10-660-357A-33

Perfect score: 626

Sequence: 1 QVQLQSGPGGLVPSFETLSL.....ARGGDGYRWGQGLTVTS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.\*
- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/PCFUS COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	530	84.7	119	3	US-09-025-769B-39
2	530	84.7	119	3	US-09-025-769B-65
3	530	84.7	119	4	US-09-490-070A-39
4	530	84.7	119	4	US-09-490-070A-65
5	530	84.7	119	4	US-09-490-153-39
6	530	84.7	119	4	US-09-490-153-65
7	530	84.7	119	4	US-09-490-324-39
8	530	84.7	119	4	US-09-490-324-65
9	520.5	83.1	122	1	US-08-360-125-11
10	520.5	83.1	122	2	US-08-450-578-11
11	520.5	83.1	122	2	US-09-017-628-11
12	520.5	83.1	122	2	US-09-014-880-11
13	520.5	83.1	122	4	US-08-450-363-11
14	520.5	83.1	122	4	US-09-467-903-11
15	519.5	83.0	473	3	US-09-049-672A-4
16	517	82.6	119	1	US-08-360-125-5
17	517	82.6	119	2	US-08-450-578-5
18	517	82.6	119	2	US-09-017-628-5
19	517	82.6	119	2	US-09-014-880-5
20	517	82.6	119	4	US-08-450-363-5
21	517	82.6	119	4	US-09-467-903-5
22	513.5	82.0	487	4	US-09-800-729-145
23	511.5	81.7	118	3	US-09-025-769B-25
24	511.5	81.7	118	4	US-09-490-070A-25
25	511.5	81.7	118	4	US-09-490-153-25
26	511.5	81.7	118	4	US-09-490-324-25
27	503	80.4	117	4	US-09-720-493-2

28	499.5	79.8	244	3	US-08-918-148-79	Sequence 79, Appl
29	499.5	79.8	244	4	US-09-138-091A-77	Sequence 77, Appl
30	496.5	79.3	120	4	US-09-424-840B-20	Sequence 20, Appl
31	496.5	79.3	172	4	US-09-472-087-7	Sequence 7, Appl
32	496.5	79.3	172	4	US-09-472-087-86	Sequence 86, Appl
33	493	78.8	118	3	US-08-545-809A-116	Sequence 116, App
34	492	78.6	142	2	US-08-480-774A-2	Sequence 2, Appl
35	479	76.5	118	3	US-08-545-809A-142	Sequence 142, App
36	476.5	76.1	278	3	US-09-260-527-3	Sequence 3, Appl
37	475	75.9	119	2	US-08-652-816A-10	Sequence 10, Appl
38	472.5	75.5	139	4	US-09-471-276-837	Sequence 837, App
39	467.5	74.7	98	1	US-08-478-039-75	Sequence 75, Appl
40	467.5	74.7	98	1	US-08-476-349A-75	Sequence 75, Appl
41	467	74.6	118	3	US-08-545-809A-123	Sequence 123, App
42	466	74.4	117	4	US-09-232-290-47	Sequence 47, Appl
43	462	73.8	155	4	US-09-471-276-888	Sequence 888, App
44	461	73.6	116	3	US-08-545-809A-140	Sequence 140, App
45	460.5	73.6	150	4	US-09-582-337-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1  
US-09-025-769B-39  
; Sequence 39, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckhuhn, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA: EP 95 11 3021.0  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-39

Query Match 84.7%; Score 530; DB 3; Length 119;  
Best Local Similarity 86.8%; Pred. No. 3.3e-45;  
Matches 105; Conservative 7; Mismatches 3; Indels 6; Gaps 3;

[illegible]

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RESULT 2
US-09-025-769B-65
; Sequence 65, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knaappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-65

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Db 119 S 119

RESULT 3  
US-09-490-070A-39  
; Sequence 39, Application US/09490070A  
; Patent No. 6696248  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Colin G. Sandercock, Esq. c/o Heller Ehrman  
; White & McAuliffe  
; STREET: 1666 K Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,070A  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Colin G. Sandercock, Esq.  
; REGISTRATION NUMBER: 31,298  
; REFERENCE/DOCKET NUMBER: 37629-0005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 912-2000  
; TELEFAX: (202) 912-2020  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
; PS-09-490-070A-39

RESULT 4  
US-09-490-070A-65  
; Sequence 65, Application US/09490070A

Patent No. 6696248  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIORITY APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-070A-65  
Query Match 84.7%; Score 530; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 3.3e-45;  
Matches 105; Conservative 7; Mismatches 3; Indels 6; Gaps 3;  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTGYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTGYHWSWIRQHPGRGLEWIGYIYSGSTN 58  
Qy 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYICAR-GGDGY---RYWGQGTLTVTS 116  
Db 59 YNPFLKSRVTISVDTSKNQFSLKLSVTAADTAVYICARWGDDGFYAMDYWGQGTLTVTS 118  
Qy 117 S 117  
Db 119 S 119  
RESULT 5  
US-09-490-153-39  
Sequence 39, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York

TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: <unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-153-39  
Query Match 84.7%; Score 530; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 3.3e-45;  
Matches 105; Conservative 7; Mismatches 3; Indels 6; Gaps 3;  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTGYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTGYHWSWIRQHPGRGLEWIGYIYSGSTN 58  
Qy 61 HNPFLKSRITISVDTSKNQFSLKLSVTAADTAVYICAR-GGDGY---RYWGQGTLTVTS 116  
Db 59 YNPFLKSRVTISVDTSKNQFSLKLSVTAADTAVYICARWGDDGFYAMDYWGQGTLTVTS 118  
Qy 117 S 117  
Db 119 S 119  
RESULT 6  
US-09-490-153-65  
Sequence 65, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York

STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9090  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-153-65  
Query Match 84.7%; Score 530; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 3.3e-45;  
Matches 105; Conservative 7; Mismatches 3; Indels 6; Gaps 3;  
QY 1 QVQLQESGPGLVKVPSETLSLTCTVSGSISSTGYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QVQLQESGPGLVKVPSETLSLTCTVSGSISSTGYHWSWIRQHPGRGLEWIGYIYSGSTN 58  
QY 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAIVYCAR--GGDGY--RYWGQGTILTVTS 116  
Db 59 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAIVYCARWGDDGFYAMDYWGQGTILTVTS 118  
QY 117 S 117  
Db 119 S 119  
RESULT 7  
US-09-490-324-39  
Sequence 39, Application US/09490324  
Patent No. 6828422  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,324  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9090  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-324-39  
Query Match 84.7%; Score 530; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 3.3e-45;  
Matches 105; Conservative 7; Mismatches 3; Indels 6; Gaps 3;  
QY 1 QVQLQESGPGLVKVPSETLSLTCTVSGSISSTGYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QVQLQESGPGLVKVPSETLSLTCTVSGSISSTGYHWSWIRQHPGRGLEWIGYIYSGSTN 58  
QY 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAIVYCAR--GGDGY--RYWGQGTILTVTS 116  
Db 59 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAIVYCARWGDDGFYAMDYWGQGTILTVTS 118  
QY 117 S 117  
Db 119 S 119  
RESULT 8  
US-09-490-324-65  
Sequence 65, Application US/09490324  
Patent No. 6828422  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,324  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769



GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Yoshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5837845ihiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,578  
FILING DATE: May 25, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:

AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-578-11  
Query Match 83.1%; Score 520.5; DB 2; Length 122;  
Best Local Similarity 82.8%; Pred. No. 2.9e-44;  
Matches 101; Conservative 8; Mismatches 8; Indels 5; Gaps 2;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGIYYSGSTY 60  
Db 1 QLQLQESGPGLVKPSSETLSLTCTVSGGSISSSYWGWIRQHPGKLEWIGSIYYSGSTY 60  
QY 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVVYCARGG-DGYRY----WQGGTLVTV 115  
Db 61 YNPFLKSRVTISVDTSKNQFSLKLSVTAADTAVVYCARGSYGGYYGMDVMQGGTTTV 120  
QY 116 SS 117  
Db 121 SS 122  
RESULT 11  
US-09-017-628-11  
; Sequence 11, Application US/09017628  
; Patent No. 5990287  
; GENERAL INFORMATION:  
; APPLICANT: HOSOKAWA, Saiko  
; APPLICANT: TAGAWA, Yoshiaki  
; APPLICANT: HIRAKAWA, Yoko  
; APPLICANT: ITO, No. 5990287ihiko  
; APPLICANT: NAGAIKE, Kazuhiro  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO  
; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
; FILE REFERENCE: 177/527361KH  
; CURRENT APPLICATION NUMBER: US/09/017,628  
; CURRENT FILING DATE: 1998-02-02  
; EARLIER APPLICATION NUMBER: 08/360,125  
; EARLIER FILING DATE: 1994-12-20  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 122  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Hybridoma producing human antibody 1-3-1  
US-09-017-628-11  
Query Match 83.1%; Score 520.5; DB 2; Length 122;  
Best Local Similarity 82.8%; Pred. No. 2.9e-44;  
Matches 101; Conservative 8; Mismatches 8; Indels 5; Gaps 2;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGIYYSGSTY 60  
Db 1 QLQLQESGPGLVKPSSETLSLTCTVSGGSISSSYWGWIRQHPGKLEWIGSIYYSGSTY 60  
QY 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVVYCARGG-DGYRY----WQGGTLVTV 115  
Db 61 YNPFLKSRVTISVDTSKNQFSLKLSVTAADTAVVYCARGSYGGYYGMDVMQGGTTTV 120  
QY 116 SS 117  
Db 121 SS 122



RESULT 12

US-09-014-880-11

Sequence 11, Application US/09014880

Patent No. 5990297

GENERAL INFORMATION:

APPLICANT: Saiko HOSOKAWA et al.

APPLICANT: Saiko HOSOKAWA

APPLICANT: Yoshiaki TAGAWA

APPLICANT: Yoko HIRAKAWA

APPLICANT: No. 6436434hiko ITO

APPLICANT: Kazuhiro NAGAIKE

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY

TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.

STREET: 2033 K Street, N.W., #800

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/014,880

FILING DATE: January 28, 1998

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/450,578

FILING DATE: May 25, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/360,125

FILING DATE: December 20, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/905,534

FILING DATE: June 29, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-721-8200

TELEFAX: 202-721-8250

TELEX:

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 122 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

CELL TYPE: Hybridoma producing human antibody 1-3-1

US-09-014-880-11

Query Match 83.1%; Score 520.5; DB 2; Length 122;

Best Local Similarity 82.8%; Pred. No. 2.9e-44;

Matches 101; Conservative 8; Mismatches 8; Indels 5; Gaps 2;

QY 1 QVLESGGGLVLPSETLSLTCTVSGGSISSGYTHSWIRQHPGRGLEWIGYVSGSTY 60

DB 1 QLOLQSGGLVLPSETLSLTCTVSGGSISSGYTHSWIRQHPGRGLEWIGYVSGSTY 60

QY 61 HNFSLKSRITISVDTSKNQFSLKSSVTAADTAVVYCARGG-DGYRY- ---WGQGLTVTV 115

DB 61 YNFSLKSRVITISVDTSKNQFSLKSSVTAADTAVVYCARGG-DGYRY- ---WGQGLTVTV 120

QY 116 SS 117

DB 121 SS 122

RESULT 13

US-08-450-363-11



RESULT 15  
US-09-049-672A-4  
; Sequence 4, Application US/09049672A  
; Patent No. 6135941  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Yue, Henry  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Baughn, Marian R.  
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/049,672A  
; FILING DATE: HEREWITH  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cerrone, Michael C.  
; REGISTRATION NUMBER: 39,132  
; REFERENCE/DOCKET NUMBER: PF-0497 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 473 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: PANCTUT01  
; CLONE: 1513264  
US-09-049-672A-4

Query Match 83.0%; Score 519.5; DB 3; Length 473;  
Best Local Similarity 81.5%; Pred. No. 1.9e-43;  
Matches 101; Conservative 7; Mismatches 9; Indels 7; Gaps 1;  
  
Qy 1 QVLEQSGPLVXPSETLSLTCTVSGSISGTYHWSWIRQHPGRGLEWIGYIYSGTY 60  
Db ||||:||||||||||||||||||||||||||:||||||:|||||||||||  
20 QVQLQSGPLVXPSETLSLTCAVSGSITSGGYYSWIRQHPGRGLEWIGYIYSGT 79  
|||:||||||||||||||||||||||||||:||||||:|||||||||||  
Qy 61 HNPFLSKSRITISVDTSKNQPSLKLSSVTAADTAIVYICAR-----GGDGYRWGGQTLV 113  
Db :||||||:||||||:||||||:||||||:||||||:||||||:||||||:||||||  
80 YNPSLKSRTIISVDTSKNQPSLKLSSVTAADTAIVYICARDDVGLRGNGMDVWGQTLV 139  
|||  
Qy 114 TVSS 117  
Db ||||  
140 TVSS 143

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Result No.	Score	Query Match	Length	DB	ID	Description
1	626	100.0	117	14	US-10-330-613-33	Sequence 33, Appl
2	626	100.0	117	14	US-10-330-530-33	Sequence 33, Appl
3	626	100.0	117	16	US-10-660-357-33	Sequence 33, Appl
4	604	96.5	117	14	US-10-330-613-5	Sequence 5, Appl
5	604	96.5	117	14	US-10-330-530-5	Sequence 5, Appl
6	604	96.5	117	16	US-10-660-357-5	Sequence 5, Appl
7	568	90.7	117	14	US-10-330-613-13	Sequence 13, Appl
8	568	90.7	117	14	US-10-330-530-13	Sequence 13, Appl
9	568	90.7	117	16	US-10-660-357-13	Sequence 13, Appl
10	552.5	88.3	118	15	US-10-309-762-138	Sequence 138, Appl
11	552	88.2	123	15	US-10-309-762-10	Sequence 10, Appl

## RESULT 2

```
US-10-330-530-33
; Sequence 33, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-33

Query Match      100.0%; Score 626; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.4e-48;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSY 60
DB 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSY 60

QY 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYYCARGDGYRYWGQGLTVTVSS 117
DB 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYYCARGDGYRYWGQGLTVTVSS 117

RESULT 3
US-10-660-357-33
; Sequence 33, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-33

Query Match      100.0%; Score 626; DB 16; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.4e-48;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSY 60
DB 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSY 60

QY 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYYCARGDGYRYWGQGLTVTVSS 117
DB 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYYCARGDGYRYWGQGLTVTVSS 117

RESULT 4
US-10-330-613-5
; Sequence 5, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
```

```
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-5

Query Match      96.5%; Score 604; DB 14; Length 117;
Best Local Similarity 94.0%; Pred. No. 5.8e-46;
Matches 110; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSY 60
DB 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSY 60

QY 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYYCARGDGYRYWGQGLTVTVSS 117
DB 61 YNPFLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGDGYRYWGQGLTVTVSS 117

RESULT 5
US-10-330-530-5
; Sequence 5, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-5

Query Match      96.5%; Score 604; DB 14; Length 117;
Best Local Similarity 94.0%; Pred. No. 5.8e-46;
Matches 110; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSY 60
DB 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSY 60

QY 61 HNPFLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGDGYRYWGQGLTVTVSS 117
DB 61 YNPFLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGDGYRYWGQGLTVTVSS 117

RESULT 6
US-10-660-357-5
; Sequence 5, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
```

; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-5

Query Match 96.5%; Score 604; DB 16; Length 117;  
Best Local Similarity 94.0%; Pred. No. 5, 8e-46;  
Matches 110; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
Qy 61 HNPSLKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGQGLTVTVSS 117  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 YNPSSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGQGLTVTVSS 117

## RESULT 7

US-10-330-613-13  
; Sequence 13, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-13

Query Match 90.7%; Score 568; DB 14; Length 117;  
Best Local Similarity 88.9%; Pred. No. 9e-43;  
Matches 104; Conservative 10; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
Qy 61 HNPSLKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGQGLTVTVSS 117  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 YNPSSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGQGLTVTVSS 117

## RESULT 8

US-10-330-530-13  
; Sequence 13, Application US/10330530  
; Publication No. US20030152514A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
; FILE REFERENCE: ABGENIX.031A  
; CURRENT APPLICATION NUMBER: US/10/330,530  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: US 60/346414  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo Sapiens

## US-10-330-530-13

Query Match 90.7%; Score 568; DB 14; Length 117;  
Best Local Similarity 88.9%; Pred. No. 9e-43; Indels 0; Gaps 0;  
Matches 104; Conservative 10; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
Qy 61 HNPSLKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGQGLTVTVSS 117  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 YNPSSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGQGLTVTVSS 117

## RESULT 9

US-10-660-357-13  
; Sequence 13, Application US/10660357  
; Publication No. US20040115205A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Eli, Menashe  
; APPLICANT: Green, Larry L.  
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
; TITLE OF INVENTION: ANTIGEN  
; FILE REFERENCE: ABGENIX.030C1  
; CURRENT APPLICATION NUMBER: US/10/660,357  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 10/330,580  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-13

Query Match 90.7%; Score 568; DB 16; Length 117;  
Best Local Similarity 88.9%; Pred. No. 9e-43; Indels 0; Gaps 0;  
Matches 104; Conservative 10; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
Qy 61 HNPSLKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGQGLTVTVSS 117  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 YNPSSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGQGLTVTVSS 117

## RESULT 10

US-10-309-762-138  
; Sequence 138, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
; FILE REFERENCE: ABGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309,762  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/337275  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 138  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-138

```
Query Match      88.3%; Score 552.5; DB 15; Length 118;
Best Local Similarity 89.0%; Pred. No. 2.1e-41;
Matches 105; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

QY 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60
Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60
QY 61 HNPSLKSRITISVDTSKNQFSLKSSVTAADTAVYYCAR--GGDGYRYWGQGLTLTVSS 117
Db 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARYGSGSDVWGQGLTLTVSS 118

RESULT 11
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-10

Query Match      88.2%; Score 552; DB 15; Length 123;
Best Local Similarity 85.4%; Pred. No. 2.5e-41;
Matches 105; Conservative 7; Mismatches 5; Indels 6; Gaps 1;

QY 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60
Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60
QY 61 HNPFLKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGGDGY-----RYWGQGLTLVT 114
Db 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARAGKYGSGSYLDYWGQGLTLVT 120
QY 115 VSS 117
Db 121 VSS 123

RESULT 12
US-10-309-762-13
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 13
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-13

Query Match      87.8%; Score 549.5; DB 15; Length 120;
Best Local Similarity 86.1%; Pred. No. 4e-41;
Matches 105; Conservative 8; Mismatches 2; Indels 7; Gaps 2;

QY 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60
Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60
QY 61 HNPFLKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGGDGYR-----WGQGLTLVT 115
Db 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAR--DGNYWYFDMWGRGLTLTV 118
QY 116 SS 117
Db 119 SS 120

RESULT 13
US-10-309-762-144
; Sequence 144, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-144

Query Match      87.8%; Score 549.5; DB 15; Length 120;
Best Local Similarity 86.1%; Pred. No. 4e-41;
Matches 105; Conservative 8; Mismatches 2; Indels 7; Gaps 2;

QY 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60
Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60
QY 61 HNPFLKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGGDGYR-----WGQGLTLVT 115
Db 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAR--DGNYWYFDMWGRGLTLTV 118
QY 116 SS 117
Db 119 SS 120

RESULT 14
US-10-309-762-9
; Sequence 9, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
```





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(CLERK) (SECRETARY)

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	523	83.5	147	2	S13519	ig heavy chain v r
2	514	82.1	140	2	S13782	ig variable region
3	510	81.5	116	2	S37456	ig mu chain - huma
4	510	81.5	130	2	S31690	ig heavy chain v r
5	507	81.0	135	2	S78051	ig heavy chain pre
6	503	80.4	121	2	S44113	ig heavy chain v r
7	498	79.6	155	2	S31511	ig heavy chain - h
8	496	79.2	155	2	S31512	ig heavy chain - h
9	493.5	78.8	139	2	S31586	ig heavy chain v r
10	493	78.8	99	2	S26801	ig heavy chain v r
11	492.5	78.7	130	2	S30534	ig heavy chain v r
12	488	78.0	128	2	S31514	ig heavy chain - h
13	484	77.3	99	2	S26802	ig heavy chain v r
14	484	77.3	99	2	S28803	ig heavy chain v r
15	480.5	76.8	129	2	S44114	ig heavy chain v r
16	479	76.5	118	2	A26340	ig heavy chain pre
17	479	76.5	123	2	S30530	ig heavy chain v r
18	476	76.0	146	2	S09711	ig heavy chain v r
19	474.5	75.8	122	2	S65912	ig v-d-j region (N
20	474.5	75.8	137	2	S31676	ig heavy chain v r
21	474	75.7	146	2	S09710	ig heavy chain v r
22	472	75.4	140	2	A49045	ig heavy chain v r
23	470	75.1	139	2	S31696	ig heavy chain v r
24	468	74.8	105	2	S44125	ig lambda chain v
25	467.5	74.7	140	2	S78052	ig heavy chain pre
26	467	74.6	99	2	S12418	ig heavy chain v r
27	464.5	74.2	110	2	S44110	ig heavy chain v-d
28	464.5	74.2	145	2	S78055	ig heavy chain pre
29	464	74.1	135	2	S31604	ig heavy chain v r

A;cross-references: EMBL:X67906; NID:g33582; PID:CAA48104.1; PID:g33583  
C.superfamily: immunoglobulin V region: immunoglobulin heavy chain

F;46-128/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 514; DB 2; Length 140;  
Best Local Similarity 82.9%; Pred. No. 2.4e-38;  
Matches 102; Conservative 7; Mismatches 6; Indels 8; Gaps 2;

QY 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISS--YYMSWRQPPGKLEWIGYIYSGSTN 77  
QY 61 HNPFLSKSRITISVDTSKNQFSLKSSVTAADTAAYVYCARG-----GDGYYWQGTTLVT 114  
DB 78 YNPSLKSRTVISVDTSKNQFSLKSSVTAADTAAYVYCARHNSSWGRFYDYWGQGTTLVT 137

QY 115 VSS 117  
DB 138 VSS 140

RESULT 3  
S37456  
IG mu chain - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S37456  
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.  
submitted to the EMBL Data Library, September 1993  
A;Description: Cloning and analysis of human IGM anti-Thyroglobulin autoantibodies from  
A;Reference number: S37453  
A;Accession: S37456  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-116 <MCI>  
A;Cross-references: EMBL:X75024; NID:g404313; PIDN:CAA52932.1; PID:g758095  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;6-90/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 510; DB 2; Length 116;  
Best Local Similarity 83.6%; Pred. No. 4.5e-38;  
Matches 97; Conservative 6; Mismatches 5; Indels 8; Gaps 1;

QY 10 GLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTYHNPFLSKSRI 69  
DB 1 GLVKPSQTLTLCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTYHNPFLSKSRV 60  
QY 70 TISVDTSKNQFSLKSSVTAADTAAYVYCARGGDGYRY-----WGQGTTLVTVSS 117  
DB 61 TISVDTSKNQFSLKSSVTAADTAAYVYCARGGYSGYIYVYVMDVWGKGTTLVTVSS 116

RESULT 4  
S31690  
IG heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31690  
R;Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31690  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-130 <CUI>  
A;Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;20-102/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 510; DB 2; Length 130;  
Best Local Similarity 79.5%; Pred. No. 5.1e-38;  
Matches 101; Conservative 7; Mismatches 7; Indels 12; Gaps 2;

QY 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
DB 6 QVQLQESGPGLVKPSSETLSLTCTVSGGSISS--YYMSWRQPPGKLEWIGYIYSGSTN 63  
QY 61 HNPFLSKSRITISVDTSKNQFSLKSSVTAADTAAYVYCARGGD-----GYRYWQGG 110  
DB 64 YNPSLKSRTVISVDTSKNQFSLKSSVTAADTAAYVYCARSSVLLWFGELLYFYDWQGG 123  
QY 111 TLVTVSS 117  
DB 124 TLVTVSS 130

RESULT 5  
S78051  
IG heavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C;Accession: S78051; S23716  
R;Harindranath, N.  
submitted to the EMBL Data Library, August 1990  
A;Reference number: S78051  
A;Accession: S78051  
A;Molecule type: mRNA  
A;Residues: 1-135 <HAR>  
A;Cross-references: EMBL:X54437; NID:g37814; PIDN:CAA38306.1; PID:g9930117  
R;Harindranath, N.; Goldfarb, I.S.; Ikenatsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin  
Int. Immunol. 3, 865-875, 1991  
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and  
patient.  
A;Reference number: S23716; MUID:92031262; PMID:1718404  
A;Accession: S23716  
A;Molecule type: mRNA  
A;Residues: 13-111 <HAW>  
A;Cross-references: EMBL:X54437  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;1-13/Domain: signal sequence (fragment) #status predicted <SIG>  
F;14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>  
F;27-111/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 507; DB 2; Length 135;  
Best Local Similarity 79.7%; Pred. No. 9.7e-38;  
Matches 98; Conservative 9; Mismatches 10; Indels 6; Gaps 1;

QY 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
DB 13 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGNTY 72  
QY 61 HNPFLSKSRITISVDTSKNQFSLKSSVTAADTAAYVYCARGG-----DGYYWQGTTLVT 114  
DB 73 FNPSLKSRTVISVDTSKNQFSLKSSVTAADTAAYVYCARLGPDDYTLGDMDVWGQGTTLVT 132  
QY 115 VSS 117  
DB 133 VSS 135

RESULT 6  
S44113  
IG heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C;Accession: S44113  
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable  
A;Reference number: S44105  
A;Accession: S44113  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-121 <HAW>

RESULT 8  
S31512  
Ig heavy chain - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S31512  
R;Chacagnier, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A;Description: Dominance of clonotypic patterns and variable gene usage of  
A;Reference number: S31509  
A;Accession: S31512  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-155 <CHA>  
A;Cross-references: EMBL:X69860; NID:q33082; PIDN:CAA49494.1;PID:q33083

RESULT 10  
S26801  
IG heavy chain V region (DP-65) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 25-Oct-1996 #text\_change 20-Jun-2000  
C:Accession: S26801; S26900  
R:Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.  
Eur. J. Immunol. 22, 1075-1082, 1992  
A:Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.  
A:Reference number: S26800; MUID:92201299; PMID:1348029  
A:Accession: S26801  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-99 <WEN>  
A:Cross-references: EMBL:Z14237; NID:g37706; PIDN:CAA78606.1; PID:g1335372  
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992  
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V  
A;Reference number: S26885; MUID:93021117; PMID:1404388  
A;Accession: S26900  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-99 <TOM>  
A;Cross-references: EMBL:Z12365; NID:g32948; PIDN:CAA78235.1; PID:g32949  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 493; DB 2; Length 99;  
Best Local Similarity 91.9%; Pred. No. 1.2e-36;  
Matches 91; Conservative 7; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
QY 61 HNPSLKSRITISVDTSKNQFSLKSSVTAADTAIVYCAR 99  
Db 61 YNPFLKSRITISVDTSKNQFSLKSSVTAADTAIVYCAR 99

RESULT 11  
S30534  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Aug-1996  
C;Accession: S30534  
R;Marette, X.  
submitted to the EMBL Data Library, October 1992  
A;Reference number: S30520  
A;Accession: S30534  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-130 <MAR>  
A;Cross-references: EMBL:Z18320  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 492.5; DB 2; Length 130;  
Best Local Similarity 74.6%; Pred. No. 1.8e-36;  
Matches 97; Conservative 10; Mismatches 10; Indels 13; Gaps 1;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTN 60  
QY 61 HNPFLKSRITISVDTSKNQFSLKSSVTAADTAIVYCAR 99  
Db 61 YNPFLKSRITISVDTSKNQFSLKSSVTAADTAIVYCAR 99

RESULT 12  
S31514  
Ig heavy chain - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S31514  
R;Chastagner, P.; Denaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto  
A;Reference number: S31509  
A;Accession: S31514  
A;Status: preliminary  
A;Molecule type: mRNA

A;Residues: 1-128 <CHA>  
A;Cross-references: EMBL:X69862; NID:g33086; PIDN:CAA49496.1; PID:g33087  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;22-106/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 488; DB 2; Length 128;  
Best Local Similarity 76.0%; Pred. No. 4.3e-36;  
Matches 92; Conservative 14; Mismatches 11; Indels 4; Gaps 1;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 8 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 67  
QY 61 HNPFLKSRITISVDTSKNQFSLKSSVTAADTAIVYCAR 99  
Db 68 YNPFLKSRITISVDTSKNQFSLKSSVTAADTAIVYCAR 99

RESULT 13  
S26802  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C;Accession: S26802  
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.  
Eur. J. Immunol. 22, 1075-1082, 1992  
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.  
A;Reference number: S26800; MUID:92201299; PMID:1348029  
A;Accession: S26802  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-99 <WEN>  
A;Cross-references: EMBL:Z14239; NID:g37708; PIDN:CAA78608.1; PID:g1335373  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 77.3%; Score 484; DB 2; Length 99;  
Best Local Similarity 90.9%; Pred. No. 7.4e-36;  
Matches 90; Conservative 7; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
QY 61 HNPFLKSRITISVDTSKNQFSLKSSVTAADTAIVYCAR 99  
Db 61 YNPFLKSRITISVDTSKNQFSLKSSVTAADTAIVYCAR 99

RESULT 14  
S26803  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C;Accession: S26803  
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.  
Eur. J. Immunol. 22, 1075-1082, 1992  
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.  
A;Reference number: S26800; MUID:92201299; PMID:1348029  
A;Accession: S26803  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-99 <WEN>  
A;Cross-references: EMBL:Z14238; NID:g37710; PIDN:CAA78607.1; PID:g1335374  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 77.3%; Score 484; DB 2; Length 99;  
Best Local Similarity 90.9%; Pred. No. 7.4e-36;  
Matches 90; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60

Qy 61 HNPSLKSRITISVDTSKNQFSLKLSSTVAADTAVYYCAR 99  
Db 61 YNPFLKSRVTISVDTSKNQFSLKLSSTVAADTAVYYCAR 99

## RESULT 15

S44114  
Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C/Accession: S44114  
R/Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable  
A/Reference number: S44105  
A/Accession: S44114  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-129 <HAW>  
A/Cross-references: EMBL:Z31579; NID:9472968; PIDN:CAA83451.1; PID:9940525  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.8%; Score 480.5; DB 2; Length 129;  
Best Local Similarity 76.0%; Pred. No. 2e-35;  
Matches 95; Conservative 11; Mismatches 10; Indels 9; Gaps 3;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSGTLSTLTCAVSGGSISSNNW-WSWVRQPPGKGLEWIGEIVHSGSTN 59

Qy 61 HNPFLKSRITISVDTSKNQFSLKLSSTVAADTAVYYCAR-----GGDG-YRYWGQGTLL 112  
Db 60 YNPFKSRVTISADTSKNQFSLKYSNVTAAADTAVYYCARRNYDFWSGGDGFDFYWGQGTLL 119

Qy 113 VTVSS 117  
Db 120 VTVSS 124

Search completed: November 9, 2005, 13:08:05  
Job time : 13.609 secs

(ENCLOSURE) TO BE OPENED



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:46:52 ; Search time 60.406 Seconds  
(without alignments)  
991.843 Million cell updates/sec

Title: US-10-660-357A-33

Perfect score: 626

Sequence: 1 QVQLFQSGPGLVKPSETLSL.....ARGGDGYRYMGQGLTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533	85.1	476	2 Q6GMX1	Q6gm1 homo sapien
2	508.5	81.2	478	2 Q72379	Q72379 homo sapien
3	487.5	77.9	465	2 Q6GMX6	Q6gm6 homo sapien
4	487	77.8	119	2 Q9UL73	Q9ul73 homo sapien
5	484.5	77.4	477	2 Q6GMX7	Q6gm7 homo sapien
6	476.5	76.1	150	2 Q95973	Q95973 homo sapien
7	475.5	76.0	496	2 Q96KX8	Q96kx8 homo sapien
8	474.5	75.8	620	2 Q96EY0	Q96ey0 homo sapien
9	473.5	75.6	576	2 Q6P4I8	Q6p4i8 homo sapien
10	472.5	75.5	130	2 Q8I2D7	Q8i2d7 homo sapien
11	466	74.4	492	2 Q72374	Q72374 homo sapien
12	462	73.8	139	2 Q86SX2	Q86sx2 homo sapien
13	440	70.3	129	1 HV2F_HUMAN	P01824 homo sapien
14	436	69.6	478	2 Q6NTH3	Q6nth3 homo sapien
15	431	68.8	595	2 Q8WUX4	Q8wux4 homo sapien
16	431	68.8	597	2 Q6GMX5	Q6gm5 homo sapien
17	431	68.8	597	2 Q9BU10	Q9bu10 homo sapien
18	431	68.8	625	2 Q96AA6	Q96aa6 homo sapien
19	428.5	68.5	146	1 HV21_HUMAN	P06331 homo sapien
20	425	67.9	597	2 Q9BQ88	Q9bqb8 homo sapien
21	417.5	66.7	136	2 Q6LBQ5	Q6lbq5 mus musculus
22	411	65.7	479	2 Q99M22	Q99m22 mus musculus
23	410.5	65.6	473	2 Q8TC83	Q8tc83 homo sapien
24	409	65.3	117	1 HV2G_HUMAN	P01825 homo sapien
25	408.5	65.3	122	2 Q9UL75	Q9ul75 homo sapien
26	398	63.6	116	2 Q723Y6	Q723y6 homo sapien
27	397	63.4	137	1 HV46_MOUSE	P01822 mus musculus
28	396	63.3	262	2 Q65ZT1	Q65zt1 mus musculus
29	393	62.8	476	2 Q6MZK7	Q6mzk7 mus musculus
30	390	62.3	113	1 HV47_MOUSE	P01823 mus musculus
31	372	59.4	117	1 HV62_MOUSE	P18533 mus musculus

32 367.5 58.7 116 1 HV61\_MOUSE  
33 366.5 58.5 116 1 HV60\_MOUSE  
34 342 54.6 121 2 Q9UL56  
35 339.5 54.2 118 2 Q811U5  
36 337.5 53.9 482 2 Q91X92  
37 336 53.7 144 1 HV43\_MOUSE  
38 335.5 53.6 135 1 HV02\_XENLA  
39 330.5 52.8 121 2 Q99NG4  
40 327 52.2 118 2 Q9UL74  
41 320 51.1 466 2 Q6IN78  
42 317 50.6 119 1 HV2C\_HUMAN  
43 316.5 50.6 606 2 Q6GMV2  
44 314 50.2 116 2 Q9UL93  
45 313.5 50.1 147 2 Q9Y509

P18532 mus musculus  
P18531 mus musculus  
Q9ul96 homo sapien  
Q811u5 mus musculus  
Q91x92 mus musculus  
P01819 mus musculus  
P20957 xenopus lae  
Q99ng4 mus musculus  
Q9ul74 homo sapien  
Q6in78 homo sapien  
P01816 homo sapien  
Q6gm92 homo sapien  
Q9ul93 homo sapien  
Q9y509 homo sapien

#### ALIGNMENTS

RESULT 1  
Q6GMX1 PRELIMINARY; PRT; 476 AA.  
AC Q6GMX1  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzyzinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073773; AAH73773.1; -  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF07654; C1-set; 3.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.





Db 20 QLOQESGPGLVKPSSETLSLCTVSGGSISSSTYWGIRQPPKGLWIGSLHNGSDY 79  
QY 61 HNPFLSKRITISVDTSKNQFSLKSLSSVTAADTAVYVCARGDG-YRYWGQGTIVTVSS 117  
Db 80 YNPSLKSRTVITSDTSKNQFSLKSLSSVTAADTAVYVCARGDGFDFWGHGTWTVSS 137

RESULT 7  
Q96KX8 PRELIMINARY; PRT; 496 AA.  
AC Q96KX8; ID Q96KX8; PRELIMINARY; PRT; 496 AA.  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DE MGC27165 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Brownstein M.J., Udén T.B., Toshiki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Casavant T.L., Scheetz T.E.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Lung;  
RC Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC016369; AAH16369.1; -.  
DR HSSP; P01876; 10W0.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 2.  
DR SMART; SM00406; IGV; 1.  
DR SMART; SM00406; IGV; 4.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 76.0%; Score 475.5; DB 2; Length 496;  
Best Local Similarity 74.2%; Pred. No. 2.1e-39;  
Matches 92; Conservative 10; Mismatches 15; Indels 7; Gaps 1;  
QY 1 QVQLQESGPGLVKPSSETLSLCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYISGSTY 60  
Db 20 QLOQESGPGLVKPSSETLSLCTVSGGSISSSTYWGIRQPPKGLWIGSLHNGSDY 79  
QY 61 HNPFLSKRITISVDTSKNQFSLKSLSSVTAADTAVYVCARGD-----DGYRYWGQGTIV 113  
Db 80 YNPSLKSRTVITSDTSKNQFSLKSLSSVTAADTAVYVCARGDYSRSGRTGIDYWGQGTIV 139

QY 114 TVSS 117  
Db 140 TVSS 143  
RESULT 8  
Q96EY0 PRELIMINARY; PRT; 620 AA.  
AC Q96EY0;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DE IGMM protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Brownstein M.J., Udén T.B., Toshiki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Casavant T.L., Scheetz T.E.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Primary B-Cells;  
RC Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011857; AAH11857.2; -.  
DR PIR; S15590; S15590.  
DR HSSP; P01820; 1G7J.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 3.  
SQ SEQUENCE 620 AA; 58125 MW; 990A1A4A6E8FF27B CRC64;

Query Match 75.8%; Score 474.5; DB 2; Length 620;  
Best Local Similarity 79.5%; Pred. No. 3.4e-39;  
Matches 97; Conservative 7; Mismatches 11; Indels 7; Gaps 2;  
QY 1 QVQLQESGPGLVKPSSETLSLCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYISGSTY 60  
Db 27 QVQLQESGPGLVKPSSETLSLCTVSGGSISS--YYWSWIRQHPAGKGLWIGRIYTSSTN 84  
QY 61 HNPFLSKRITISVDTSKNQFSLKSLSSVTAADTAVYVCAR-----GGDGYRYWGQGTIV 115  
Db 85 YNPSLKSRTVITSDTSKNQFSLKSLSSVTAADTAVYVCASQPWELPTVGLFYWGQGTIV 144

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Qy 116 SS 117
Db 145 SS 146

RESULT 9
Q6P418 PRELIMINARY; PRT; 576 AA.
ID Q6P418
AC Q6P418
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGH protein.
GN Name=IGH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RA Strausberg R.;
RL EMBL; BC063384; AAH63384.1; -
DR HSSP; P01820; 1A7N.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00407; Igcl; 3.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 576 AA; 75.6% Score 473.5; DB 2; Length 576;
Query Match 75.6%; Score 473.5; DB 2; Length 576;
Best Local Similarity 78.5%; Pred. No. 4e-39;
Matches 95; Conservative 8; Mismatches 13; Indels 5; Gaps 2;

Qy 1 QVQLQSGGPGLVKPSKPSLTLCTVSGSISSTGYTHSWIRHQRGLGWIGYISGSTY 60
Db 27 QVQLQSGGPGLVKPSGLTSLTCAVSGSISSSNN-WSWVRPPGKGLWIGYISGSTN 85
Qy 61 HNPGLSKRITISVDTSKNQFSLKLSVTAADTAIVYCA-----WGQGLTVTVS 116

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Db 86 YNPGLSKRVTISVDTSKNQFSLKLSVTAADTAIVYCASLGDIIYYGNDVWGQGLTVTVS 145
Qy 117 S 117
Db 146 S 146

RESULT 10
Q81ZD7 PRELIMINARY; PRT; 130 AA.
ID Q81ZD7
AC Q81ZD7
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 26, Last annotation update)
DE Anti-thyroglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jang Y.-J., Chung J., Park J.-Y.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AY145445; AAN64329.1; -
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 130
SQ SEQUENCE 130 AA; 13901 MW; 036131FC6EC1551E CRC64;

Query Match 75.5%; Score 472.5; DB 2; Length 130;
Best Local Similarity 73.1%; Pred. No. 1e-39;
Matches 95; Conservative 11; Mismatches 11; Indels 13; Gaps 3;

Qy 1 QVQLQSGGPGLVKPSKPSLTLCTVSGSISSTGYTHSWIRHQRGLGWIGYISGSTY 59
Db 1 QVQLQSGGPGLVKPSKPSLTLCTVSGSISSTGYTHSWIRHQRGLGWIGYISGSTY 60
Qy 60 ----YHNPGLSKRITISVDTSKNQFSLKLSVTAADTAIVYCA-----RGDGY---RYW 107
Db 61 SGSPYVAPSLRSRVIIISVDTSKNQLSLRLSSVTAADTAIVYCA-----RGDGY---RYW 107
Qy 108 GQGLTVTVSS 117
Db 121 GQGLTVTVSS 130

RESULT 11
Q72374 PRELIMINARY; PRT; 492 AA.
ID Q72374
AC Q72374
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKF2p686C02218 (Fragment).
GN Name=DKF2p686C02218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wienann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
EMBL; BX538077; CAD98001.1; -
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.

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DR InterPro; IPR003597; Ig ci.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A1576F0CA74B CRC64;

Query Match 74.4%; Score 466; DB 2; Length 492;
Best Local Similarity 72.7%; Pred. No. 1.9e-38;
Matches 88; Conservative 16; Mismatches 13; Indels 4; Gaps 1;

QY 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSTGYHMSWIRQHPGRGLEWIGYIYSGSTY 60
Db 32 QLQESGPGLVKPFSETLSLTCTVSGGSVSNRYNGWIRQPPGKLEWIGSIYYNENTY 91
QY 61 HNPGLSKRITISVDTSKNQFSLKSSVTAADTAVYTCARGDG----YRWGQGLTVTVS 116
Db 92 YSPSLKSLRTIFVDTSKHFSRLTSVTAADTAVYTCVRHVEGPGYGNFDPWGQGLTVTVS 151
QY 117 S 117
Db 152 S 152

RESULT 12
Q86SX2 PRELIMINARY; PRT; 139 AA.
AC Q86SX2
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line) of
DE Homo sapiens (human) (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248300; CAD62627.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 73.8%; Score 462; DB 2; Length 139;
Best Local Similarity 89.9%; Pred. No. 1.2e-38;
Matches 89; Conservative 6; Mismatches 2; Indels 2; Gaps 1;

QY 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSTGYHMSWIRQHPGRGLEWIGYIYSGSTY 60
Db 33 QVQLQESGPGLVKPFSETLSLTCTVSGGSISS--YRWSWIRQPPGKLEWIGIYIYSGSTN 90
QY 61 HNPGLSKRITISVDTSKNQFSLKSSVTAADTAVYTCAR 99
Db 91 YNPGLSKRITISVDTSKNQFSLKSSVTAADTAVYTCAR 129

Query Match 70.3%; Score 440; DB 1; Length 129;
Best Local Similarity 64.3%; Pred. No. 1.9e-36;
Matches 83; Conservative 15; Mismatches 19; Indels 12; Gaps 1;

QY 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSTGYHMSWIRQHPGRGLEWIGYIYSGSTY 60
Db 1 RLQQLQESGPGLVKPFSETLSLTCTVSGGPIRRRTGYWGWIRQPPGKLEWIGIYIYSGSIY 60
QY 61 HNPGLSKRITISVDTSKNQFSLKSSVTAADTAVYTCARGG-----DGYYRWG 108
Db 61 YNPGLRGRVITISVDTSKNQFSLNLRMSAADTAMYYCARGNPPPPYDYGTSDDGIDVWG 120
QY 109 QGTLVTVSS 117
Db 121 QGTTVTVSS 129

RESULT 14
Q6NYH3 PRELIMINARY; PRT; 478 AA.
ID Q6NYH3
AC Q6NYH3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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RESULT 13
HV2F_HUMAN STANDARD; PRT; 129 AA.
ID HV2F_HUMAN
AC P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-II region WAH.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE.
RX MEDLINE=8222235; PubMed=6806818;
RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
RT immunoglobulin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
CC -!- MISCELLANEOUS: This chain was isolated from an IgD myeloma
CC protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02099; D2HUWA.
DR HSSP; P01820; IG7J.
DR GlycoSuiteDB; P01824; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 113
FT NON_TER 129
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 70.3%; Score 440; DB 1; Length 129;
Best Local Similarity 64.3%; Pred. No. 1.9e-36;
Matches 83; Conservative 15; Mismatches 19; Indels 12; Gaps 1;

QY 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSTGYHMSWIRQHPGRGLEWIGYIYSGSTY 60
Db 1 RLQQLQESGPGLVKPFSETLSLTCTVSGGPIRRRTGYWGWIRQPPGKLEWIGIYIYSGSIY 60
QY 61 HNPGLSKRITISVDTSKNQFSLKSSVTAADTAVYTCARGG-----DGYYRWG 108
Db 61 YNPGLRGRVITISVDTSKNQFSLNLRMSAADTAMYYCARGNPPPPYDYGTSDDGIDVWG 120
QY 109 QGTLVTVSS 117
Db 121 QGTTVTVSS 129

RESULT 14
Q6NYH3 PRELIMINARY; PRT; 478 AA.
ID Q6NYH3
AC Q6NYH3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

```



(CLASS) NAME: [illegible]



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:43:32 ; Search time 74.6015 Seconds  
(without alignments)  
627.306 Million cell updates/sec

Title: US-10-660-357A-37

Perfect score: 651

Sequence: 1 QVQLQESGPGLVKPSSETLSL.....WLVPDAFDWQGTMTSVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_16Dec04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	651	100.0	121	7 ADC99808	Adc99808 Anti-huma
2	651	100.0	121	7 ADD05412	Add05412 Anti-MUC1
3	651	100.0	121	7 ADF09850	Adf09850 Human ant
4	598	91.9	121	7 ADC99780	Adc99780 Anti-huma
5	598	91.9	121	7 ADD05384	Add05384 Anti-MUC1
6	598	91.9	121	7 ADF09822	Adf09822 Human ant
7	597	91.7	121	7 ADC99772	Adc99772 Anti-huma
8	597	91.7	121	7 ADC99788	Adc99788 Anti-huma
9	597	91.7	121	7 ADD05376	Add05376 Anti-MUC1
10	597	91.7	121	7 ADD05392	Add05392 Anti-MUC1
11	597	91.7	121	7 ADF09814	Adf09814 Human ant
12	597	91.7	121	7 ADF09830	Adf09830 Human ant
13	562.5	86.4	243	8 ADO58076	Ado58076 S9 cell d
14	554	85.1	125	5 ADF03871	Adf03871 Murine-ex
15	547	84.0	121	5 ADF03884	Adf03884 Human ant
16	546	83.9	123	6 ADA89258	Ada89258 Human ant
17	544.5	83.6	121	5 ABB07171	Abb07171 ebvHgm M
18	544.5	83.6	121	5 ADI26658	Adi26658 Human ant
19	543	83.4	125	7 ADF03868	Adf03868 Murine-ex
20	543	83.4	125	7 ADF03876	Adf03876 Murine-ex
21	541.5	83.2	122	7 ADF03885	Adf03885 Murine-ex
22	541.5	83.2	122	7 ADF03889	Adf03889 Murine-ex
23	539	82.8	125	7 ADF03983	Adf03983 Murine-ex
24	539	82.8	446	8 ADK52356	Adk52356 Human ant
25	538.5	82.7	120	2 AAW90287	Aaw90287 Human ant

## ALIGNMENTS

### RESULT 1

ADC99808

ID ADC99808 standard; protein; 121 AA.

XX AC ADC99808;

XX AC

DT 01-JAN-2004 (first entry)

XX DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 37.

XX KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
XX KW cytotostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
XX KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
XX KW lung cancer; human.

XX OS Homo sapiens.

XX PN WC2003057838-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041581.

XX PR 28-DEC-2001; 2001US-0346299P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J;

XX DR WPI; 2003-597113/55.

XX DR N-PSDB; ADC99810.

XX PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
or condition associated with expression of MUC18 in a patient, e.g.  
tumors, cancers, and other malignancies.

XX PS Claim 1; SEQ ID NO 37; 78pp; English.

XX CC The invention relates to a novel isolated monoclonal antibody comprising  
a heavy or light chain amino acid or a heavy or light chain variable  
domain where the antibody binds to MUC18. The monoclonal antibody of the  
invention demonstrates cytostatic activity and may be useful for treating  
a disease or condition associated with the expression of MUC18 on the  
cell surface such as tumours, specifically melanoma, oesophageal,  
pancreatic or colorectal tumours, carcinomas, particularly cervical  
carcinomas and cervical intraepithelial neoplasia and cancers including  
colorectal, breast or lung cancer, as well as other malignancies. The  
current sequence is that of the anti-human MUC18 monoclonal antibody

Adp22272 Human ant  
Adp03887 Murine-ex  
Adp03931 Murine-ex  
Adp03884 Murine-ex  
Adj36929 Anti-CD40  
Adp43199 Human ova  
Aaw27554 Human Ab  
Adj18676 Antibody  
Adp03864 Murine-ex  
Adp03862 Murine-ex  
Adl9313 Heavy cha  
Adp03933 Murine-ex  
Adp03973 Murine-ex  
Adi22106 Anti-plat  
Ade28491 Human ant  
Ade28471 Human ant  
Adp03984 Murine-ex  
ABg92888 Human imm  
Aay15126 Anti-muri  
Ade28447 Human ant

26 537.5 82.6 118 8 ADP22272  
27 537.5 82.6 122 7 ADP03887  
28 537.5 82.6 122 7 ADP03931  
29 537.5 82.6 122 7 ADP03884  
30 536.5 82.4 143 6 ABJ36929  
31 536.5 82.4 193 5 ABP43199  
32 536 82.3 119 2 AAW27554  
33 536 82.3 119 6 ABJ18676  
34 534.5 82.1 120 7 ADP03864  
35 534.5 82.1 120 7 ADP03862  
36 534.5 82.1 128 8 ADS19313  
37 533.5 82.0 122 7 ADP03933  
38 532 81.7 119 7 ADP03973  
39 532 81.7 119 8 ADI22106  
40 532 81.7 121 7 ADE28491  
41 532 81.7 466 7 ADE28471  
42 531.5 81.6 121 7 ADP03984  
43 530.5 81.5 126 5 ABG92888  
44 530.5 81.5 246 3 AAY15126  
45 529 81.3 121 7 ADE28447

CC heavy chain protein of the invention.

XX SQ Sequence 121 AA;

Query Match 100.0%; Score 651; DB 7; Length 121;  
Best Local Similarity 100.0%; Pred. No. 2.7e-47;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGPGLVVPSETLSLTCTVSGSISTYVWSWIRPPGKLEWIGIYYTGTNTYN 60  
DB 1 QVQLQSGPGLVVPSETLSLTCTVSGSISTYVWSWIRPPGKLEWIGIYYTGTNTYN 60

QY 61 PSLSKRVTVSDTSKNQFSLKLSVTAADTAVYYCARDPGQWLVPDAFDIWGGTWSVVS 120  
DB 61 PSLSKRVTVSDTSKNQFSLKLSVTAADTAVYYCARDPGQWLVPDAFDIWGGTWSVVS 120

QY 121 S 121

DB 121 S 121

RESULT 2

ADD05412  
ID ADD05412 standard; protein; 121 AA.

XX AC ADD05412;

XX DT 01-JAN-2004 (first entry)

XX DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 37.  
XX KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
XX KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.

XX OS Homo sapiens.

XX PN WO2003057006-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041582.

XX PR 28-DEC-2001; 2001US-0346460P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J, Bar-Eli M;

XX DR WPI; 2003-577496/54.

XX DR N-PSDB; ADD05414.

XX PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
XX PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
XX PT associated with melanoma, or increasing survival of an animal having a  
XX PT metastatic tumor.

XX PS Claim 1; SEQ ID NO 37; 87pp; English.

XX CC The invention relates to a novel monoclonal antibody used for inhibiting  
XX CC tumour growth in an animal. The tumour inhibition process comprises  
XX CC selecting an animal in need of treatment for a tumour, providing a  
XX CC monoclonal antibody comprising a heavy chain amino acid, where the  
XX CC antibody consists of any one of 10 fully defined sequences of 117-123  
XX CC amino acids given in the specification, and where the monoclonal antibody  
XX CC binds MUC18, and contacting the tumour with the antibody resulting in  
XX CC inhibited proliferation of the cells. The monoclonal antibody has  
XX CC cytostatic and can be used in the production of a vaccine. The monoclonal  
XX CC antibodies against the MUC18 antigen are useful for diagnosing and  
XX CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or  
XX CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
XX CC increasing survival of an animal having a metastatic tumour. This  
XX CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
XX CC protein of the invention.

XX SQ Sequence 121 AA;

Query Match 100.0%; Score 651; DB 7; Length 121;  
Best Local Similarity 100.0%; Pred. No. 2.7e-47;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGPGLVVPSETLSLTCTVSGSISTYVWSWIRPPGKLEWIGIYYTGTNTYN 60

DB 1 QVQLQSGPGLVVPSETLSLTCTVSGSISTYVWSWIRPPGKLEWIGIYYTGTNTYN 60

QY 61 PSLSKRVTVSDTSKNQFSLKLSVTAADTAVYYCARDPGQWLVPDAFDIWGGTWSVVS 120

DB 61 PSLSKRVTVSDTSKNQFSLKLSVTAADTAVYYCARDPGQWLVPDAFDIWGGTWSVVS 120

QY 121 S 121

DB 121 S 121

RESULT 3

ADF09850  
ID ADF09850 standard; protein; 121 AA.

XX AC ADF09850;

XX DT 12-FEB-2004 (first entry)

XX DE Human anti-MUC18 monoclonal antibody heavy chain #10.

XX KW cell proliferation inhibition; MUC18 tumour antigen;  
XX KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
XX KW carcinoma; cancer; malignancy; heavy chain; human.

XX OS Homo sapiens.

XX PN WO2003057837-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041580.

XX PR 28-DEC-2001; 2001US-0346414P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J;

XX DR WPI; 2003-598367/56.

XX DR N-PSDB; ADF09852.

XX PT Inhibiting cell proliferation associated with expression of MUC18 tumour  
XX PT antigen, involves incubating and inhibiting cell by administering anti-  
XX PT MUC18 monoclonal antibody.

XX PS Claim 1; SEQ ID NO 37; 83pp; English.

XX CC The invention comprises a method for inhibiting cell proliferation  
XX CC associated with expression of MUC18 tumour antigen. The method involves  
XX CC administering anti-MUC18 monoclonal antibody. The method of the invention  
XX CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
XX CC proliferation associated with the expression of MUC18 tumour antigen, the  
XX CC method is preferably useful for inhibiting tumour metastasis. The method  
XX CC is useful for inhibiting cell proliferation in patients with tumours,  
XX CC carcinomas, cancer and other malignancies. The present amino acid  
XX CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
XX CC monoclonal antibody.

XX SQ Sequence 121 AA;

Query Match 100.0%; Score 651; DB 7; Length 121;  
Best Local Similarity 100.0%; Pred. No. 2.7e-47;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPESETLSLTCTVSGGSIITYYWSWIRQPGKLEWIGIYYTGTNTYYN 60  
 Db 1 QVQLQESGPGLVKPESETLSLTCTVSGGSIITYYWSWIRQPGKLEWIGIYYTGTNTYYN 60  
 QY 61 PSLKSRVTVSVDTSKNQFSLKNSVTAAADTAATVYYCARDPGQWLVPDAFDIWGQGTMTVS 120  
 Db 61 PSLKSRVTVSVDTSKNQFSLKNSVTAAADTAATVYYCARDPGQWLVPDAFDIWGQGTMTVS 120  
 QY 121 S 121  
 Db 121 S 121

## RESULT 4

ADC99780  
 ID ADC99780 standard; protein; 121 AA.

XX AC ADC99780;

XX DT 01-JAN-2004 (first entry)

XX DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 9.

XX KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
 KW cytotstatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
 KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
 KW lung cancer; human.

XX OS Homo sapiens.

XX PN WO2003057838-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041581.

XX PR 28-DEC-2001; 2001US-0346299P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J;

XX WPI; 2003-587113/55.

XX DR N-PSDB; ADC99782.

XX PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
 PT or condition associated with expression of MUC18 in a patient, e.g.  
 PT tumors, cancers, and other malignancies.

XX PS Claim 1; SEQ ID NO 9; 78pp; English.

XX CC The invention relates to a novel isolated monoclonal antibody comprising  
 CC a heavy or light chain amino acid or a heavy or light chain variable  
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
 CC invention demonstrates cytostatic activity and may be useful for treating  
 CC a disease or condition associated with the expression of MUC18 on the  
 CC cell surface such as tumours, specifically melanoma, oesophageal,  
 CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
 CC carcinomas and cervical intraepithelial neoplasia and cancers including  
 CC colorectal, breast or lung cancer, as well as other malignancies. The  
 CC current sequence is that of the anti-human MUC18 monoclonal antibody  
 CC heavy chain protein of the invention.

XX SQ Sequence 121 AA;

Query Match 91.9%; Score 598; DB 7; Length 121;

Best Local Similarity 90.9%; Pred. No. 7.9e-43;

Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPESETLSLTCTVSGGSIITYYWSWIRQPGKLEWIGIYYTGTNTYYN 60

Db 1 QVQLQESGPGLVKPESETLSLTCTVSGGSIITYYWSWIRQPGKLEWIGIYYTGTNTYYN 60

QY 61 PSLKSRVTVSVDTSKNQFSLKNSVTAAADTAATVYYCARDPGQWLVPDAFDIWGQGTMTVS 120  
 Db 61 PSLKSRVTVSVDTSKNQFSLKNSVTAAADTAATVYYCARDPGQWLVPDAFDIWGQGTMTVS 120  
 QY 121 S 121  
 Db 121 S 121

## RESULT 5

ADD05384  
 ID ADD05384 standard; protein; 121 AA.

XX AC ADD05384;

XX DT 01-JAN-2004 (first entry)

XX DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 9.

XX KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
 KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.

XX OS Homo sapiens.

XX PN WO2003057006-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041582.

XX PR 28-DEC-2001; 2001US-0346460P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J, Bar-Eli M;

XX WPI; 2003-577496/54.

XX DR N-PSDB; ADD05386.

XX PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
 PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
 PT associated with melanoma, or increasing survival of an animal having a  
 PT metastatic tumor.

XX PS Claim 1; SEQ ID NO 9; 87pp; English.

XX CC The invention relates to a novel monoclonal antibody used for inhibiting  
 CC tumour growth in an animal. The tumour inhibition process comprises  
 CC selecting an animal in need of treatment for a tumour, providing a  
 CC monoclonal antibody comprising a heavy chain amino acid, where the  
 CC antibody consists of any one of 10 fully defined sequences of 117-123  
 CC amino acids given in the specification, and where the monoclonal antibody  
 CC binds MUC18, and contacting the tumour with the antibody resulting in  
 CC inhibited proliferation of the cells. The monoclonal antibody has  
 CC cytostatic and can be used in the production of a vaccine. The monoclonal  
 CC antibodies against the MUC18 antigen are useful for diagnosing and  
 CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or  
 CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
 CC increasing survival of an animal having a metastatic tumour. This  
 CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
 CC protein of the invention.

XX SQ Sequence 121 AA;

Query Match 91.9%; Score 598; DB 7; Length 121;

Best Local Similarity 90.9%; Pred. No. 7.9e-43;

Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPESETLSLTCTVSGGSIITYYWSWIRQPGKLEWIGIYYTGTNTYYN 60

Db 1 QVQLQESGPGLVKPESETLSLTCTVSGGSIITYYWSWIRQPGKLEWIGIYYTGTNTYYN 60



ADC99788  
 ID ADC99788 standard; protein; 121 AA.  
 XX AC  
 XX AC ADC99788;  
 XX DT  
 XX DT 01-JAN-2004 (first entry)  
 XX DE  
 XX DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 17.  
 XX KW  
 XX KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
 XX KW cytosolic; melanoma; oesophageal; pancreatic; colorectal tumour;  
 XX KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
 XX KW lung cancer; human.  
 XX OS  
 XX OS Homo sapiens.  
 XX PN  
 XX PN WO2003057838-A2.  
 XX XX  
 XX PD 17-JUL-2003.  
 XX PF  
 XX PF 26-DEC-2002; 2002WO-US041581.  
 XX PR  
 XX PR 28-DEC-2001; 2001US-0346299P.  
 XX PA  
 XX PA (ABGE-) ABGENIX INC.  
 XX PI  
 XX PI Gudas J;  
 XX PT  
 XX PT WPI; 2003-587113/55.  
 XX DR  
 XX DR N-PSDB; ADC99790.  
 XX PS  
 XX PS New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
 XX PT or condition associated with expression of MUC18 in a patient, e.g.  
 XX PT tumors, cancers, and other malignancies.  
 XX PS  
 XX PS Claim 1; SEQ ID NO 17; 78pp; English.  
 XX CC  
 XX CC The invention relates to a novel isolated monoclonal antibody comprising  
 XX CC a heavy or light chain amino acid or a heavy or light chain variable  
 XX CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
 XX CC invention demonstrates cytostatic activity and may be useful for treating  
 XX CC a disease or condition associated with the expression of MUC18 on the  
 XX CC cell surface such as tumours, specifically melanoma, oesophageal,  
 XX CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
 XX CC carcinomas and cervical intraepithelial neoplasia and cancers including  
 XX CC colorectal, breast or lung cancer, as well as other malignancies. The  
 XX CC current sequence is that of the anti-human MUC18 monoclonal antibody  
 XX CC heavy chain protein of the invention.  
 XX SQ

Query Match 91.78; Score 597; DB 7; Length 121;  
 Best Local Similarity 90.9%; Pred. No. 9.6e-43;  
 Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 QVQLQESGPGLVKPESETLSLTCTVSGGSIISTYVSWIRQPPGKLEWIGIYYTNTYYN 60  
 Db 1 QVQLQESGPGLVKPESETLSLTCTVSGGSIISTYVSWIRQPPGKLEWIGIYYTNTSYN 60  
 Qy 61 PSLKSRVTVSVDTSKNQFSLKLSVTAADTAIVYCARDPGQWLVPDAFDIWGQGTWVS 120  
 Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAIVYCARDQGWLLPDAFDIWGQGTWVS 120  
 Qy 121 S 121  
 Db 121 S 121

RESULT 9  
 ADD05376  
 ID ADD05376 standard; protein; 121 AA.  
 XX AC  
 XX AC ADD05376;

XX DT  
 XX DT 01-JAN-2004 (first entry)  
 XX DE  
 XX DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID NO 1.  
 XX KW  
 XX KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
 XX KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
 XX OS  
 XX OS Homo sapiens.  
 XX PN  
 XX PN WO2003057006-A2.  
 XX XX  
 XX PD 17-JUL-2003.  
 XX PF  
 XX PF 26-DEC-2002; 2002WO-US041582.  
 XX PR  
 XX PR 28-DEC-2001; 2001US-0346460P.  
 XX PA  
 XX PA (ABGE-) ABGENIX INC.  
 XX PI  
 XX PI Gudas J, Bar-Eli M;  
 XX DR  
 XX DR WPI; 2003-577496/54.  
 XX DR  
 XX DR N-PSDB; ADD05378.  
 XX PT  
 XX PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
 XX PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
 XX PT associated with melanoma, or increasing survival of an animal having a  
 XX PT metastatic tumor.  
 XX PS  
 XX PS Claim 1; SEQ ID NO 1; 87pp; English.  
 XX CC  
 XX CC The invention relates to a novel monoclonal antibody used for inhibiting  
 XX CC tumour growth in an animal. The tumour inhibition process comprises  
 XX CC selecting an animal in need of treatment for a tumour, providing a  
 XX CC monoclonal antibody comprising a heavy chain amino acid, where the  
 XX CC antibody consists of any one of 10 fully defined sequences of 117-123  
 XX CC amino acids given in the specification, and where the monoclonal antibody  
 XX CC binds MUC18, and contacting the tumour with the antibody resulting in  
 XX CC inhibited proliferation of the cells. The monoclonal antibody has  
 XX CC cytostatic and can be used in the production of a vaccine. The monoclonal  
 XX CC antibodies against the MUC18 antigen are useful for diagnosing and  
 XX CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or  
 XX CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
 XX CC increasing survival of an animal having a metastatic tumour. This  
 XX CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
 XX CC protein of the invention.  
 XX SQ

Query Match 91.7%; Score 597; DB 7; Length 121;  
 Best Local Similarity 90.9%; Pred. No. 9.6e-43;  
 Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 QVQLQESGPGLVKPESETLSLTCTVSGGSIISTYVSWIRQPPGKLEWIGIYYTNTYYN 60  
 Db 1 QVQLQESGPGLVKPESETLSLTCTVSGGSIISTYVSWIRQPPGKLEWIGIYYTNTSYN 60  
 Qy 61 PSLKSRVTVSVDTSKNQFSLKLSVTAADTAIVYCARDPGQWLVPDAFDIWGQGTWVS 120  
 Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAIVYCARDQGWLLPDAFDIWGQGTWVS 120  
 Qy 121 S 121  
 Db 121 S 121

RESULT 10  
 ADD05392  
 ID ADD05392 standard; protein; 121 AA.  
 XX AC  
 XX AC ADD05392;

DT 01-JAN-2004 (first entry)  
 XX Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 17.  
 DE monoclinal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
 XX antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
 KW Homo sapiens.  
 OS  
 XX WO2003057006-A2.  
 PN  
 XX 17-JUL-2003.  
 PD  
 XX 26-DEC-2002; 2002WO-US041582.  
 PF  
 XX 28-DEC-2001; 2001US-0346460P.  
 PR  
 XX (ABGE-) ABGENIX INC.  
 PA  
 XX Gudas J, Bar-Eli M;  
 PI  
 XX WPI; 2003-577496/54.  
 DR  
 XX N-PSDB; ADD05394.  
 DT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
 XX treating tumors, inhibiting tumor growth, inhibiting cell invasion  
 XX associated with melanoma, or increasing survival of an animal having a  
 XX metastatic tumor.  
 XX  
 XX Claim 1; SEQ ID NO 17; 87pp; English.  
 XX  
 XX The invention relates to a novel monoclonal antibody used for inhibiting  
 XX tumour growth in an animal. The tumour inhibition process comprises  
 XX selecting an animal in need of treatment for a tumour, providing a  
 XX monoclonal antibody comprising a heavy chain amino acid, where the  
 XX antibody consists of any one of 10 fully defined sequences of 117-123  
 XX amino acids given in the specification, and where the monoclonal antibody  
 XX binds MUC18, and contacting the tumour with the antibody resulting in  
 XX inhibited proliferation of the cells. The monoclonal antibody has  
 XX cytostatic and can be used in the production of a vaccine. The monoclonal  
 XX antibodies against the MUC18 antigen are useful for diagnosing and  
 XX treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or  
 XX tumour metastasis), inhibiting cell invasion associated with melanoma, or  
 XX increasing survival of an animal having a metastatic tumour. This  
 XX sequence represents an anti-MUC18 antibody heavy chain, variable region,  
 XX protein of the invention.  
 XX  
 XX Sequence 121 AA;  
 XX  
 XX Query Match 91.7%; Score 597; DB 7; Length 121;  
 XX Best Local Similarity 90.9%; Pred. No. 9.6e-43;  
 XX Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
 XX  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIITYYWSWIRQPPGKLEWIGIYYTGTNYN 60  
 DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIITYYWSWIRQPPGKLEWIGIYYTGTNYN 60  
 QY 61 PSLKSRVTYSVDTSKNQFSLKLSNVTAAADTAVYVCARDPQGLVLPDADFIDWGQGTWVS 120  
 DB 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGLWLLPDAFDIDWGQGTWVS 120  
 QY 121 S 121  
 DB 121 S 121  
 RESULT 11  
 ADF09814  
 ID ADF09814 standard; protein; 121 AA.  
 XX  
 XX ADF09814;  
 AC  
 XX 12-FEB-2004 (first entry)  
 DT

XX Human anti-MUC18 monoclonal antibody heavy chain #1.  
 DE cell proliferation inhibition; MUC18 tumour antigen;  
 XX anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
 KW carcinoma; cancer; malignancy; heavy chain; human.  
 XX  
 OS Homo sapiens.  
 XX WO2003057837-A2.  
 PN  
 XX 17-JUL-2003.  
 PD  
 XX 26-DEC-2002; 2002WO-US041580.  
 PF  
 XX 28-DEC-2001; 2001US-0346414P.  
 PR  
 XX (ABGE-) ABGENIX INC.  
 PA  
 XX Gudas J;  
 PI  
 XX WPI; 2003-598367/56.  
 DR  
 XX N-PSDB; ADF09816.  
 DT Inhibiting cell proliferation associated with expression of MUC18 tumor  
 XX antigen, involves incubating and inhibiting cell by administering anti-  
 XX MUC18 monoclonal antibody.  
 XX  
 XX Claim 1; SEQ ID NO 1; 83pp; English.  
 XX  
 XX The invention comprises a method for inhibiting cell proliferation  
 XX associated with expression of MUC18 tumour antigen. The method involves  
 XX administering anti-MUC18 monoclonal antibody. The method of the invention  
 XX is useful for inhibiting cell (e.g. melanoma or tumour cell)  
 XX proliferation associated with the expression of MUC18 tumour antigen, the  
 XX method is preferably useful for inhibiting tumour metastasis. The method  
 XX is useful for inhibiting cell proliferation in patients with tumours,  
 XX carcinomas, cancer and other malignancies. The present amino acid  
 XX sequence represents a heavy chain from an MUC18 tumour antigen-specific  
 XX monoclonal antibody.  
 XX  
 XX Sequence 121 AA;  
 XX  
 XX Query Match 91.7%; Score 597; DB 7; Length 121;  
 XX Best Local Similarity 90.9%; Pred. No. 9.6e-43;  
 XX Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
 XX  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIITYYWSWIRQPPGKLEWIGIYYTGTNYN 60  
 DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIITYYWSWIRQPPGKLEWIGIYYTGTNYN 60  
 QY 61 PSLKSRVTYSVDTSKNQFSLKLSNVTAAADTAVYVCARDPQGLVLPDADFIDWGQGTWVS 120  
 DB 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGLWLLPDAFDIDWGQGTWVS 120  
 QY 121 S 121  
 DB 121 S 121  
 RESULT 12  
 ADF09830  
 ID ADF09830 standard; protein; 121 AA.  
 XX  
 XX ADF09830;  
 AC  
 XX 12-FEB-2004 (first entry)  
 DT Human anti-MUC18 monoclonal antibody heavy chain #5.  
 DE cell proliferation inhibition; MUC18 tumour antigen;  
 XX anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
 KW carcinoma; cancer; malignancy; heavy chain; human.  
 XX

XX OS Homo sapiens.  
 XX PN WO2003057837-A2.  
 XX PD 17-JUL-2003.  
 XX PF 26-DEC-2002; 2002WO-US041580.  
 XX PR 28-DEC-2001; 2001US-0346414P.  
 XX PA (ABGE-) ABGENIX INC.  
 XX PI Gudas J;  
 XX WPI; 2003-598367/56.  
 XX DR N-PSDB; ADF09832.  
 XX PT Inhibiting cell proliferation associated with expression of MUC18 tumor  
 PT antigen, involves incubating and inhibiting cell by administering anti-  
 PT MUC18 monoclonal antibody.  
 XX PS Claim 1; SEQ ID NO 17; 83pp; English.  
 XX CC The invention comprises a method for inhibiting cell proliferation  
 CC associated with expression of MUC18 tumour antigen. The method involves  
 CC administering anti-MUC18 monoclonal antibody. The method of the invention  
 CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
 CC proliferation associated with the expression of MUC18 tumour antigen, the  
 CC method is preferably useful for inhibiting tumour metastasis. The method  
 CC is useful for inhibiting cell proliferation in patients with tumours,  
 CC carcinomas, cancer and other malignancies. The present amino acid  
 CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
 CC monoclonal antibody.  
 XX SQ Sequence 121 AA;  
 Query Match 91.7%; Score 597; DB 7; Length 121;  
 Best Local Similarity 90.9%; Pred. No. 9.6e-43;  
 Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISITYYWSWIRQPPGKLEWIGIYYTNTYNN 60  
 DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISITYYWSWIRQPPGKLEWIGIYYTNTYNN 60  
 QY 61 PSLKSRVTISVDTSKNQFSLKNSVTAADTAVYYCARDPGQWLVPDADFINGQGTWTVS 120  
 DB 61 PSLKSRVTISVDTSKNQFSLKNSVTAADTAVYYCARDPGQWLVPDADFINGQGTWTVS 120  
 QY 121 S 121  
 DB 121 S 121  
 RESULT 13  
 ADO58076  
 ID ADO58076 standard; protein; 243 AA.  
 AC ADO58076;  
 XX DT 12-AUG-2004 (first entry)  
 XX DE S9 cell derived human scFvVL-VH protein.  
 XX KW B cell; surface immunoglobulin; Ig; binding site; antigen; human CD28;  
 KW closed system; detection laser-beam; catcher tube;  
 KW electrochemical device; fluorescence activated cell sorter; FACS;  
 KW antibody variable region; human.  
 XX OS Homo sapiens.  
 XX PN WO2004044584-A1.

PD 27-MAY-2004.  
 XX 12-NOV-2003; 2003WO-EP012664.  
 XX PR 13-NOV-2002; 2002EP-00025335.  
 XX PA (MICR-) MICROMET AG.  
 XX PI Baeuerle P, Hoffmann P, Weinberger S, Kischel R;  
 XX WPI; 2004-449579/42.  
 XX DR N-PSDB; ADO58077.  
 XX PT Identifying a B cell carrying a surface immunoglobulin molecule having a  
 PT binding site for an antigen of interest, useful for constructing  
 PT therapeutic antibodies, comprises contacting a sample with the antigen  
 PT and a receptor.  
 XX PS Claim 22; SEQ ID NO 76; 156pp; English.  
 XX CC The invention relates to a novel method for identifying a B cell carrying  
 CC a surface immunoglobulin (Ig) molecule having a binding site for an  
 CC antigen of interest. The method comprises contacting a sample putatively  
 CC containing the B cell with the antigen of interest and with a receptor  
 CC specifically binding to the Ig molecule, and assessing the presence of  
 CC the detectable signal. The invention further comprises: an antibody  
 CC generated by the method above which is specific for human CD28 or  
 CC comprising an amino acid(s) sequence(s) given in the specification,  
 CC and/or are encoded by a nucleic acid sequence(s) also given in the  
 CC specification; and a device for assessing the presence of a detectable  
 CC signal defined above, where the device comprises a closed system for the  
 CC detection laser-beam and a catcher tube, and where the B cell of interest  
 CC can be collected as a single cell by means of an electrochemical device,  
 CC which is triggered by an electric signal generated by the fluorescence  
 CC activated cell sorter (FACS) device, where the electrochemical device  
 CC moves the nozzle of the steady catcher tube liquid stream for a  
 CC programmed time over a collecting tube, microtiter plate or other  
 CC container after a B cell is sorted. The method is useful for identifying  
 CC a B cell carrying a surface Ig molecule having a binding site for an  
 CC antigen of interest. The method is also useful for cloning of antibody  
 CC variable regions from the identified B cells, which may subsequently be  
 CC employed in the construction of proteins such as antibodies or its  
 CC fragments or derivatives useful in therapeutic approaches. The method is  
 CC useful as an alternative to phage display for the gain of antibodies or  
 CC its fragments. This sequence represents an S2 cell derived human  
 CC polypeptide of the invention.  
 XX SQ Sequence 243 AA;  
 Query Match 86.4%; Score 562.5; DB 8; Length 243;  
 Best Local Similarity 88.4%; Pred. No. 1.6e-39;  
 Matches 107; Conservative 8; Mismatches 5; Indels 1; Gaps 1;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISITYYWSWIRQPPGKLEWIGIYYTNTYNN 60  
 DB 124 QVQLQESGPGLVKPSSETLSLTCTVSGSISITYYWSWIRQPPGKLEWIGIYYTNTYNN 183  
 QY 61 PSLKSRVTISVDTSKNQFSLKNSVTAADTAVYYCARDPGQWLVPDADFINGQGTWTVS 120  
 DB 184 PSLKSRVTISVDTSKNQFSLKNSVTAADTAVYYCARDPGQWLVPDADFINGQGTWTVS 242  
 QY 121 S 121  
 DB 243 S 243  
 RESULT 14  
 ADP03871  
 ID ADP03871 standard; protein; 125 AA.  
 XX AC ADP03871;  
 XX DT 29-JUL-2004 (first entry)

XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 11.  
 XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytosolic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX OS Unidentified.  
 XX WO2003048328-A2.  
 XX PN 12-JUN-2003.  
 XX PD  
 XX PF 02-DEC-2002; 2002WO-US038550.  
 XX PR 03-DEC-2001; 2001US-0337275P.  
 XX PA (ABGE-) ABGENIX INC.  
 XX PI Gudas J, Foltz I, Handa M, Gallo M;  
 XX WIPI; 2003-523295/49.  
 XX PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX PS Claim 1; SEQ ID NO 11; 89pp; English.

XX CC The invention relates to a novel isolated monoclonal antibody (mAb)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytostatic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.

XX SQ Sequence 125 AA;

Query Match 85.1%; Score 554; DB 7; Length 125;  
 Best Local Similarity 85.6%; Pred. No. 4.1e-39;  
 Matches 107; Conservative 8; Mismatches 6; Indels 4; Gaps 2;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIST--YYNSWIRQPPKGLWGIYYTGTNY 58  
 Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYNSWIRQHPGKGLWGIYYSGNTY 60  
 Qy 59 YNPSLKRVTVDTSKNQSLKNSVTAADTAVYYCARDPGQWLV--PPAFDIWGQGTM 116  
 Db 61 YNPSLKRITISVDTSKNQSLKNSVTAADTAVYYCARTYFDLTGYPDPAFDIWGQGTM 120

Qy 117 VSVSS 121

Db 121 VTVSS 125

RESULT 15

ABG92884

ID ABG92884 standard; protein; 121 AA.

AC ABG92884;

XX 19-NOV-2002 (first entry)

XX Human immunoglobulin variable light domain #1.

XX KW Immunoglobulin; variable heavy chain; variable light chain; human;  
 KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;  
 KW immunologic deficiency syndrome; blood protein disorder; nephritis;  
 KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;  
 KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;  
 KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;  
 KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;  
 KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;  
 KW Pneumocystis carni infection; cardiovascular disorder; atherosclerosis;  
 KW Lymphocytopenia.  
 XX OS Homo sapiens.  
 XX PN WO200264612-A2.  
 XX PD 22-AUG-2002.  
 XX PF 08-FEB-2002; 2002WO-US003634.  
 XX PR 09-FEB-2001; 2001US-00779880.  
 PR 09-FEB-2001; 2001WO-US004153.  
 PR 12-JUN-2001; 2001US-0297257P.  
 PR 08-AUG-2001; 2001US-0310458P.  
 PR 12-OCT-2001; 2001US-0328447P.  
 PR 21-DEC-2001; 2001US-0341725P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Roschke V, Rosen CA, Ruben SM;  
 XX WIPI; 2002-643455/59.  
 XX N-PSDB; ABS68607.  
 XX PT New human G-protein Chemokine Receptor gene (HDGNR10) useful for  
 PT treating, preventing, ameliorating or monitoring diseases or disorders  
 PT associated with aberrant expression of HDGNR10 e.g. cancer.  
 XX Example 55; Fig 4; 562pp; English.

XX The invention describes an isolated polynucleotide encoding a first  
 CC antibody at least 95-100% identical to a second antibody consisting of an  
 CC amino acid sequence comprising at least one, two or three CDR regions of  
 CC a variable heavy (VH) or variable light (VL) domain of the antibody  
 CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,  
 CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody  
 CC is useful treating, preventing, ameliorating, prognosing or monitoring  
 CC cancers or other diseases or disorders e.g. immunologic deficiency  
 CC syndromes such as blood protein disorders and ataxia telangiectasia,  
 CC inflammation associated disorders such as endotoxin lethality, nephritis  
 CC and inflammatory bowel disease, conditions associated with an increase in  
 CC certain haematopoietic cells such as histiocytosis, defective or aberrant  
 CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,  
 CC an infectious disease, an autoimmune disease such as Addison's disease,  
 CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative  
 CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or  
 CC poxvirus infection, a Pneumocystis carni infection, Kaposi's sarcoma,  
 CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a  
 CC disease or disorder associated with aberrant expression of novel human G-  
 CC protein chemokine receptor (CCR5) HDGNR10. This is the amino acid  
 CC sequence of human immunoglobulin sequence associated with the antibodies  
 CC against HDGNR10

XX SQ Sequence 121 AA;

Query Match 84.0%; Score 547; DB 5; Length 121;

Best Local Similarity 86.0%; Pred. No. 1.6e-38;  
 Matches 104; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISTYYNSWIRQPPKGLWGIYYTGTNY 60  
 Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISFFYNSWIRQPPKGLWIGRIYTGNTNY 60



Qy	61	PSLKSRTVTSVDTSKQFSLKLSVTAAADTAIVYICARDPGOWLPDPAFDINGQGTMVSVS	120
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Db	121 S	121	

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Job time : 75.6015 secs

(CANC) 2000-01-01 00:00:00

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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55 ; Search time 18.802 Seconds  
(without alignments)  
480.403 Million cell updates/sec

Title: US-10-660-357A-37

Perfect score: 651

Sequence: 1 QVQLQESGPGLVKPSSETLSL.....WLVPDAFDWQGTMTSVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*

2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	538.5	82.7	120	4	US-09-424-840B-20
2	536	82.3	119	3	US-09-025-769B-39
3	536	82.3	119	3	US-09-025-769B-65
4	536	82.3	119	4	US-09-490-070A-39
5	536	82.3	119	4	US-09-490-070A-65
6	536	82.3	119	4	US-09-490-153-39
7	536	82.3	119	4	US-09-490-153-65
8	536	82.3	119	4	US-09-490-324-39
9	536	82.3	119	4	US-09-490-324-65
10	525.5	80.7	118	3	US-09-025-769B-25
11	525.5	80.7	118	4	US-09-490-070A-25
12	525.5	80.7	118	4	US-09-490-153-25
13	525.5	80.7	118	4	US-09-490-324-25
14	525.5	80.7	244	4	US-09-138-091A-77
15	525.5	80.7	244	4	US-09-138-091A-77
16	520.5	80.0	473	3	US-09-049-672A-4
17	513	78.8	117	4	US-09-720-493-2
18	511	78.5	142	2	US-08-480-774A-2
19	510.5	78.4	122	1	US-08-360-125-11
20	510.5	78.4	122	2	US-08-450-578-11
21	510.5	78.4	122	2	US-09-017-628-11
22	510.5	78.4	122	2	US-09-014-880-11
23	510.5	78.4	122	4	US-08-450-363-11
24	510.5	78.4	122	4	US-09-467-903-11
25	498.5	76.6	487	4	US-09-800-729-145
26	497.5	76.4	172	4	US-09-472-087-7
27	497.5	76.4	172	4	US-09-472-087-86

28 496.5 76.3 139 4 US-09-471-276-837 Sequence 837, Appl  
29 496 76.2 119 1 US-08-360-125-5 Sequence 5, Appli  
30 496 76.2 119 2 US-08-450-578-5 Sequence 5, Appli  
31 496 76.2 119 2 US-09-017-628-5 Sequence 5, Appli  
32 496 76.2 119 2 US-09-014-880-5 Sequence 5, Appli  
33 496 76.2 119 4 US-08-450-363-5 Sequence 5, Appli  
34 496 76.2 119 4 US-09-467-903-5 Sequence 5, Appli  
35 491 75.4 123 3 US-08-793-450-4 Sequence 4, Appli  
36 488 75.0 116 3 US-08-545-809A-140 Sequence 140, Appl  
37 488 75.0 472 3 US-08-733-450-8 Sequence 8, Appli  
38 482.5 74.1 98 1 US-08-478-039-75 Sequence 75, Appl  
39 482.5 74.1 98 1 US-08-476-349A-75 Sequence 75, Appl  
40 482.5 74.1 278 3 US-09-260-527-3 Sequence 3, Appli  
41 480 73.7 119 2 US-08-652-816A-10 Sequence 10, Appl  
42 480 73.7 155 4 US-09-471-276-888 Sequence 888, Appl  
43 478 73.4 117 4 US-09-232-290-47 Sequence 47, Appl  
44 477 73.3 118 3 US-08-545-809A-142 Sequence 142, Appl  
45 475.5 73.0 139 4 US-09-203-768A-2 Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
US-09-424-840B-20  
; Sequence 20, Application US/09424840B  
; Patent No. 6790938  
; GENERAL INFORMATION:  
; APPLICANT: Berchtold, Peter  
; APPLICANT: Escher, Robert F. A.  
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES  
; FILE REFERENCE: 100564-09049  
; CURRENT APPLICATION NUMBER: US/09/424,840B  
; CURRENT FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: DE 19820663.1  
; PRIOR FILING DATE: 1998-05-08  
; PRIOR APPLICATION NUMBER: DE 19755227.7  
; PRIOR FILING DATE: 1997-12-12  
; PRIOR APPLICATION NUMBER: DE 19723904.8  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 20  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-424-840B-20

Query Match 82.7%; Score 538.5; DB 4; Length 120;  
Best Local Similarity 85.4%; Pred. No. 1.9e-46;  
Matches 105; Conservative 6; Mismatches 7; Indels 5; Gaps 3;  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSTYYWSMIQPPGKGLEWIGYIYTGNTYYN 60  
Db 1 QVQLKESGPGLVKPSSETLSLTCTVSGSGSTYYWSMIQPPGKGLEWIGYIYTGNTYYN 60  
Qy 61 PSLSKRVTVSDPFSKNQFSLKLSVTAADTAADVYCA--RDPGQWLVPDAFDWQGTMTVS 118  
Db 61 PSLSKRVTSVDTFSKNQFSLKLSVTAADTAADVYCARLNDG-W--NDGFDWQGTMTV 117  
Qy 119 VSS 121  
Db 118 VSS 120  
RESULT 2  
US-09-025-769B-39  
; Sequence 39, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic



APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-070A-39

Query Match 82.3%; Score 536; DB 4; Length 119;  
Best Local Similarity 85.1%; Pred. No. 3.4e-46;  
Matches 103; Conservative 7; Mismatches 9; Indels 2; Gaps 1;  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISITYYWSWIRQPPGKGLEWIGYIYTGNTYIN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISITYYWSWIRQPPGKGLEWIGYIYSGSTNYN 60  
Qy 61 PSLKSRVTISVDTSKNQPSLKLNSVTAADTAIVYICARDPQGWLPDAPDINGQGTMSVS 120  
Db 61 PSLKSRVTISVDTSKNQPSLKLNSVTAADTAIVYICARDPQGWLPDAPDINGQGTMTVS 118  
Qy 121 \$ 121  
Db 119 \$ 119

RESULT 5  
US-09-490-070A-65  
Sequence 65, Application US/09490070A  
Patent No. 6696248  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
White & McAuliffe  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-070A-65  
Query Match 82.3%; Score 536; DB 4; Length 119;  
Best Local Similarity 85.1%; Pred. No. 3.4e-46;  
Matches 103; Conservative 7; Mismatches 9; Indels 2; Gaps 1;  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISITYYWSWIRQPPGKGLEWIGYIYTGNTYIN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISITYYWSWIRQPPGKGLEWIGYIYSGSTNYN 60  
Qy 61 PSLKSRVTISVDTSKNQPSLKLNSVTAADTAIVYICARDPQGWLPDAPDINGQGTMSVS 120  
Db 61 PSLKSRVTISVDTSKNQPSLKLNSVTAADTAIVYICARDPQGWLPDAPDINGQGTMTVS 118  
Qy 121 \$ 121  
Db 119 \$ 119  
RESULT 6  
US-09-490-153-39  
Sequence 39, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:



Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGYIYSGSTNYN 60  
QY 61 PSLKSRVTVSVDTSKQFSLKLSNVTAAATAVYYCARDPGQWLVPDAPFDIWGQGTWVS 120  
Db 61 PSLKSRVTISVDTSKQFSLKLSNVTAAATAVYYCARDPGQWLVPDAPFDIWGQGTWVS 118

QY 121 S 121  
Db 119 S 119

## RESULT 9

US-09-490-324-65

; Sequence 65, Application US/09490324

; Patent No. 6828422

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; Pack, Peter

; Ilag, Vic

; Ge, Liming

; Moroney, Simon

; Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish &amp; Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10021

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/490,324

; FILING DATE: 24-Jan-2000

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/025,769

; FILING DATE: 18-FEB-1998

; APPLICATION NUMBER: EP 95 11 3021.0

; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: James F. Haley, Jr., Esq.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: MORPHO/5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)596-9000

; TELEFAX: (212)596-9090

; INFORMATION FOR SEQ ID NO: 65:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 119 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 65:

US-09-490-324-65

Query Match 82.3%; Score 536; DB 4; Length 119;  
Best Local Similarity 85.1%; Pred. No. 3.4e-46;  
Matches 103; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGYIYSGSTNYN 60

Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGYIYSGSTNYN 60

QY 61 PSLKSRVTVSVDTSKQFSLKLSNVTAAATAVYYCARDPGQWLVPDAPFDIWGQGTWVS 120  
Db 61 PSLKSRVTISVDTSKQFSLKLSNVTAAATAVYYCARDPGQWLVPDAPFDIWGQGTWVS 118





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; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25

Query Match      80.7%; Score 525.5; DB 4; Length 118;
Best Local Similarity 84.3%; Pred. No. 3.8e-45;
Matches 102; Conservative 8; Mismatches 8; Indels 3; Gaps 1;

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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISTYYWSWIRQPPGKLEWIGIYYTNTYYN 60

Qy 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAATVYVCARDPGQWLVPDAFDIWGQGTWVS 120
Db 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAATVYVCARDPGQWLVPDAFDIWGQGTWVS 120

Qy 121 S 121
Db 118 S 118

RESULT 14
US-08-918-148-79
; Sequence 79, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 79
; LENGTH: 244
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-79

Query Match      80.7%; Score 525.5; DB 3; Length 244;
Best Local Similarity 82.6%; Pred. No. 9.2e-45;
Matches 102; Conservative 8; Mismatches 8; Indels 3; Gaps 1;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISTYYWSWIRQPPGKLEWIGIYYTNTYYN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISTYYWSWIRQPPGKLEWIGIYYTNTYYN 60

Qy 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAATVYVCARDPGQWLVPDAFDIWGQGTWVS 120
Db 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAATVYVCARDPGQWLVPDAFDIWGQGTWVS 120

Qy 121 S 121
Db 118 S 118

RESULT 15
US-09-138-091A-77
; Sequence 77, Application US/09138091A
; Patent No. 6737249
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: 9491-013-27
; CURRENT APPLICATION NUMBER: US/09/138,091A
; CURRENT FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: US 60/056,736
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: single chain antibody (scFv) fragments
US-09-138-091A-77

Query Match      80.7%; Score 525.5; DB 4; Length 244;
Best Local Similarity 82.6%; Pred. No. 9.2e-45;
Matches 100; Conservative 12; Mismatches 2; Indels 7; Gaps 2;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISTYYWSWIRQPPGKLEWIGIYYTNTYYN 60
Db 3 QVQLQESGPGLVKPSSETLSLTCTVSGSISTYYWSWIRQPPGKLEWIGIYYTNTYYN 62

Qy 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAATVYVCARDPGQWLVPDAFDIWGQGTWVS 120
Db 63 PSLKSRVTISVDTSKNQFSLKLSVTAADTAATVYVCARDPGQWLVPDAFDIWGQGTWVS 120

Qy 121 S 121
Db 116 S 116

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(2020) 2020 2020 2020

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2005, 11:40:37 ; Search time 67.2222 Seconds  
(without alignments)  
753.137 Million cell updates/sec

Title: US-10-660-357A-37

Perfect score: 651

Sequence: 1 QVQLQESGPGLVKPSSETLSL.....WLVPDADFIMWGQGTWVSVS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
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- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
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- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US10F\_PUBCOMB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
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- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	651	100.0	121	14	US-10-330-613-37
2	651	100.0	121	14	US-10-330-530-37
3	651	100.0	121	16	US-10-660-357-37
4	598	91.9	121	14	US-10-330-613-9
5	598	91.9	121	14	US-10-330-530-9
6	598	91.9	121	16	US-10-660-357-9
7	597	91.7	121	14	US-10-330-613-1
8	597	91.7	121	14	US-10-330-613-17
9	597	91.7	121	14	US-10-330-530-1
10	597	91.7	121	14	US-10-330-530-17
11	597	91.7	121	16	US-10-660-357-1

12	597	91.7	121	16	US-10-660-357-17	Sequence 17, Appl
13	554	85.1	125	15	US-10-309-762-11	Sequence 11, Appl
14	552	84.8	142	17	US-10-893-576-37	Sequence 37, Appl
15	547.5	84.1	118	15	US-10-292-088-142	Sequence 142, App
16	547	84.0	121	14	US-10-067-800-60	Sequence 60, Appl
17	547	84.0	121	18	US-10-994-679-60	Sequence 60, Appl
18	546	83.9	123	15	US-10-371-942-102	Sequence 102, App
19	544.5	83.6	121	14	US-10-010-729-11	Sequence 11, Appl
20	544	83.6	121	17	US-10-893-576-191	Sequence 191, App
21	543.5	83.5	118	15	US-10-292-088-109	Sequence 109, App
22	543	83.4	125	15	US-10-309-762-8	Sequence 8, Appl1
23	543	83.4	125	15	US-10-309-762-16	Sequence 16, Appl
24	541.5	83.2	122	15	US-10-309-762-25	Sequence 25, Appl
25	541.5	83.2	122	15	US-10-309-762-29	Sequence 29, Appl
26	541	83.1	119	17	US-10-937-596-23	Sequence 23, Appl
27	539	82.8	125	15	US-10-309-762-153	Sequence 153, App
28	539	82.8	446	17	US-10-644-277-62	Sequence 62, Appl
29	538.5	82.7	120	16	US-10-844-424-20	Sequence 20, Appl
30	537.5	82.6	118	17	US-10-727-155-178	Sequence 178, App
31	537.5	82.6	122	15	US-10-309-762-24	Sequence 24, Appl
32	537.5	82.6	122	15	US-10-309-762-27	Sequence 27, Appl
33	537.5	82.6	122	15	US-10-309-762-71	Sequence 71, Appl
34	537.5	82.6	141	15	US-10-309-762-90	Sequence 90, Appl
35	537	82.5	148	17	US-10-893-576-31	Sequence 31, Appl
36	536.5	82.4	139	17	US-10-893-576-39	Sequence 39, Appl
37	536.5	82.4	143	16	US-10-693-629-44	Sequence 44, Appl
38	536.5	82.4	193	15	US-10-264-049-4331	Sequence 4331, Ap
39	536	82.3	119	14	US-10-125-687-5	Sequence 5, Appl1
40	536	82.3	119	18	US-10-596-191-5	Sequence 5, Appl1
41	534.5	82.1	120	15	US-10-309-762-4	Sequence 4, Appl1
42	534.5	82.1	120	15	US-10-309-762-102	Sequence 102, App
43	534.5	82.1	128	15	US-10-173-551-24	Sequence 24, Appl
44	533.5	82.0	122	15	US-10-309-762-73	Sequence 73, Appl
45	533.5	82.0	141	15	US-10-309-762-94	Sequence 94, Appl

ALIGNMENTS

RESULT 1  
US-10-330-613-37  
; Sequence 37, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; PRIOR FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 37  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-37

Query Match 100.0%; Score 651; DB 14; Length 121;  
Best Local Similarity 100.0%; Pred. No. 2.4e-51;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISTYVSWIRQPPGKLEWIGYIYTGNTYIN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISTYVSWIRQPPGKLEWIGYIYTGNTYIN 60  
Qy 61 PSLSKRVTVSDVTSKNOFSLKLNSTAAADTAVYVPCARDPGQMLVPDADFIMWGQGTWVSVS 120  
Db 61 PSLSKRVTVSDVTSKNOFSLKLNSTAAADTAVYVPCARDPGQMLVPDADFIMWGQGTWVSVS 120  
Qy 121 s 121

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Db      121 S 121

RESULT 2
US-10-330-530-37
; Sequence 37, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-37

Query Match      100.0%; Score 651; DB 14; Length 121;
Best Local Similarity 100.0%; Pred. No. 2.4e-51;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QVQLQESGPGLVKPSSETLSLTCTVSGGISITYYMSWIRQPPGKGLEWIGYIYTGNTYYN 60
Db      1 QVQLQESGPGLVKPSSETLSLTCTVSGGISITYYMSWIRQPPGKGLEWIGYIYTGNTYYN 60
Qy      61 PSLKSRVTVSVDTSKNQFSLKLSVTAADTAVYYCARDPGQWLVPDAFDIWGGQTMVSVS 120
Db      61 PSLKSRVTVSVDTSKNQFSLKLSVTAADTAVYYCARDPGQWLVPDAFDIWGGQTMVSVS 120
Qy      121 S 121
Db      121 S 121

RESULT 3
US-10-660-357-37
; Sequence 37, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-37

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Best Local Similarity 100.0%; Pred. No. 2.4e-51;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 QVQLQESGPGLVKPSSETLSLTCTVSGGISITYYMSWIRQPPGKGLEWIGYIYTGNTYYN 60
Qy      61 PSLKSRVTVSVDTSKNQFSLKLSVTAADTAVYYCARDPGQWLVPDAFDIWGGQTMVSVS 120
Db      61 PSLKSRVTVSVDTSKNQFSLKLSVTAADTAVYYCARDPGQWLVPDAFDIWGGQTMVSVS 120

Db      121 S 121
Qy      121 S 121

RESULT 4
US-10-330-613-9
; Sequence 9, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-9

Query Match      91.9%; Score 598; DB 14; Length 121;
Best Local Similarity 90.9%; Pred. No. 1.5e-46;
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy      1 QVQLQESGPGLVKPSSETLSLTCTVSGGISITYYMSWIRQPPGKGLEWIGYIYTGNTYYN 60
Db      1 QVQLQESGPGLVKPSSETLSLTCTVSGGISITYYMSWIRQPPGKGLEWIGYIYTGNTYYN 60
Qy      61 PSLKSRVTVSVDTSKNQFSLKLSVTAADTAVYYCARDPGQWLVPDAFDIWGGQTMVSVS 120
Db      61 PSLKSRVTVSVDTSKNQFSLKLSVTAADTAVYYCARDPGQWLVPDAFDIWGGQTMVSVS 120
Qy      121 S 121
Db      121 S 121

RESULT 5
US-10-330-530-9
; Sequence 9, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-9

Query Match      91.9%; Score 598; DB 14; Length 121;
Best Local Similarity 90.9%; Pred. No. 1.5e-46;
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy      1 QVQLQESGPGLVKPSSETLSLTCTVSGGISITYYMSWIRQPPGKGLEWIGYIYTGNTYYN 60
Db      1 QVQLQESGPGLVKPSSETLSLTCTVSGGISITYYMSWIRQPPGKGLEWIGYIYTGNTYYN 60
Qy      61 PSLKSRVTVSVDTSKNQFSLKLSVTAADTAVYYCARDPGQWLVPDAFDIWGGQTMVSVS 120
Db      61 PSLKSRVTVSVDTSKNQFSLKLSVTAADTAVYYCARDPGQWLVPDAFDIWGGQTMVSVS 120
Qy      121 S 121
Db      121 S 121
```

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQCGQWLLPDAFDIWGQGTWTVS 120  
121 S 121  
|  
Db 121 S 121

## RESULT 6

US-10-660-357-9  
; Sequence 9, Application US/10660357  
; Publication No. US20040115205A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-El, Menashe  
; APPLICANT: Green, Larry L.  
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
; FILE REFERENCE: ABGENIX.030C1  
; CURRENT APPLICATION NUMBER: US/10/660,357  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 10/330,580  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-9

Query Match 91.9%; Score 598; DB 16; Length 121;  
Best Local Similarity 90.9%; Pred. No. 1.5e-46;  
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTYYWSMIROPPGKLEWIGIYYTGTNYN 60  
|  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTYYWSMIROPPGKLEWIGIYYTGTNYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDPCQWLVPDAFDIWGQGTWTVS 120  
|  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQCGQWLLPDAFDIWGQGTWTVS 120

QY 121 S 121  
|  
Db 121 S 121

## RESULT 7

US-10-330-613-1  
; Sequence 1, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-1

Query Match 91.7%; Score 597; DB 14; Length 121;  
Best Local Similarity 90.9%; Pred. No. 1.9e-46;  
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTYYWSMIROPPGKLEWIGIYYTGTNYN 60  
|  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTYYWSMIROPPGKLEWIGIYYTGTNYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDPCQWLVPDAFDIWGQGTWTVS 120  
|  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQCGQWLLPDAFDIWGQGTWTVS 120  
121 S 121  
|  
Db 121 S 121

## RESULT 8

US-10-330-613-17  
; Sequence 17, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-17

Query Match 91.7%; Score 597; DB 14; Length 121;  
Best Local Similarity 90.9%; Pred. No. 1.9e-46;  
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTYYWSMIROPPGKLEWIGIYYTGTNYN 60  
|  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTYYWSMIROPPGKLEWIGIYYTGTNYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDPCQWLVPDAFDIWGQGTWTVS 120  
|  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQCGQWLLPDAFDIWGQGTWTVS 120

QY 121 S 121  
|  
Db 121 S 121

## RESULT 9

US-10-330-530-1  
; Sequence 1, Application US/10330530  
; Publication No. US20030152514A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
; FILE REFERENCE: ABGENIX.031A  
; CURRENT APPLICATION NUMBER: US/10/330,530  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: US 60/346414  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-530-1

Query Match 91.7%; Score 597; DB 14; Length 121;  
Best Local Similarity 90.9%; Pred. No. 1.9e-46;  
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTYYWSMIROPPGKLEWIGIYYTGTNYN 60  
|  
|

Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYYTWTSNYN 60  
QY 61 PSLKSRVTISVDTSKNQFSLKLSNVTAAADVYVCARDPGQWMLPDAFDIWGGQTMVSVS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADVYVCARDQGWMLLPDAFDIWGGQTMVTVS 120  
QY 121 S 121  
Db 121 S 121

## RESULT 10

US-10-330-530-17  
; Sequence 17, Application US/10330530  
; Publication No. US20030152514A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
; FILE REFERENCE: ABGENIX.031A  
; CURRENT APPLICATION NUMBER: US/10/330,530  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: US 60/346414  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-530-17

Query Match 91.7%; Score 597; DB 14; Length 121;  
Best Local Similarity 90.9%; Pred. No. 1.9e-46;  
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYYTWTSNYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYYTWTSNYN 60  
QY 61 PSLKSRVTISVDTSKNQFSLKLSNVTAAADVYVCARDPGQWMLPDAFDIWGGQTMVSVS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADVYVCARDQGWMLLPDAFDIWGGQTMVTVS 120  
QY 121 S 121  
Db 121 S 121

## RESULT 11

US-10-660-357-1  
; Sequence 1, Application US/10660357  
; Publication No. US20040115205A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Eli, Menashe  
; APPLICANT: Green, Larry L.  
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
; FILE REFERENCE: ABGENIX.030C1  
; CURRENT APPLICATION NUMBER: US/10/660,357  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 10/330,580  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-1

Query Match 91.7%; Score 597; DB 16; Length 121;  
Best Local Similarity 90.9%; Pred. No. 1.9e-46;  
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYYTWTSNYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYYTWTSNYN 60  
QY 61 PSLKSRVTISVDTSKNQFSLKLSNVTAAADVYVCARDPGQWMLPDAFDIWGGQTMVSVS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADVYVCARDQGWMLLPDAFDIWGGQTMVTVS 120  
QY 121 S 121  
Db 121 S 121

## RESULT 12

US-10-660-357-17  
; Sequence 17, Application US/10660357  
; Publication No. US20040115205A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Eli, Menashe  
; APPLICANT: Green, Larry L.  
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
; FILE REFERENCE: ABGENIX.030C1  
; CURRENT APPLICATION NUMBER: US/10/660,357  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 10/330,580  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-17

Query Match 91.7%; Score 597; DB 16; Length 121;

Best Local Similarity 90.9%; Pred. No. 1.9e-46;  
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYYTWTSNYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYYTWTSNYN 60  
QY 61 PSLKSRVTISVDTSKNQFSLKLSNVTAAADVYVCARDPGQWMLPDAFDIWGGQTMVSVS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADVYVCARDQGWMLLPDAFDIWGGQTMVTVS 120  
QY 121 S 121  
Db 121 S 121

## RESULT 13

US-10-309-762-11  
; Sequence 11, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
; FILE REFERENCE: ABGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309,762  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/337275  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 125



(1234) 5678 9012 3456



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OM protein - protein search, using sw model

Run on: November 9, 2005, 12:25:58 ; Search time 13.0401 Seconds  
(without alignments)  
892.802 Million cell updates/sec

Title: US-10-660-357A-37

Perfect score: 651

Sequence: 1 QVQLQESGPGLVKPSSETLSL.....WLVPDAFDIWGQGTWVSVS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	537	82.5	140	2 137782	Ig variable region
2	536	82.3	155	2 131512	Ig heavy chain - h
3	531	81.6	155	2 131511	Ig heavy chain - h
4	527	81.0	130	2 131690	Ig heavy chain v r
5	524	80.5	147	2 131519	Ig heavy chain v r
6	522.5	80.3	139	2 131586	Ig heavy chain v r
7	517	79.4	135	2 131586	Ig heavy chain pre
8	515.5	79.2	118	2 131586	Ig heavy chain v r
9	512.5	78.7	130	2 131586	Ig heavy chain v r
10	507.5	78.0	137	2 131676	Ig heavy chain v r
11	498	76.5	121	2 131676	Ig heavy chain v r
12	497	76.3	105	2 131676	Ig heavy chain v r
13	492.5	75.7	140	2 131676	Ig heavy chain v r
14	489	75.1	97	2 131676	Ig heavy chain pre
15	488	75.0	116	2 131676	Ig heavy chain pre
16	488	75.0	123	2 131676	Ig heavy chain v r
17	486	74.7	97	2 131676	Ig heavy chain v r
18	485	74.5	146	2 131676	Ig heavy chain v r
19	484	74.3	99	2 131676	Ig heavy chain v r
20	484	74.3	99	2 131676	Ig heavy chain v r
21	483.5	74.3	110	2 131676	Ig heavy chain v r
22	483	74.2	140	2 131676	Ig heavy chain v r
23	483	74.2	140	2 131676	Ig heavy chain v r
24	477.5	73.3	129	2 131676	Ig heavy chain v r
25	477	73.0	118	2 131676	Ig heavy chain pre
26	475	73.0	99	2 131676	Ig heavy chain pre
27	475	73.0	146	2 131676	Ig heavy chain v r
28	471	72.4	99	2 131676	Ig heavy chain v r
29	470.5	72.3	126	2 131676	Ig heavy chain V4.

30	469.5	72.1	118	2	S24443	Ig heavy chain v r
31	469	72.0	135	2	S31604	Ig heavy chain v r
32	469	72.0	140	2	A24770	hypothetical hybri
33	468.5	72.0	145	2	S78055	Ig heavy chain pre
34	468	71.9	97	2	PH0876	Ig heavy chain v r
35	468	71.9	143	2	B49028	Ig heavy chain v r
36	466	71.6	220	2	A49444	Ig gamma-1 heavy c
37	465	71.4	99	2	S12412	Ig heavy chain v r
38	462	71.0	99	2	S26800	Ig heavy chain v r
39	462	71.0	124	2	S31684	Ig heavy chain v r
40	462	71.0	129	1	D2H0WA	Ig heavy chain v r
41	461.5	70.9	137	2	S31585	Ig heavy chain v r
42	461	70.8	97	2	S26804	Ig heavy chain v r
43	461	70.8	116	2	S18557	Ig heavy chain v r
44	460.5	70.7	98	2	S12421	Ig heavy chain v r
45	460	70.7	116	2	S37456	Ig mu chain - huma

ALIGNMENTS

RESULT 1

I37782

Ig variable region (VDJ) (clone T23-9) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999

C;Accession: I37782; S25476

R;Demaision, C.; Chastagner, P.; Theze, J.; Zouali, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A;Title: Somatic diversification in the heavy chain variable region genes expressed by

A;Reference number: A36876; MUID:94119917; PMID:8290556

A;Accession: I37782

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140 <RES>

A;Cross-references: EMBL:X67906; NID:G33582; PIDN:CAA48104.1; PID:G33583

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;46-128/Domain: immunoglobulin homology <IMW>

Query Match 82.5%; Score 537; DB 2; Length 140;  
Best Local Similarity 84.3%; Pred. No. 1.le-40;  
Matches 102; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Qy	1	QVQLQESGPGLVKPSSETLSLCTVSGSISTYYWSWIRQPPGKLEWIGYIYGTNTVYN	60
Db	20	QVQLQESGPGLVKPSSETLSLCTVSGSISTYYWSWIRQPPGKLEWIGYIYGTNTVYN	79
Qy	61	PSLKSRTVTSVDTSKNQFSLKLSVTAADTAATVYTCARDPQGWLPDADFQGTWVSVS	120
Db	80	PSLKSRTVTSVDTSKNQFSLKLSVTAADTAATVYTCARDPQGWLPDADFQGTWVSVS	139
Qy	121	S 121	
Db	140	S 140	

RESULT 2

S31512

Ig heavy chain - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999

C;Accession: S31512

R;Chastagner, P.; Demaision, C.; Theze, J.; Zouali, M.

submitted to the EMBL Data Library, December 1992

A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA au

A;Reference number: S31509

A;Accession: S31512

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-155 <CHA>

A;Cross-references: EMBL:X69860; NID:G33082; PIDN:CAA49494.1; PID:G33083

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 536; DB 2; Length 155;  
Best Local Similarity 82.1%; Pred. No. 1.5e-40;  
Matches 101; Conservative 8; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPESETLSLTCTVSGSISTYYWMIROPPGKLEWIGYIYTGNTYYN 60  
DB 33 QVQLQESGPGLVKPESETLSLTCTVSGSISTYYWMIROPPGKLEWIGYIYTGNTYYN 92

QY 61 PSLKSRVTVSVDTSKNQFSLKLSVTAADTAVYYCARDPG--QWLVPDAFDIWGQGTWVS 118  
DB 93 PPIKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGGSISSWYIYGGNDVWGQGTITV 152

QY 119 VSS 121  
DB 153 VSS 155

#### RESULT 3

S31511  
Ig heavy chain - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S31511  
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto-  
A;Reference number: S31509  
A;Accession: S31511  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-155 <CHA>  
A;Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 81.6%; Score 531; DB 2; Length 155;  
Best Local Similarity 82.1%; Pred. No. 4.2e-40;  
Matches 101; Conservative 7; Mismatches 13; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPESETLSLTCTVSGSISTYYWMIROPPGKLEWIGYIYTGNTYYN 60  
DB 33 QVQLQESGPGLVKPESETLSLTCTVSGSISTYYWMIROPPGKLEWIGYIYTGNTYYN 92

QY 61 PSLKSRVTVSVDTSKNQFSLKLSVTAADTAVYYCARDPG--QWLVPDAFDIWGQGTWVS 118  
DB 93 PPIKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGGSISSWYIYGGNDVWGQGTITV 152

QY 119 VSS 121  
DB 153 VSS 155

#### RESULT 4

S31690  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31690  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31690  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-130 <CUI>  
A;Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;20-102/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 527; DB 2; Length 130;  
Best Local Similarity 81.1%; Pred. No. 7.8e-40;  
Matches 103; Conservative 8; Mismatches 8; Indels 8; Gaps 2;

QY 1 QVQLQESGPGLVKPESETLSLTCTVSGSISTYYWMIROPPGKLEWIGYIYTGNTYYN 60  
DB 6 QVQLQESGPGLVKPESETLSLTCTVSGSISTYYWMIROPPGKLEWIGYIYTGNTYYN 65

QY 61 PSLKSRVTVSVDTSKNQFSLKLSVTAADTAVYYCARDP-----QWLVPDAFDIWGQ 114  
DB 66 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGSSVLLMFGELLY--YFDYWGQ 123

QY 115 TMVSVSS 121  
DB 124 TLVTVSS 130

#### RESULT 5

S31519  
Ig heavy chain V region precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31519  
R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.  
Nucleic Acids Res. 19, 673, 1991  
A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked  
A;Reference number: S31519; MUID:91187691; PMID:2011536  
A;Accession: S31519  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-147 <MOR>  
A;Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;41-125/Domain: immunoglobulin homology <IMM>

Query Match 80.5%; Score 524; DB 2; Length 147;  
Best Local Similarity 82.9%; Pred. No. 1.6e-39;  
Matches 102; Conservative 9; Mismatches 8; Indels 4; Gaps 3;

QY 1 QVQLQESGPGLVKPESETLSLTCTVSGSI--STYYWMIROPPGKLEWIGYIYTGNTY 58  
DB 27 QQLQLQESGPGLVKPESETLSLTCTVSGSISSSSYWMIROPPGKLEWIGSIYSGSTY 86

QY 59 YNPGLKSRVTVSVDTSKNQFSLKLSVTAADTAVYYCARDPGQWLVPDAFDIWGQGTWVS 118  
DB 87 YNPGLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR-PLLWP-GEFLDYWGQGTTLVT 144

QY 119 VSS 121  
DB 145 VSS 147

#### RESULT 6

S31586  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31586  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31586  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-139 <CUI>  
A;Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 522.5; DB 2; Length 139;  
Best Local Similarity 85.1%; Pred. No. 2.1e-39;  
Matches 103; Conservative 7; Mismatches 10; Indels 1; Gaps 1;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISITYYMSWIRQPPGKGLEWIGIYYTGTNTY 60  
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGSISITYYMSWIRQPPGKLEWIGIRIYTSNSTYN 79  
  
QY 61 PSLSKRVTVSVSDTSKNQFSLKNSVTAADTAVYYCARDPGQWLVPDADFIDWQGTMTVS 120  
Db 80 PSLSKRVTVSVSDTSKNQFSLKNSVTAADTAVYYCARDPGQWLVPDADFIDWQGTMTVS 138  
  
QY 121 S 121  
Db 139 S 139  
  
RESULT 7  
S78051  
Ig heavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C;Accession: S78051; S23716  
R;Harindranath, N.  
submitted to the EMBL Data Library, August 1990  
A;Reference number: S78051  
A;Accession: S78051  
A;Molecule type: mRNA  
A;Residues: 1-135 <HAR>  
A;Cross-references: EMBL:X54437; NID:G37814; PIDN:CAA38306.1; PID:G930117  
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.B.; Wilder, R.L.; Notkins  
Int. Immunol. 3, 865-875, 1991  
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h  
patient.  
A;Reference number: S23716; MUID:92031262; PMID:1718404  
A;Accession: S23716  
A;Molecule type: mRNA  
A;Residues: 13-111 <HAW>  
A;Cross-references: EMBL:X54437  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;1-13/Domain: signal sequence (fragment) #status predicted <SIG>  
F;14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>  
F;27-111/Domain: immunoglobulin homology <IMM>  
  
Query Match 79.4%; Score 517; DB 2; Length 135;  
Best Local Similarity 80.6%; Pred. No. 6.2e-39;  
Matches 100; Conservative 11; Mismatches 9; Indels 4; Gaps 3;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISITYYMSWIRQPPGKLEWIGIYYTGTNTY 58  
Db 13 QVQLQESGPGLVKPSSETLSLTCTVSGSISIRGSHYWGIRQPPGKLEWIGIYYTGTNTY 72  
  
QY 59 YNPSSLKRVTVSVSDTSKNQFSLKNSVTAADTAVYYCARDPGQWLVPDADFIDWQGTMTV 117  
Db 73 YNPSSLKRVTVSVSDTSKNQFSLKNSVTAADTAVYYCARDPGQWLVPDADFIDWQGTMTV 131  
  
QY 118 SVSS 121  
Db 132 TVSS 135  
  
RESULT 8  
S20780  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C;Accession: S20780  
R;Wortari, F.; Wang, J.; Schroeder, H.W.  
submitted to the EMBL Data Library, April 1992  
A;Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.  
A;Reference number: S20764  
A;Accession: S20780

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-118 <WOR>  
A;Cross-references: EMBL:Z11958; NID:G33893; PIDN:CAA78015.1; PID:G33894  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;15-97/Domain: immunoglobulin homology <IMM>  
  
Query Match 79.2%; Score 515.5; DB 2; Length 118;  
Best Local Similarity 82.6%; Pred. No. 7.3e-39;  
Matches 100; Conservative 8; Mismatches 10; Indels 3; Gaps 1;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISITYYMSWIRQPPGKLEWIGIYYTGTNTY 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISITYYMSWIRQPPGKLEWIAFIRYTGSTYN 60  
  
QY 61 PSLSKRVTVSVSDTSKNQFSLKNSVTAADTAVYYCARDPGQWLVPDADFIDWQGTMTVS 120  
Db 61 PSLSKRVTVSVSDTSKNQFSLKNSVTAADTAVYYCARDPGQWLVPDADFIDWQGTMTVS 117  
  
QY 121 S 121  
Db 118 S 118  
  
RESULT 9  
S30534  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Aug-1996  
C;Accession: S30534  
R;Marette, X.  
submitted to the EMBL Data Library, October 1992  
A;Reference number: S30520  
A;Accession: S30534  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-130 <MAR>  
A;Cross-references: EMBL:Z18320  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>  
  
Query Match 78.7%; Score 512.5; DB 2; Length 130;  
Best Local Similarity 80.0%; Pred. No. 1.5e-38;  
Matches 104; Conservative 7; Mismatches 10; Indels 9; Gaps 3;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISITYYMSWIRQPPGKLEWIGIYYTGTNTY 58  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISITYYMSWIRQPPGKLEWIGIRIYTSNSTYN 60  
  
QY 59 YNPSSLKRVTVSVSDTSKNQFSLKNSVTAADTAVYYCARDPGQWLVPDADFIDWQGTMTV 111  
Db 61 YNPSSLKRVTVSVSDTSKNQFSLKNSVTAADTAVYYCARDPGQWLVPDADFIDWQGTMTV 120  
  
QY 112 GQGTMTVS 121  
Db 121 GQGTMTVS 130  
  
RESULT 10  
S31676  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31676  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31676  
A;Status: preliminary  
A;Molecule type: mRNA

A;Residues: 1-137 <GUI>  
A;Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>  
  
Query Match 78.0%; Score 507.5; DB 2; Length 137;  
Best Local Similarity 82.0%; Pred. No. 4.4e-38;  
Matches 100; Conservative 8; Mismatches 9; Indels 5; Gaps 2;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIRQPPGKGLWIGIYYTGTNTY 60  
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIRQPPGKGLWIGIYYTGTNTY 79  
  
QY 61 PSLKSRVTVSVDTSKNQFSLKNSVTAADTAVYYCARD-PGQWLVPDAPFDINGQGTMTVS 119  
Db 80 PSLKSRVTMTSVDTSKNQFSLKLSVTAADTAVYYCARDAPLMY---GMDVMVQGGTTVT 135  
  
QY 120 SS 121  
Db 136 SS 137  
  
RESULT 11  
S44113  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C;Accession: S44113  
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable  
A;Reference number: S44105  
A;Accession: S44113  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-121 <HAW>  
A;Cross-references: EMBL:Z31389; NID:g472967; PIDN:CAA83264.1; PID:g940524  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>  
  
Query Match 76.5%; Score 498; DB 2; Length 121;  
Best Local Similarity 78.9%; Pred. No. 2.6e-37;  
Matches 97; Conservative 9; Mismatches 13; Indels 4; Gaps 2;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGG--SISYYWWSWIRQPPGKGLWIGIYYTGTNTY 58  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGYISSSSYWGWTRQPPGKGLWIGIYYSGSY 60  
  
QY 59 YNPSLKSRVTVSVDTSKNQFSLKNSVTAADTAVYYCARDPPGQWLVPDAPFDINGQGTMTVS 118  
Db 61 YNPSLKSRVTLSVDTSKNQFSLKLSVTAADTGVYYCSRLSGGY--SDFDYMSQGTLT 118  
  
QY 119 VSS 121  
Db 119 VSS 121  
  
RESULT 12  
S44125  
Ig lambda chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C;Accession: S44125  
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable  
A;Reference number: S44105  
A;Accession: S44125  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-105 <HAW>

A;Cross-references: EMBL:Z31383; NID:g472978; PIDN:CAA83258.1; PID:g940535  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-97/Domain: immunoglobulin homology <IMM>  
  
Query Match 76.3%; Score 497; DB 2; Length 105;  
Best Local Similarity 92.9%; Pred. No. 2.8e-37;  
Matches 92; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIRQPPGKGLWIGIYYTGTNTY 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIRQPPGKGLWIGIYYTGTNTY 60  
  
QY 61 PSLKSRVTVSVDTSKNQFSLKNSVTAADTAVYYCARDP 99  
Db 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARNP 99  
  
RESULT 13  
S78052  
Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C;Accession: S78052; S23717  
R;Harindranath, N.  
submitted to the EMBL Data Library, August 1990  
A;Reference number: S78051  
A;Accession: S78052  
A;Molecule type: mRNA  
A;Residues: 1-140 <HAR>  
A;Cross-references: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118  
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Norkin  
Int. Immunol. 3, 865-875, 1991  
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and  
patient.  
A;Reference number: S23716; MUID:92031262; PMID:1718404  
A;Accession: S23717  
A;Molecule type: mRNA  
A;Residues: 15-111 <HAW>  
A;Cross-references: EMBL:X54441  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>  
F;15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>  
F;29-111/Domain: immunoglobulin homology <IMM>  
  
Query Match 75.7%; Score 492.5; DB 2; Length 140;  
Best Local Similarity 75.4%; Pred. No. 9.5e-37;  
Matches 95; Conservative 11; Mismatches 15; Indels 5; Gaps 1;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIRQPPGKGLWIGIYYTGTNTY 60  
Db 15 QVQLQGWAGLLKPSSETLSLTCAVYGGSPSGYYWWSWIRQPPGKGLWIGIYHSGSTNY 74  
  
QY 61 PSLKSRVTVSVDTSKNQFSLKNSVTAADTAVYYCARDPG----OWLVPDAPFDINGQGT 115  
Db 75 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGGSVLRFLEWLLYPAPFDYWGQGT 134  
  
QY 116 MVSVSS 121  
Db 135 LVTVSS 140  
  
RESULT 14  
S26906  
Ig heavy chain V region (DP-71 / VH 4.11 / 4.15) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S26906; S09421; S12415  
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of  
A;Reference number: S26885; MUID:93021117; PMID:1404388

Search completed: November 9, 2005, 13:08:05  
Job time : 13.0401 secs

A;Accession: S26906  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-97 <TOM>  
A;Cross-references: EMBL:Z12371; NID:g32962; PIDN:CAA78241.1; PID:g32963  
A;Note: designated DP-71  
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.  
EMBO J. 8, 3741-3748, 1989  
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.  
A;Reference number: S09421; MUID:90059975; PMID:2511001  
A;Accession: S09421  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-97 <SAN>  
A;Cross-references: EMBL:X56355  
A;Note: designated 4.11  
A;Accession: S12415  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-97 <SA2>  
A;Cross-references: EMBL:X56359  
A;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 75.1%; Score 489; DB 2; Length 97;  
Best Local Similarity 93.8%; Pred. No. 1.3e-36;  
Matches 91; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYTGNTYYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYSGSTNYN 60

Qy 61 PSLKSRVTVSVDTSKNQFSLKLSNVTAAADTAVYYCAR 97  
Db 61 PSLKSRVTISVDTSKNQFSLKLSNVTAAADTAVYYCAR 97

RESULT 15  
B26340  
IG heavy chain precursor V-II region (71-4) - human  
C;Species: Homo sapiens (man)  
C;Date: 05-Jun-1988 #sequence\_revision 30-Jun-1991 #text\_change 23-Jul-1999  
C;Accession: B26340  
R;Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo, T.  
J. Mol. Biol. 190, 529-541, 1986  
A;Title: Organization and evolution of variable region genes of the human immunoglobulin  
A;Reference number: A26340; MUID:87061007; PMID:3097326  
A;Accession: B26340  
A;Molecule type: DNA  
A;Residues: 1-116 <KOD>  
A;Cross-references: GB:X05711; NID:g33602; PIDN:CAA29183.1; PID:g296660  
A;Note: the authors translated the codon GAG for residue 25 as Gln  
C;Genetics:  
A;Introns: 16/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-116/Product: Ig heavy chain V region 71-4 #status predicted <MAT>  
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 488; DB 2; Length 116;  
Best Local Similarity 92.8%; Pred. No. 1.9e-36;  
Matches 90; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYTGNTYYN 60  
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSVSYWSWIRQPPGKGLEWIGYIYSGSTNYN 79

Qy 61 PSLKSRVTVSVDTSKNQFSLKLSNVTAAADTAVYYCAR 97  
Db 80 PSLKSRVTISVDTSKNQFSLKLSNVTAAADTAVYYCAR 116

(CLINT) 10/10/10

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:46:52 ; Search time 62.4712 Seconds  
(without alignments)  
991.843 Million cell updates/sec

Title: US-10-660-357A-37

Perfect score: 651

Sequence: 1 QVQLQESGPGLVKPKSETLSL.....WLVPDAFDINGQGMVSVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	538	82.6	476	2	Q6GMX1
2	513	78.8	119	2	Q9UL73
3	505.5	77.6	478	2	Q7Z379
4	504.5	77.5	465	2	Q6GMX6
5	503.5	77.3	620	2	Q96EY0
6	502.5	77.2	477	2	Q6GMX7
7	495	76.0	139	2	Q86SX2
8	487	74.8	492	2	Q7Z374
9	485.5	74.6	150	2	Q95973
10	474.5	72.9	496	2	Q96KX8
11	465.5	71.5	576	2	Q6P418
12	462	71.0	129	1	HV2F HUMAN
13	452	69.4	478	2	Q6NVH3
14	449.5	69.0	146	1	HV21 HUMAN
15	448	68.8	595	2	Q8WUX4
16	448	68.8	597	2	Q6GMX5
17	448	68.8	597	2	Q9BU10
18	448	68.8	625	2	Q96AA6
19	444	68.2	597	2	Q9BQB8
20	441.5	67.8	130	2	Q81ZD7
21	431	66.2	117	1	HV23 HUMAN
22	420.5	64.6	116	2	Q7Z3Y6
23	418.5	64.3	473	2	Q8TC63
24	406	62.4	479	2	Q99W22
25	402	61.8	476	2	Q6MZX7
26	401.5	61.7	122	2	Q9UL75
27	397.5	61.1	136	2	Q6LBQ5
28	396	60.8	137	1	HV46 MOUSE
29	392	60.2	262	2	Q65Z11
30	391	60.1	113	1	HV47 MOUSE
31	370.5	56.9	116	1	HV61_MOUSE

32	369.5	56.8	116	1	HV60 MOUSE
33	369.5	56.8	482	2	Q91X92
34	365	56.2	117	1	HV62 MOUSE
35	360.5	55.4	121	2	Q99NG4
36	353	54.2	144	1	HV43_MOUSE
37	350.5	53.8	135	1	HV02_XENLA
38	343.5	52.8	118	2	Q811U5
39	343.5	52.8	613	2	Q8WUK1
40	342	52.5	470	2	Q6PJA4
41	339	52.1	118	2	Q9UL74
42	339	52.1	466	2	Q6IN78
43	333	51.2	240	2	Q65ZC9
44	331.5	50.9	118	2	Q9UL91
45	331	50.8	121	2	Q9UL96

## ALIGNMENTS

RESULT 1  
Q6GMX1  
ID Q6GMX1 PRELIMINARY; PRT; 476 AA.  
AC Q6GMX1;  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DE Hypothetical protein.  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
ON NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Richards S., Worley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
DR EMBL; BC073773; AAH73773.1; -;  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF07654; C1-set; 3.  
DR Pfam; PF00047; IG; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.

Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

KW Hypothetical protein.  
SQ SEQUENCE 476 AA; 52286 MW; 622AABASC62DDE9D CRC64;  
Query Match 82.6%; Score 538; DB 2; Length 476;  
Best Local Similarity 81.2%; Pred. No. 7.5e-45;  
Matches 104; Conservative 10; Mismatches 6; Indels 8; Gaps 3;  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSI--YYWSWIRQPPGKLEWIGYIYTGNTY 58  
Db 20 QVQLQESGPGLVKPSQTSLSLTCTVSGGSISSGGYYWSWIRQPPGKLEWIGYIYSGSTY 79  
Qy 59 YNPSLSKRVTVSVDTSKNQFSKLNSVTAADTAATVYFCARDPGOW-----LVPADFIDWQ 113  
Db 80 YNPSLSKRVTVSVDTSKNQFSKLNSVTAADTAATVYFCAR-AGVWGSFRSWAIDGFNIWQ 138  
Qy 114 GTMVSVSS 121  
Db 139 GTMVTVSS 146  
RESULT 2  
Q9UL73 PRELIMINARY; PRT; 119 AA.  
AC Q9UL73;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;  
RX Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M., Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035041; AAD56277.1; -.  
DR PIR; PH0876; PH0876.  
DR PIR; S12416; S12416.  
DR HSP; P01820; IG7J.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
FT NON TER 1  
FT NON TER 119  
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;  
Query Match 78.8%; Score 513; DB 2; Length 119;  
Best Local Similarity 81.8%; Pred. No. 5e-43;  
Matches 99; Conservative 8; Mismatches 12; Indels 2; Gaps 2;  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIYYWSWIRQPPGKLEWIGYIYTGNTY 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIYWSWIRQPPGKLEWIGYIYSGSTY 60  
Qy 61 PSLKSRVTVSVDTSKNQFSKLNSVTAADTAATVYFCARDPGOWLVPADFIDWQGTWVS 120  
Db 61 PSLKSRVTVSVDTSKNQFSKLNSVTAADTAATVYFCAR-LSNW-GPYVFDWQGTTLVTS 118  
Qy 121 S 121  
Db 119 S 119  
RESULT 3  
Q7Z379 PRELIMINARY; PRT; 478 AA.  
ID Q7Z379

AC Q7Z379;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein DKFZp686K04218 (Fragment).  
GN Name=DKFZp686K04218;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RA Bloecker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX538066; CAD97996.1; -.  
DR HSP; P01820; IG7J.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
FT NON TER 1  
FT NON TER 1  
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;  
Query Match 77.6%; Score 505.5; DB 2; Length 478;  
Best Local Similarity 76.4%; Pred. No. 1.2e-41;  
Matches 94; Conservative 18; Mismatches 6; Indels 5; Gaps 2;  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSI--YYWSWIRQPPGKLEWIGYIYTGNTY 58  
Db 19 QVQLQESGPGLVKPSQTSLSLTCTVSGGSISSGGYFWSWIRQPPGKLEWIGYIYSGSTY 78  
Qy 59 YNPSLSKRVTVSVDTSKNQFSKLNSVTAADTAATVYFCARDPGOWLVPADFIDWQGTWVS 118  
Db 79 YNPSLSKRVTVSVDTSKNQFSKLNSVTAADTAATVYFCARGVG--LGTAFDINGQGTVT 135  
Qy 119 VSS 121  
Db 136 VSS 138  
RESULT 4  
Q6GMX6 PRELIMINARY; PRT; 465 AA.  
ID Q6GMX6  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,



RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,  
RA Whiting M., Madan A., Young A.C., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073766; AAH73766.1; -  
DR InterPro; IPR003599; IG-like.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR Pfam; PF00047; ig; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00406; IGV; 1.  
DR SMART; SM00407; IGcl; 3.  
DR PROSITE; PS0835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein\_  
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FD8B1386E CRC64;

Query Match 77.5%; Score 504.5; DB 2; Length 465;  
Best Local Similarity 82.6%; Pred. No. 1.5e-41;  
Matches 100; Conservative 8; Mismatches 8; Indels 5; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIITYYWSWIRQPPGKLEWIGYIYTGNTYYN 60  
DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSIITYYWSWIRQPPGKLEWIGYIYTGNTYYN 79  
QY 61 PSLSKRVTVSDTSKNQFSLKLSVTAADTAVYYCARDPGQWLVPDADFHWGQGTWVS 120  
DB 80 PSLSKRVTVSDTSKNQFSLKLSVTAADTAVYYCARDPGQWLVPDADFHWGQGTWVS 134  
QY 121 S 121  
DB 135 S 135

RESULT 5  
Q96EYO PRELIMINARY; PRT; 620 AA.  
ID Q96EYO PRELIMINARY; PRT; 620 AA.  
AC Q96EYO;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE IGHM protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011857; AAH11857.2; -  
DR PIR; S15590; S15590.  
DR HSP; P01820; IG7J.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;

Query Match 77.3%; Score 503.5; DB 2; Length 620;  
Best Local Similarity 81.1%; Pred. No. 2.6e-41;  
Matches 99; Conservative 8; Mismatches 12; Indels 3; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIITYYWSWIRQPPGKLEWIGYIYTGNTYYN 60  
DB 27 QVQLQESGPGLVKPSSETLSLTCTVSGGSIITYYWSWIRQPPGKLEWIGYIYTGNTYYN 86  
QY 61 PSLSKRVTVSDTSKNQFSLKLSVTAADTAVYYCARDPGQWLVPDADFHWGQGTWVS 119  
DB 87 PSLSKRVTVSDTSKNQFSLKLSVTAADTAVYYCARDPGQWLVPDADFHWGQGTWVS 144  
QY 120 SS 121  
DB 145 SS 146

RESULT 6  
Q6GMX7 PRELIMINARY; PRT; 477 AA.  
ID Q6GMX7 PRELIMINARY; PRT; 477 AA.  
AC Q6GMX7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smillius D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL EMBL: BC073765; AAH73765.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF07654; Cl-set; 2.
DR Pfam: PF00047; ig; 3.
DR SMART: SM00409; IG; 4.
DR SMART: SM00407; IGC1; 3.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS00835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CF85 CRC64;

Query Match 77.2%; Score 502.5; DB 2; Length 477;
Best Local Similarity 81.0%; Pred. No. 2.5e-41;
Matches 98; Conservative 9; Mismatches 11; Indels 3; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISTYVSWIRQPPGKLEWIGIYYTGTYYN 60
DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSTYVSWIRQPPGKLEWIGIYSHGTTYN 79
QY 61 PSLSKRVTVSVDTSKNQFSLKLSVTAADTAVYVCARDPQQLVPDAFDIWGGTVMVSVS 120
DB 80 PSLSKRVTVSVDTSKNQFSLKLSVTAADTAVYICAHG-SSW--DFAFDIWGGTTLTVTS 136
QY 121 S 121
DB 137 S 137

RESULT 7
Q86SX2 PRELIMINARY; PRT; 139 AA.
AC Q86SX2; 2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line) of
DE Homo sapiens (human) (Fragment).
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
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DR EMBL: BX248300; CAD62627.1; -.
DR HSSP: P01820; 1G7J.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 76.0%; Score 495; DB 2; Length 139;
Best Local Similarity 93.9%; Pred. No. 3.6e-41;
Matches 92; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISTYVSWIRQPPGKLEWIGIYYTGTYYN 60
DB 33 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSTYVSWIRQPPGKLEWIGIYVSGSTYN 92
QY 61 PSLSKRVTVSVDTSKNQFSLKLSVTAADTAVYVCARD 98
DB 93 PSLSKRVTVSVDTSKNQFSLKLSVTAADTAVYVCARD 130

RESULT 8
Q7Z374 PRELIMINARY; PRT; 492 AA.
ID Q7Z374
AC Q7Z374; 2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686C02218 (Fragment).
GN Name=DKFZp686C02218;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX538077; CAD98001.1; -.
DR HSSP: P01820; 1G7J.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF07654; Cl-set; 2.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS00835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 74.8%; Score 487; DB 2; Length 492;
Best Local Similarity 75.4%; Pred. No. 8.8e-40;
Matches 95; Conservative 8; Mismatches 13; Indels 10; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIS--TYVSWIRQPPGKLEWIGIYYTGTNTY 58
DB 32 QVQLQESGPGLVKPSSETLSLTCTVSGGSISNRNYWGNIQPPGKLEWIGISYYTNTY 91
QY 59 YNPFLSKRVTVSVDTSKNQFSLKLSVTAADTAVYVCARD---DPGQWLVPDAFDIWGGT 115
DB 92 YSPFLSKRLTIFVDTSKNHFSLRLTSVTAADTAVYICVRHVEGPGYGM-----FDPWGGT 146
QY 116 MVSVS 121
DB 147 LVTVS 152

RESULT 9
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O95973
ID O95973 PRELIMINARY; PRT; 150 AA.
AC O95973;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE V44 heavy chain variable region precursor (fragment).
GN Name=IGM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suh C.-H., Song C.-H., Lee S.-K.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RE EMBL; AF103795; AAC79084.1; -
DR PIR; S31673; S31673.
DR HSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig v.
DR SMART; SM00406; IGV; 1_
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 >150 V44 heavy chain variable region.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 74.6%; Score 485.5; DB 2; Length 150;
Best Local Similarity 77.2%; Pred. No. 3.4e-40;
Matches 95; Conservative 11; Mismatches 10; Indels 7; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSI--YYNWSWIRPPKGLWIGIYYTQNTY 58
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSYWGWIRPPKGLWIGIYYTQNTY 79
QY 59 YNPSLKSRTVSVDTSKNQPSLKLNSVTAADTAVYVCARDPGQWLVPDAFDINGQTMVS 118
Db 80 YNPSLKSRTVSVDTSKNQPSLKLNSVTAADTAVYVCARDPGQWLVPDAFDINGQTMVS 134
QY 119 VSS 121
Db 135 VSS 137

RESULT 10
Q96KX8 PRELIMINARY; PRT; 496 AA.
AC Q96KX8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC27165 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
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Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RE EMBL; BC016369; AAH16369.1; -
DR HSP; P01876; IGW0.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 72.9%; Score 474.5; DB 2; Length 496;
Best Local Similarity 74.8%; Pred. No. 1.5e-38;
Matches 95; Conservative 9; Mismatches 14; Indels 9; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSI--STVYWSWIRPPKGLWIGIYYTQNTY 58
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSYWGWIRPPKGLWIGIYYTQNTY 79
QY 59 YNPSLKSRTVSVDTSKNQPSLKLNSVTAADTAVYVCARDPGQWLVPDAFDINGQ 114
Db 80 YNPSLKSRTVSVDTSKNQPSLKLNSVTAADTAVYVCARDPGQWLVPDAFDINGQ 136
QY 115 TMVSVSS 121
Db 137 TLTVTVSS 143

RESULT 11
Q6P4I8 PRELIMINARY; PRT; 576 AA.
ID Q6P4I8;
AC Q6P4I8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHD protein.
GN Names=IGHD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
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Qy 61 PSLKSRVTVSVDTSKNQFSIKLNSVTAADTAVVYCAR-----DPGQWLVPD---AFDIMG 112  
Db 87 PSLKSRVTIISVDTSKKQLSLKSSVNAADTAVVYCARVITRASPG-----TDGRYGMVWG 142  
Qy 113 QGTWVSVS 121  
Db 143 QGTTTVVS 151

Search completed: November 9, 2005, 13:05:52  
Job time : 63.4712 secs